

A-77N: Ed Hart.

Access DB# 119047

SEARCH REQUEST FORM

Scientific and Technical Information Center

CRFE

Requester's Full Name Celine Qian Examiner # 78710 Date: 4/8/04
Alt Unit 1636 Phone Number 306-2-0777 Serial Number 101090458
Mail Box and Bldg Room Location 2A89 Results Format Preferred (circle) PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need. MEJ

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention Novel ABCAS Transporter and uses thereof

Inventors (please provide full names): Chen, Hongyu et al.

Earliest Priority Filing Date: 3/1/2001

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO: 4, also do an oligo search of SEQ ID NO: 4

Also search a nucleic acid molecule encoding SEQ ID NO: 5.

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher _____	NA Sequence (#) <u>2</u> STN _____	
Searcher Phone # _____	AA Sequence (#) <u>1</u> <u>Reverse to NA</u>	
Searcher Location _____	Structure (#) _____	Questel/Other _____
Date Searcher Assigned <u>4/8/04</u>	Bibliographic _____	On Line _____
Date Completed <u>4/15/04</u>	Citation _____	Lexis Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>POH</u>
Client Prep Time _____	Patent Family _____	WWW/Internet _____
Other Time _____	Other _____	Other _____



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 119047

TO: Celine Qian
Location: rem/2a89/2c70
Art Unit: 1636
Thursday, April 15, 2004

Case Serial Number: 10/090458

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Qian,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



STIC SEARCH RESULT FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .nrpm and .nrpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

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OM nucleic - nucleic search, using sw model

Run on: April 12, 2004, 00:54:04 ; Search time 252 Seconds
(without alignments)
12056.969 Million cell updates/sec

Title: US-10-090-458-4
Perfect score: 5475
Sequence: 1 gcgtccgcgcctcgacag.....cataaagcaatgtgaagtt 5475

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	760.2	13.9	974	4	US-09-833-381-1085
2	319.2	5.8	485	4	US-09-621-976-409
3	319.2	5.8	1350	4	US-09-833-381-1082
4	159.2	2.9	5894	3	US-08-665-259-24
5	159.2	2.9	5894	3	US-08-762-500-24
6	159.2	2.9	6525	3	US-08-762-500-74
7	137.6	2.5	7860	4	US-09-526-193A-2
8	103.4	1.9	1064	4	US-08-858-207A-88
9	97.4	1.8	728	4	US-09-833-381-1087
10	92.2	1.7	5625	4	US-08-961-527-1
11	83.8	1.5	450	4	US-09-621-976-2582
12	83.4	1.5	463	4	US-09-621-976-2581
13	83.4	1.5	478	4	US-09-621-976-2583
14	80.8	1.5	465	4	US-09-833-381-1080
15	80.6	1.5	795	4	US-08-961-527-264
16	77.8	1.4	8536	4	US-08-956-171E-278
17	77.2	1.4	696	4	US-09-134-001C-987
18	75.8	1.4	1026	4	US-09-134-001C-1205
19	75	1.4	774	4	US-09-107-532A-412
20	74.6	1.4	1664976	4	US-08-916-421B-1
21	72.2	1.3	768	4	US-09-107-532A-1681
22	71	1.3	1664976	4	US-08-916-421B-1
23	69.8	1.3	990	4	US-09-107-532A-1190
24	69.8	1.3	28626	4	US-09-596-002-15
25	69.2	1.3	969	4	US-09-107-532A-1008
26	68	1.2	7963	4	US-08-956-171E-168
27	67.4	1.2	1599	4	US-09-543-681A-474

28	67	1.2	527	4	US-09-833-381-1083	Sequence 1083, Ap
c 29	66.8	1.2	19124	2	US-08-487-826B-13	Sequence 13, Appl
30	66.2	1.2	714	4	US-09-134-000C-1821	Sequence 1821, Ap
c 31	65.8	1.2	4848	4	US-08-961-527-185	Sequence 185, App
32	65.8	1.2	5717	4	US-08-961-527-102	Sequence 102, App
33	65	1.2	1770	4	US-09-328-352-3466	Sequence 3466, Ap
34	64.8	1.2	1785	4	US-09-543-681A-1356	Sequence 1356, Ap
35	64.6	1.2	3144	4	US-08-961-527-224	Sequence 224, App
c 36	64.6	1.2	6273	4	US-08-961-527-21	Sequence 21, Appl
c 37	64	1.2	16397	4	US-08-956-171E-205	Sequence 205, App
c 38	63.2	1.2	4093	4	US-08-956-171E-108	Sequence 108, App
c 39	63	1.2	353	4	US-09-833-381-384	Sequence 384, App
40	63	1.2	14672	4	US-08-961-527-111	Sequence 111, App
41	62.6	1.1	711	4	US-09-134-000C-1433	Sequence 1433, Ap
42	62.6	1.1	7218	1	US-08-232-463-14	Sequence 14, Appl
43	62.4	1.1	1554	4	US-09-134-000C-1110	Sequence 1110, Ap
44	62.4	1.1	580073	4	US-08-545-528D-1	Sequence 1, Appl1
45	62	1.1	2163	4	US-09-134-000C-2226	Sequence 2226, Ap

ALIGNMENTS

RESULT 1
US-09-833-381-1085
; Sequence 1085, Application US/098333381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1085
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1085

Query Match	13.9%	Score 760.2;	DB 4;	Length 974;
Best Local Similarity	99.0%;	Pred. No. 8.6e-168;		
Matches 765;	Conservative 0;	Mismatches 8;	Indels 0;	Gaps 0;
QY	83	CGGCTCGGGCCCTGAGGTTTATTTCAGAAAACATGTCCTACTGCAATTAGGGAGGTAGGAGT	142	
Db	202	CTGCCCCCGCCACAGGTTTATTTCAGAAAACATGTCCTACTGCAATTAGGGAGGTAGGAGT	261	
QY	143	TTGGAGACAGACCAGAACACTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAA	202	
Db	262	TTGGAGACAGACCAGAACACTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAA	321	
QY	203	GAGTAGTGTTCAGGAAATTCCTTTTCCACTATTTTTCCTATTTTGGTTAATATTATTAG	262	
Db	322	GAGTAGTGTTCAGGAAATTCCTTTTCCACTATTTTTCCTATTTTGGTTAATATTATTAG	381	
QY	263	CATGATGCATCCAAATAAGAAATATGAAGAAGTGCCTTAATATAGAACTCAATCCTATGGA	322	
Db	382	CATGATGCATCCAAATAAGAAATATGAAGAAGTGCCTTAATATAGAACTCAATCCTATGGA	441	
QY	323	CAAGTTTACTCTTTCTAATCTAATTTCTTGGATATATCTCCAGTGACTAATATTACAGCAG	382	
Db	442	CAAGTTTACTCTTTCTAATCTAATTTCTTGGATATATCTCCAGTGACTAATATTACAGCAG	501	
QY	383	CATCATGCAGAAAGTGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATAC	442	
Db	502	CATCATGCAGAAAGTGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATAC	561	
QY	443	AAATGAAAAAGAAATGTTAAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGGT	502	

Db 562 AAATGAAAAAAGAAATGTTAAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGGT 621
QY 503 TTTCAAAGACTCCATGTCCATGAACCTTCGTTTTTTTCTCTGATATGATCCAGTATCTTC 562
Db 622 TTTCAAAGACTCCATGTCCATGAACCTTCGTTTTTTTCTCTGATATGATCCAGTATCTTC 681
QY 563 TATTTATATGGATTCAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTC 622
Db 682 TATTTATATGGATTCAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTC 741
QY 623 CTCAGGTTTCACAGTTTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAA 682
Db 742 CTCAGGTTTCACAGTTTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAA 801
QY 683 TGTTCCTCTTTGGAAGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAACTGCTGT 742
Db 802 TGTTCCTCTTTGGAAGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAACTGCTGT 861
QY 743 TGTAGAAATAGATACCTTTCCCGAGGAGTAATTTTAAATATACCTAGTTATAGCATTTTC 802
Db 862 TGTAGAAATAGATACCTTTCCCGAGGAGTAATTTTAAATATACCTAGTTATAGCATTTTC 921
QY 803 ACCTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAA 855
Db 922 ACCTTTTGGATACCTTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAA 974

RESULT 2
US-09-621-976-409
; Sequence 409, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 409
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 185..484
US-09-621-976-409

Query Match 5.8%; Score 319.2; DB 4; Length 485;
Best Local Similarity 99.1%; Pred. No. 4.3e-65;
Matches 321; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 91 GCCCTGAGSTTTATTCAGAAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGAC 150
Db 162 GCGCCAGGTTTATTCAGAAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGAC 221
QY 151 AGACCAGAACACTTCTACTGAAGNATTACTTAAATTAATGCAGAACCAAAAAGAGTAGTG 210
Db 222 AGACCAGAACACTTCTACTGAAGNATTACTTAAATTAATGCAGAACCAAAAAGAGTAGTG 281
QY 211 TTCAGGAAATCTTTTTCCACTATTTTTTTTATTTTGGTTAATATTAATTAGCATGATGC 270
Db 282 TTCAGGAAATCTTTTTCCACTATTTTTTTTATTTTGGTTAATATTAATTAGCATGATGC 341
QY 271 ATCCAAATAAGAAATATGAAGAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTA 330
Db 342 ATCCAAATAAGAAATATGAAGAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTA 401
QY 331 CTCTTTCTAATCTAATTTCTTGGATATACCTCCAGTGACTAATATTACAAGCAGCATCATGC 390
Db 402 CTCTTTCTAATCTAATTTCTTGGATATACCTCCAGTGACTAATATTACAAGCAGCATCATGC 461

QY 391 AGAAAGTGTCTACTGATCATCTAC 414
Db 462 AGAAAGTGTCTACTGATCATCTAC 485
RESULT 3
US-09-833-381-1082
; Sequence 1082, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1082
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1082

Query Match 5.8%; Score 319.2; DB 4; Length 1350;
Best Local Similarity 59.6%; Pred. No. 6.6e-65;
Matches 610; Conservative 0; Mismatches 383; Indels 31; Gaps 3;
QY 3966 GAGGAGAAACCATCCATTATGTGTCAGCAATTTTGCATAAAGAATATGATGACAAGAAAGAT 4025
Db 6 GATGAGAAACCTGTTATAATTGCCAGCTGTCTACACAAAGAATATGCAGGCCAAGAA 65
QY 4026 TTTCTCTCTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTCTGTGTGAAA 4085
Db 66 AGTTGCTTTTCAAAGAGGAAGAAAAATAGCAGCAAGAAATATCTCTTCTGTGTCAA 125
QY 4086 AAAGGAGAGATCTTAGGACTATTTGGGTCCAAATGGTGTGGCAAAAGCACAATTATTAAT 4145
Db 126 GAAGATGAAATTTTGGGATTGCTAGGACCCCAATGGTGTGTGAAAAAGTTTCATCTATTAGA 185
QY 4146 ATTCTGTTGGTGATATTGAAACCAACTTCAGGCCAGGTATTTTAGGAGATTAATCTTCA 4205
Db 186 ATGATATCTGGGATCACAAAGCCAACTGCTGGAGAGGTGGAACTGAAAGGCTGCAGTTCA 245
QY 4206 GAGACAAAGTGAAGATGATGATTCAGTGAAGTGTATGGTGTACTGTCTCCTCAGATAAACCT 4265
Db 246 G-----TTTGGGCCACCTGGGTACTGCCCTCAAGAGAACGTG 284
QY 4266 TTGTGGCCAGATACTACATTGTCAGGAACATTTTGAATTTATGGAGCTGTCAAAGGAATG 4325
Db 285 CTGTGGCCCATGCTGACGTTGAGGGAACACCTGGAGGTGTATGTCCGTCAAGGGGCTC 344
QY 4326 AGTGCAAGTGACATGAAAGAAAGTCATAAGTCGAATAACACATGCACCTTGATTTAAAGAA 4385
Db 345 AGGAAAGCGGACGCGAGGCTCGCCATCGCAAGATTAGTGAGTGCTTTCAAACTGCATGAG 404
QY 4386 CATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAAAACGAAAGTTGTGTTTGTCT 4445
Db 405 CAGCTGAATGTTCTCTGTGCAGAAATTAACAGCAGGAATCACGAGAAAGTTGTGTTTGTG 464
QY 4446 CTAAGTATGCTAGGGAATCCTCAGATTACTTTTGCTAGTAGAACCATCTACAGGTATGGAT 4505
Db 465 CTGAGCCTCCTGGGAAACTCCCTTCCGTGCTCCTGGTAGAACCATCTACGGGCATAGAC 524
QY 4506 CCCA-AAGCCAAACAGCACATGTGGCGAGCAATTTCGAAGTGCATTTTAAACAGAAAGCG 4564
Db 525 CCCACAGGGCAGCCAGCAATGTGGCAGGCAATCCAGGCACTCGTTAAAAACACAGAGAG 584
QY 4565 GGCTGCTATTCTGACCACCTCACTATATATGGAGGAGGCAGAGGCTGTCTGTGATCGAGTAGC 4624
Db 585 AGGTGTCTCTGACCCACCCCAATACCTGGCTGAGGCGGAGGCTTGTGTGACCGTGTGGC 644

QY 4625 TATCATGGTGTCTGGCAGTTAAGATGTATCGGAACAGTACAAACATCTAAAGAGTAAATT 4684
Db |||||
QY 4685 TGGAAAAGGCTACTTTTGGAAAATTAAATTGAAGGACTGGATAGAAAACCTAGAAGTAGA 4744
Db |||||
QY 4745 CCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAGGAAAGTTTTTC 4804
Db |||||
QY 4805 TTCTATTTTGGCTTATAAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTTCAAAATCTTTTTT 4864
Db |||||
QY 4865 TAAGCTGGAAGAAGCTAAACATGCTTTTGGCCATTGAAGAATATAGCTTTTCTCAAGCAAC 4924
Db |||||
QY 4925 ATTGGAACAGGTTTTTTAGAACTCACTAAAGAAACAAGAGGAGGAAGATAATAGTTGTGG 4984
Db |||||
QY 4985 AACT 4988
Db |||||
QY 996 AATT 999

RESULT 4
US-08-665-259-24
; Sequence 24, Application US/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountaint Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..5053
US-08-665-259-24
Query Match 2.9%; Score 159.2; DB 3; Length 5894;
Best Local Similarity 48.0%; Pred. No. 2.4e-27;
Matches 554; Conservative 0; Mismatches 588; Indels 12; Gaps 3;
QY 1317 ATGTCACACTTAATAGTATATTTCTATGTCTCTTGGCTGTCTATCTTGTATCAAGTCAAT 1376
Db |||||
QY 1377 CCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTTCATATTGTTCA 1436
Db |||||
QY 1437 AAGACAAAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAATATATTAGTTT 1496
Db |||||
QY 1497 AGTGAAATTTAGCCAGTTTCTTTCAGAAATTTGAGGAAAAGAACCCATAAGAAATTAGT 1556
Db |||||
QY 1557 GGTATTCAGAAGACATACAGAAAGAAAGGGTGAATGTGAGGGCTTTTGAGAAATTTGTCA 1616
Db |||||
QY 1617 TTTGACATATATGAGGTCAGATTACTGCTTACTTTGGCCACAGTGGAAACAGGAAAAGAGT 1676
Db |||||
QY 1677 ACATTGATGAATATTTCTTGTGGACTCTGCCCCACCTTCTGTATGGTGTTCATCTATATAT 1736
Db |||||
QY 1737 GGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAATGATTGGCATTTGT 1796
Db |||||
QY 1797 CCACAGTTAGATATACACTTTGTATGTTTTTGACAGTAGAAGAAAATTTTATCAATTTTGGCT 1856
Db |||||
QY 1857 TCAATCAAAGGGATACCAGCCCAACATATAATACAGAAAGTGCAGAAAGTTTACTAGAT 1916
Db |||||
QY 1917 TTAGACATGCAGACTATCAAAGATAACCAAGCTAATTAAGTGGTGGTCAAAAAGA 1976
Db |||||
QY 1977 AAGCTGTCAATTAGGAATTTGCTGTTCTTGGGAACCCAAAGATACCTGCTGATGAACCA 2036
Db |||||
QY 2037 ACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGAAAA 2096
Db |||||
QY 2097 GCCAATCGGGTGACAGTGTTCAGTACTCTATTTTCATGGATGAAGCTGACATCTTTCAGAT 2156
Db |||||
QY 2157 AGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTGTTCTTCAATGTTCTCAAA 2216
Db |||||
QY 2217 AGTAAATGGGGATCGGCTACCGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCACAGAA 2276
Db |||||
QY 2276 AGTAAATGGGGATCGGCTACCGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCACAGAA 2276
Db |||||

Qy	2277	TCTCTTTCTTCTACTGGTTAAACAACATATACCTGGAGCTACTTTATTATCAACAGAAATGAC	2336
Db	2255	GACATCTCCAGCTGGTCCACCACCAACGTGCCCAACGCCACGCTGGAGAGCAGCGCTGGG	2314
Qy	2337	CAACAACITGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCAGGTTTGTGTTTTCT	2396
Db	2315	GCCGAGCTGTCTTTTCATCCTTCCCAGAGAGAGCAGCAGGTTTGAAGGTCCTCTTGCT	2374
Qy	2397	GCCCTAGACAGTCATTCAAATTTGGGTGTCATTTC---TTATGGTGTGTTTCCATGACGACT	2453
Db	2375	AAACTGGAGAGAAGACAGAAAGAGCTGGGCATTGCCAGCTTTGGGGCATCCCATCACCACC	2434
Qy	2454	TTGGAAGACGTATT	2467
Db	2435	ATGGAGGAAGTCTT	2448

RESULT 5
US-08-762-500-24
; Sequence 24, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IGS-9.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..5053
US-08-762-500-24

	Query Match	2.9%;	Score 159.2;	DB 3;	Length 5894;
	Best Local Similarity	48.0%;	Pred. No. 2.4e-27;		
	Matches 554;	Conservative	0;	Mismatches 588;	Indels 12; Gaps 3;
QY	1317	ATGCTCACACTTAATAGTATATTCTATGTCTCTCTTGGCTGTCTATCTTGATCAAGTCATT	1376		
Db	1304	ATGCTGCTGTGGACTCTGTGCTCTATGGCCTGGTGACCTGGTACATGAGGCCGCTCTTC	1363		
QY	1377	CCAGGGGAATTTGGCTTACGGAGATCATCTTTATATATTTTCTGAAGCCTTCATATTGGTCA	1436		
Db	1364	CCAGGGCAGTTCGGCGTGCCTCAGCCCTGGTACTTCTTTCATCATGCCCTCCTATTGGTGT	1423		
QY	1437	AAGAGCAAAAGAAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAATAATTAGTTTTT	1496		
Db	1424	GGGAAGCCAAGGGCGTTTCAGGGAAGGAGGAAGAAGACAGTGACCCCGAGAAAAGCACTC	1483		
QY	1497	AGTGAAATTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAACGCCATAAGAATTAGT	1556		
Db	1484	AGAAACGAGTACTTTGAAGCCGAGCCAGAGGACCTGG--TGCGGGGATCAAGATCAAG	1540		
QY	1557	GGTATTCAGAAAGACATACAGAAAGAGGGTGAAAATGTGAGGCTTTTGAGAAAATTTGTCA	1616		
Db	1541	CACCTGTCCAAGGTGTTTCAGGGTGGGAAATAAGGACAGGGCGGCCGTGAGAGACCTGAAC	1600		
QY	1617	TTTGACATATATGAGGTCAGATTACTGCCTTACTTTGGCCACAGTGGAAACAGGAAAAGT	1676		
Db	1601	CTCAACCTGTACGAGGGACAGATCACCGTCTGCTGGGCCACAAACGGTGCCGGAAAGACC	1660		
QY	1677	ACATTGATGAATATTCTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCACTCTATATAT	1736		
Db	1661	ACCACCTCTCCATGCTCACAGGTCTCTTTCCCCCACCAGTGGACGGGATACATCAGC	1720		
QY	1737	GGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAATTTATCAATTTTGGCT	1796		
Db	1721	GGGTATGAATTTCCAG-----GACATGGTTTCAGATCCGGAAGAGCCCTGGGCTGTGC	1774		
QY	1797	CCACAGTTAGATATACACTTTGTGATGTTTGACAGTAGAAGAAAATTTATCAATTTTGGCT	1856		
Db	1775	CCGCAGCACGACATCTCTGTTTGACAACTTGACAGTCGCAGAGCACTTTATTTCACGCC	1834		
QY	1857	TCAATCAAAGGATACCAGCCAAACAATATAATAACAAGAAAGTGCAGAGGTTTACTAGAT	1916		
Db	1835	CAGCTGAAGGGCTGTACGTGAGAAAGTGCCCTGGAAGAAAGTCAAGCAGATGCTGCACATC	1894		
QY	1917	TTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGTGGTCAAAAAAGA	1976		
Db	1895	ATCGGCCTGGAGGACAAGTGGAACCTCACGGAGCCGCTTCTTGAGCGGGGCATGAGGCGC	1954		
QY	1977	AAGCTGTCAATTAGGAATTGCTGTTCTTTGGGAACCCAAAGATACTGCTGCTAGATGAACCA	2036		
Db	1955	AAGCTCTCCATCGGCATCGCCCTCATCGCAGGCTCCAAGGTGCTGATCTGGACGAGCCC	2014		
QY	2037	ACAGCTGGAATGGACCCCTGTTCTTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAA	2096		
Db	2015	ACCTCGGCATGGACGCCATCTCCAGGAGGGCCCATCTGGGATCTTCTTCAGCGGCAGAAA	2074		
QY	2097	GCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCAGAT	2156		
Db	2075	AGTGACCGCACCATCGTGTGACCAACCCACTTCATGGACGAGGCTGACCTGCTGGGAGAC	2134		
QY	2157	AGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTGTTCTTCAATGTTCTCTCAAA	2216		
Db	2135	CGCATCGCCCATATGGCCAAAGGGGAGCTGCAGTGTCTCGGGTCTCTCGTGTCTCTCAAG	2194		
QY	2217	AGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAAATATTGTGCCACAGAA	2276		
Db	2195	CAGAAATACGGTCCGGCTATCACATGACGCTGGTGAAGGAGCCGCACTGCAACCCGGAA	2254		
QY	2277	TCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTACACAGAAATGAC	2336		
Db	2255	GACATCTCCAGCTGGTCCACCACCAAGTGCACCAACGCCACGCTGGAGAGCAGCGCTGGG	2314		
QY	2337	CAACAACTTGTGTATAGCTTGCCCTTTCAAGGACATGGACAAAATTTTCAGGTTTGTCTTCT	2396		

Db 2315 GCCGAGCTGTCTTTCATCCTCCAGAGAGACGACAGGTTTGAAGGTCCTTTGCT 2374
Qy 2397 GCCCTAGACAGTCATTCAAAATTTGGGTGTCAATTC---TTATGGTGTTCATGACGACT 2453
Db 2375 AAACCTGGAGAAGAGCAGAAAGAGCTGGGCATTGCCAGCCTTTGGGGCATCCATCACCACC 2434
Qy 2454 TTGGAAGACGTATT 2467
Db 2435 ATGGAGGAAGTCTT 2448

RESULT 6

US-08-762-500-74
; Sequence 74, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6525 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 573..5684
US-08-762-500-74

Query Match 2.9%; Score 159.2; DB 3; Length 6525;
Best local Similarity 48.0%; Pred. No. 2.5e-27;
Matches 554; Conservative 0; Mismatches 588; Indels 12; Gaps 3;
Qy 1317 ATGCTCACACTTAATAGTATATCTATGCTCTTGGCTGTCTATCTTGTATCAAGTCATT 1376

Db 1935 ATGCTGCTGGACTCTGTGCTCTATGGCCTGGTGACCTGGTACATGGAGGCGCTCTTC 1994
Qy 1377 CCAGGGGAATTTGGCTTACGAGATCATCTTTATATTTTCTGAAGCCTTCATATTTGCTCA 1436
Db 1995 CCAGGCGAGTTGCGCGTGCCTCAGCCCTGGTACTTCTTCATCATGCCCTCCTATTTGGTGT 2054
Qy 1437 AAGAGCAAAAGAAATTAATGAGGAGTTATCAGAGGGCAATGTTAATGGAATATTAGTTTT 1496
Db 2055 GGGAAGCCAAAGGCGGTTGCGAGGAAGGAGGAAGACAGTACCCCGAGAAAGCACTC 2114
Qy 1497 AGTGAATATTAGCCAGTTTCTTTCAGAAATTTGTAGGAAAGAACCCATAAGAAATTAGT 1556
Db 2115 AGAAACGAGTACTTTGAAGCCGAGCCAGAGGACCTGG--TGGCGGGGATCAAGATCAAG 2171
Qy 1557 GGTATTTCAGAAAGACATACAGAAAGAGGTTGAAATATGTGAGGCTTTTGAGAAATTTGTCA 1616
Db 2172 CACCTGTCCAAGGTGTTCAAGGTGGGAAATAAGGACAGGCGCGCGTTCAGAGACCTGAAC 2231
Qy 1617 TTTGACATATATGAGGGTCAGATTACTGCTTACTTGGCCACAGTGGAAACAGGAAAGAGT 1676
Db 2232 CTCACCTGTACGAGGGACAGATCACCGTCTCTGCTGGCCACAAACGGTCCCGGGAAGACC 2291
Qy 1677 ACATTGATGAATATTTCTTTGTGACTCTGCCCCACCTTCTGATGGTTTTCATCTATATAT 1736
Db 2292 ACCACCTCTCCATGCTCAGAGTCTCTTTTCCCCCACCAGTGGACGGGCATACATCAGC 2351
Qy 1737 GGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAATGATTGGCATTGTTGT 1796
Db 2352 GGGTATGAAATTTCCAG-----GACATGGTTTCAGATCCGGAAGAGCCTGGGCTGTGC 2405
Qy 1797 CCACAGTTAGATATACACTTTGATGTTTTCAGAGTAGAGAAATTTATCAATTTTGGCT 1856
Db 2406 CCGCAGCAGGACATCTCTGTTTGACAACTTGACAGTTCGAGAGCACCTTTATTTCTACGCC 2465
Qy 1857 TCAATCAAAAGGGATACCAGCCAAACAATATAACAAGAGTGCAGAAAGTTTACTAGAT 1916
Db 2466 CAGCTGAAGGGCCTGTACGTCAGAAAGTGCCTGAAGAGTCAAGCAGATGCTGCACATC 2525
Qy 1917 TTAGACATGCAGACTATCAAAGATAACCAAGCTAAATAATTAAGTGGTGGTCAAAAAGA 1976
Db 2526 ATCGGCTGGAGGACAAAGTGAACACTCAGGAGCGGCTCTCTGAGCGGGGCGATGAGCGC 2585
Qy 1977 AAGCTCTCATTAGGAATGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAACCA 2036
Db 2586 AAGCTCTCCATCGGCATCGCCCTCATCGAGGCTCCAGGCTGCTGCTGATCTGAGCGAGCC 2645
Qy 2037 ACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGAAA 2096
Db 2646 ACCTCGGCGATGGACGCGCATCTCCAGGAGGGCCATCTGGATCTTCTCAGCGGCGAGAA 2705
Qy 2097 GCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGAGAT 2156
Db 2706 AGTGACCGCACCATCGTGTGCTGACCAACCCACTTTCATGAGGAGGCTGACCTGCTGGAGAC 2765
Qy 2157 AGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTGTTCTTCAATGTTCTCTCAA 2216
Db 2766 CGCATCGCCCATCATGGCCAAAGGGGAGCTGCAGTGTGCGGGTCTCTCGCTGTTCTCTCAAG 2825
Qy 2217 AGTAATGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACAGAA 2276
Db 2826 CAGAAATACGGTCCCGGCTATCAGATGACGCTGTTGAAGGAGCGGCACTGCAACCCGGAA 2885
Qy 2277 TCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAATGAC 2336
Db 2886 GACATCTCCAGCTGGTCCACCAACCGTCCCAACCGCAGCTGGAGAGCAGCGCTGGG 2945
Qy 2337 CAACAACCTTGTATAGCTTTCCTTTCAAGGACATGGCAAAATTTTCAGGTTTGTGTTTCT 2396
Db 2946 GCCGAGTGTCTTTTCATCTCTCCAGAGAGAGCAGCAGAGTTTGAAGGTCTCTTTGCT 3005
Qy 2397 GCCCTAGACAGTCATTCAAATTTGGGTGTCTATTC---TTATGGTGTTTCCATGACGACT 2453
Db 3006 AAACCTGGAGAAGAGCAGAAAGAGCTGGGCATTGCCAGCTTTGGGGCATCCATCACCACC 3065

QY	4126	GCAAAAGCACAATATTAAATATCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTAT	4188
DB	263	GTAAGTCAACAACGATTAAAAATGTTGACAGGGATTTTAAAAACCGACATCTGGTTTTTGTC	322
QY	4186	TTTTAGGAGATTATTTCTTCAGAGACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTT	4245
DB	323	GCATTAAATGGGAAGATTCTCAAGAAAAATCGTCAGGATTATGTTAAGGATATTGGTGTG	382
QY	4246	ACTGTCCTCAGATAAACCTTTGTGGCCAGATACTACATTCAGGAACATTTTGAAATTT	4305
DB	383	TTTTTGGGCAACGCACCCAGCTTTGGTGGGATTTGSCCTTTACAAGAGACATACTCAGTTT	442
QY	4306	ATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAGAAAGTCAATAAGTCGAATAACAC	4365
DB	443	TAAAAAGAAATTTATGATGTCCTGATGCAGTATTTCAAAAAACGCATGGATTTTTAAATG	502
QY	4366	ATGCACTTGATTTTAAAAAACAATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCA	4425
DB	503	ATGTTTTAGACTTGAAGAGTTTATTAAAGGATCCTGTGCGGACACTATCATTAGGTCAAC	562
QY	4426	AACGAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTTGCTAGATG	4485
DB	563	GTATGAGAGCGGATATTGGGCCCTCCTTGCTCCACAATCCCAAAGTTCTTTTTTTAGATG	622
QY	4486	AACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTG	4545
DB	623	AGCGACCATTTGGTTTGGACGTTTCGGTTAAGGATAATATTCTGTCGGGCATTTACTCAGA	682
QY	4546	CATTTAAAAACAGAAAAGCGGCTGCTATTCTGACCACTCACTATATGGAGAGGCAGAGG	4605
DB	683	TCAATCAAGAGGAAGAAACTACCATTTCTTTTGACCACTCACGATTTGAGTGATTTGA-G	741
QY	4606	CTGTCGTGTGATCGACTAGCTATCATGGTGTCTGGCAGTTTAAGATGTATCGGAACAGTAC	4665
DB	742	CAATTTGTGATCGGATTTTTCATGATTGACAAGGGGCAAGAGATTTTTTGATGGAAACAGTGA	801
QY	4666	AACATCTAAAGAGTAAATTTTGAAA	4690
DB	802	GCCAACTCAAGGAGACCTTTGGTAA	826

RESULT 9

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US-09-833-381-1087
; Sequence 1087, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1087
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(728)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1087

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	Query Match	1.8%	Score 97.4;	DB 4;	Length 728;
	Best Local Similarity	49.8%;	Pred. No. 2.7e-13;		
	Matches 308;	Conservative 0;	Mismatches 301;	Indels 10;	Gaps 2;
QY	2971	ATAGTGGCGCTTTAAATGTGATGCATT	CAGAAAAGGACTATGTTTTTG	CAGCTGTTTCA	3030
Db	53	ACAATGGAGCTATCATAGTTTTCTGGTAAAC	CAAAAGGANTATAGATTTTCAGTTTGCTGTA	112	

QY	3031	ACAGTACTATGGTTTATCTTTACCTATATATAGTGAATATCATTAGTAACCTACTATCTTT	3090
DB	113	ATACCAAGAGATTGCACGTGTTTCCAAATCTTATGAATATATCAGCAATGGGCTACTTC	172
QY	3091	ATCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTA	3150
DB	173	AAATGTTTAAATCACACACAATATTCGAATTGAGTCAAGCCCATTTCCCTC-----TTA	226
QY	3151	CTGATATAGTTTTTAAAAATGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTA	3210
DB	227	GCCACATAGGACTCTGGACTGGGTGCCGATGGTTCCTTTTCTTATTTTGGTTCAT	286
QY	3211	CTGCAATGCCACCTTACTTTTGCCATGGAAATGCAGAGAATCATAGAATCAAAGCTTATA	3270
DB	287	GTAGCATTTCTCCTTATATCACCATGCGCAGCATCAGTGATTACAAGAAAAATGCTAAGT	346
QY	3271	CTCAACTTAAACTTTTCAGGTCTTTTGGCATCTGCATATTTGGATTGGACAAGCTGTTGTTG	3330
DB	347	CCCAGCTATGGATTTCAGGCTCTACACTTCTGCTTACTGGTGTGGGAGGCACACTAGTGG	406
QY	3331	ATATCCCCTTATTTTTTATCATCTTATTTTGATGCTAGGAAGCTTATTTGGCATTTTCATT	3390
DB	407	GACGTCAGCTCTCTCATTTTAAATTCCTTTTAAATGTATTTAATTTCTACATAGAAAAAC	466
QY	3391	ATGGATTATATTTTTTAT---ACTGTAAAGTTCCTTGCTGTGGTTTTTTTGCCTTATTGGT	3446
DB	467	ATGCAGTACCTTCTTATTACAAGCCAAATTTGTTGTTTGGTTATAGTTACTCTCTGGT	526
QY	3447	TATGTTCCATCAGTTATTTCTGTTCACTTATATTGCTTCTTTCACCTTTTAAGAAAAATTTTA	3506
DB	527	TATGCAGCTTCTCTTGTCTTCTTCATATATATGATATCATTTATTTTTCGCAAAAAGAGA	586
QY	3507	AATACCAAGAAATTTTGGTCATTTATCTATTTCTGTGGCAGCGTTGGCTTGTTATTTGCAATC	3566
DB	587	AAAAACAGTGGCCTTTGGTCATTTTACTTCTTTTTTGGCTCACCATCATGTTTTTCCATCA	646
QY	3567	ACTGAAATAAACTTTCTTTTA	3585
DB	647	CTTTAATCAATCATTTTTGA	665

RESULT 10

US-08-961-527-1
; Sequence 1, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5625 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-1

Query Match      1.7%; Score 92.2; DB 4; Length 5625;
Best Local Similarity 46.2%; Pred. No. 9.9e-12;
Matches 307; Conservative 0; Mismatches 358; Indels 0; Gaps 0;

QY 4026 TTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTCTGTGTGAAA 4085
Db 2132 TTTATTCATCCTGAAAGCAGACCTTTGAAGCGGTCAAGGATTTGACCTTTGAGGTTCCA 2191
QY 4086 AAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTCTGCGCAAAAGCACAATTATTAAAT 4145
Db 2192 AAAGGCGAGATTTAGGATTTATCGGGCAAAATGGTCTGCGCAAGTCGACAACCAATAAA 2251
QY 4146 ATTCTGGTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGAGATTATCTTCA 4205
Db 2252 ATGCTGACAGGAATTTGAAACCAACATCTGGTTTTTGTGCGATTAAACGGCAAGATTCCC 2311
QY 4206 GAGACAAGTGAAGATGATGATTCACCTGAAGTGATGGGTACTGTCTCAGATAAACCCCT 4265
Db 2312 CAGGACATCGGCAAGATTATGTCAAGATATTGGCGTAGTCTTTGGACAACGCCACCCAG 2371
QY 4266 TTGTGGCCAGATACTACATTGCAGGAACATTTTGAAATTTATGGAGCTGTCAAAGGAATG 4325
Db 2372 CTATGGTGGATTGGCTCTGCAAGAGACCTACACTGTCTTAAAGAGATTATGATGTG 2431
QY 4326 AGTGCAAGTGACATGAAAGAGTCAATAAGTCGAATAACACATGCACCTTGATTTAAAGAA 4385
Db 2432 CCAGACTCGCTCTTTTCATAAGCGTATGGACTTTTGAATGAAGTCTTGGATTGAGGAC 2491
QY 4386 CATCTTCAGAAGACTGTAAAGAACTACCTGCAGGAATCAACGAAAGTTGTGTTTGCT 4445
Db 2492 TTTATCAAGGATCCCGTGGGACTCTTTCACTGGGACACCGGATCGGGCGGATATTGCG 2551
QY 4446 CTAAGTATGTAGGGAATCCTCAGATTACTTTGTAGATGAACCATCTACAGGTATGGAT 4505
Db 2552 GCCTCCTTGTCCCAATCCCAAGGTCTTTTGTAGATGAGCCGACCATTTGTTTGGAC 2611
QY 4506 CCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAATCGCATTTAAACACAGAAAGCGG 4565
Db 2612 GTTTCGGTTAAGGATAATATTCTGTCGGGCAATTACTCAGATCAATCAAGAGGAAGAACT 2671
QY 4566 GCTGCTATTCTGACCACTCACTATATGAGGAGGAGGAGGCTGTCTGTATCGAGTAGCT 4625
Db 2672 ACCATTCTTTGACCACCTCAGGATTTGAGTGATATTGAGCAACTTTGTATCGGATTTTC 2731
QY 4626 ATCATGGTGTCTGGGCGAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTAAATTT 4685
Db 2732 ATGATTGACAAGGGGCAAGAGATTTTGTATGGAACGGTGTGACCAACTCAAGGAGACCTTT 2791
QY 4686 GAAA 4690
Db 2792 GGTA 2796
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RESULT 11
US-09-621-976-2582
; Sequence 2582, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
```

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; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2582
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 69..308
US-09-621-976-2582

Query Match      1.5%; Score 83.8; DB 4; Length 450;
Best Local Similarity 60.2%; Pred. No. 3.2e-10;
Matches 139; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 4796 AAGTTTTTCTTCTATTTTGGCTTATATAAAATTCCTAAGGAAGATGTTCCCTTTTCA 4855
Db 74 AAAATATCTCTCTTTAATGGCGTATAAGTTACCTGTGGAGATGTCCACCTCTATCTCG 133
QY 4856 ATCTTTTTTAAAGCTGGAAGAAAGTAAACATGCTTTTGGCATTGAAGAATATAGCTTTTC 4915
Db 134 GGCTTTTCAAGTTAGAGGCGATGAAACAGACCTTCAACCTGGAGGAATACAGCCTCTC 193
QY 4916 TCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCCTAAAGAACAAAGAGGAGGATAA 4975
Db 194 TCAGGCTACCTTGGAGCAGGTATTTTAGAACTCTGTAAAGAGCAGGAGCTGGGAAATGT 253
QY 4976 TAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAAACACAAAGAAGA 5026
Db 254 TGATGATAAAATTGATACAACAGTTGAATGGAACCTTCTCCACACAGGAAGA 304
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RESULT 12
US-09-621-976-2581
; Sequence 2581, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2581
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..328
US-09-621-976-2581
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Query Match      1.5%; Score 83.4; DB 4; Length 463;
Best Local Similarity 60.3%; Pred. No. 4.1e-10;
Matches 138; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 4798 GTTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCCCTTTTCA 4857
Db 96 GATATTCCTCTTTAATGGCGTATAAGTTACCTGTGGAGGATGTCCACCTCTATCTCGGC 155
QY 4858 CTTTTTTTAAAGCTGGAAGAAAGTAAACATGCTTTTGGCATTGAAGAATATAGCTTTTCTC 4917
Db 156 CCTTTTCAAGTTAGAGGCGATGAAACAGACCTTCAACCTGGAGGAATACAGCCTCTCTC 215
QY 4918 AAGCAACATTTGGAACAGGTTTTTGTAGAACTCCTAAAGAACAAAGAGGAGGATATA 4977
Db 216 AGGCTACCTTGGAGCAGGTATTTCTTAGAACTCTGTAAAGAGCAGGAGCTGGGAAATGTTG 275
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QY 4978 GTTGTGGAACCTTTAAACAGCAGCACACTTTGGTGGGAACGAAACAACAAGA 5026
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RESULT 13
US-09-621-976-2583
; Sequence 2583, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2583
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..328
US-09-621-976-2583

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Best Local Similarity 60.3%; Pred. No. 4.1e-10;
Matches 138; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
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QY 4858 CTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTCCCATTTGAAGAATATAGCTTTTCTC 4917
Db 156 CCTTTTCAAGTTAGAGGGCGATGAACAGACCTTCAACCTGGAGGAATACAGCCTCTCTC 215
QY 4918 AAGCAACATTGGAACAGGTTTTTGTAGAACTCAGTAAAGAACAGAGGAGGAAGATAATA 4977
Db 216 AGGCTACCTTGGAGCAGGTTATCTTTAGAACTCTGTAAAGAGCAGGAGCTGGGAAATGTTG 275
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RESULT 14
US-09-833-381-1080
; Sequence 1080, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1080
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1080

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Db 464 TG 465

RESULT 15
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; Sequence 264, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: Hp Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

; TOPOLOGY: linear									
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Best Local Similarity 48.3%; Pred. No. 2.3e-09;									
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	4664	85.2	5262	9	US-09-971-121-5	Sequence 5, Appli
4	4572	83.5	4929	9	US-09-971-121-1	Sequence 1, Appli
5	4408	80.5	4785	9	US-09-971-121-3	Sequence 3, Appli
6	2826	51.6	5463	13	US-10-090-458-1	Sequence 1, Appli
7	2739	50.0	3268	15	US-10-094-749-984	Sequence 984, App
8	2713	49.6	4917	13	US-10-090-458-3	Sequence 3, Appli
9	1991	36.4	3347	15	US-10-108-260A-160	Sequence 160, App
10	1497	27.3	1548	10	US-09-822-846-97	Sequence 97, Appl
11	1343	24.5	3928	10	US-09-822-846-98	Sequence 98, Appl
12	744	13.6	1818	14	US-10-204-887-32	Sequence 32, Appl
13	743	13.6	974	9	US-09-833-381-1085	Sequence 1085, Ap
14	742	13.6	1943	15	US-10-108-260A-1424	Sequence 1424, Ap
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22	376	6.9	1346	9	US-09-962-436-337	Sequence 337, App	
23	376	6.9	1346	9	US-09-880-107-3406	Sequence 3406, Ap	
24	376	6.9	1346	9	US-09-954-531-1033	Sequence 1033, Ap	
25	376	6.9	1346	14	US-10-171-581-333	Sequence 333, App	
26	331	6.0	476	9	US-09-867-701-4362	Sequence 4362, Ap	
C	27	324	469	9	US-09-880-107-1883	Sequence 1883, Ap	
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C	36	207	709	15	US-10-027-632-115304	Sequence 115304, A	
37	193	3.5	1478	15	US-10-242-355-971	Sequence 971, App	
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41	144	2.6	566	14	US-10-029-386-2801	Sequence 2801, Ap	
42	128	2.3	315	9	US-09-783-590-9786	Sequence 9786, Ap	
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45	39	0.7	60	10	US-09-908-975-10033	Sequence 10033, A	

ALIGNMENTS

RESULT 1
US-10-090-458-4
; Sequence 4, Application US/10090458
; Publication No. US20020123107A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCAS TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090,458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 25
; OTHER INFORMATION: n = A,T,C or G
US-10-090-458-4

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Best Local Similarity	100.0%;	Pred. No. 0;		
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4261 ACCCTTTGTGGCCAGATACATTTGCAGGAACATTTTGAATTTTATGGAGCTGTCAAAG 4320
Db |||||
4261 ACCCTTTGTGGCCAGATACATTTGCAGGAACATTTTGAATTTTATGGAGCTGTCAAAG 4320
QY |||||
4321 GAATGAGTGCAAGTGACATGAAAGAGTCAATAAGTCGAATAACACATGCATTTGATTTAA 4380
Db |||||
4321 GAATGAGTGCAAGTGACATGAAAGAGTCAATAAGTCGAATAACACATGCATTTGATTTAA 4380
QY |||||
4381 AAGAACATCTTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTTGTGTT 4440
Db |||||
4381 AAGAACATCTTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTTGTGTT 4440
QY |||||
4441 TTGCTCTAAGTATGCTAGGAAATCCTCAGATTACTTTTGTAGATGAACCATCTACAGGTA 4500
Db |||||
4441 TTGCTCTAAGTATGCTAGGAAATCCTCAGATTACTTTTGTAGATGAACCATCTACAGGTA 4500
QY |||||
4501 TGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGCAATTTAAAAACAGAA 4560

Db 4501 TGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAAAAACAGAA 4560

QY 4561 AGCGGGTCTATTCTGACCACTCACTATATGGAGGAGCAGAGGCTGTCTGTGATCGAG 4620

Db 4561 AGCGGGTCTATTCTGACCACTCACTATATGGAGGAGCAGAGGCTGTCTGTGATCGAG 4620

QY 4621 TAGCTATCATGGTGTCTGGGCAAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTA 4680

Db 4621 TAGCTATCATGGTGTCTGGGCAAGTTAAGATGTATCGGAACAGTACAACATCTAAAGAGTA 4680

QY 4681 AATTGGAAAAAGGCTACTTTTTGGAAATTAATTTGAAGACTGGATAGAAAACTAGAAG 4740

Db 4681 AATTGGAAAAAGGCTACTTTTTGGAAATTAATTTGAAGACTGGATAGAAAACTAGAAG 4740

QY 4741 TAGACCGCTTCAAGAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGAAAAAGTT 4800

Db 4741 TAGACCGCTTCAAGAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGAAAAAGTT 4800

QY 4801 TTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTTCAAACTTT 4860

Db 4801 TTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTTCAAACTTT 4860

QY 4861 TTTTAAAGCTGGAAGAGCTAAACATGCTTTTGGCAATGGAAGATATAGCTTTTCTCAAG 4920

Db 4861 TTTTAAAGCTGGAAGAGCTAAACATGCTTTTGGCAATGGAAGATATAGCTTTTCTCAAG 4920

QY 4921 CAACATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAAAGAGGAGGAAGATAAGTT 4980

Db 4921 CAACATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACAAAGAGGAGGAAGATAAGTT 4980

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Db 5041 GAATTTGTATTTTGGTCTGCTTACTGGGACTTCTTTTCTTTTCTTTTCACTTAATTTAACTT 5100

QY 5101 TGGTTTAAAAAGTTTTTTTATTGGGAATGGTAACCTGGAGAACCAAGACGCACTTGAATTT 5160

Db 5101 TGGTTTAAAAAGTTTTTTTATTGGGAATGGTAACCTGGAGAACCAAGACGCACTTGAATTT 5160

QY 5161 TTCTAAGCTCCTTAATTGAAATGCTGTGGTGTGTGTTTGTCTTTTCTTTTAAATAAAACG 5220

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Db 5221 TATGTATAAATAAGTGAAGCTGCATGTTGTATTGGAAGTATATTGAACTATATAGTTGT 5280

QY 5281 ATGTCACTTTTTCACCAATTCAGAAACAGTGTCTTGAATTTGTGATTTTAAAGGAATTGT 5340

Db 5281 ATGTCACTTTTTCACCAATTCAGAAACAGTGTCTTGAATTTGTGATTTTAAAGGAATTGT 5340

QY 5341 AATAGAATAGTTTATTTTAAAGTTATCTTTAAAGTTTATGCCATCTTTCTTTAAATAAGTAC 5400

Db 5341 AATAGAATAGTTTATTTTAAAGTTATCTTTAAAGTTTATGCCATCTTTCTTTAAATAAGTAC 5400

QY 5401 GTAATGTTCCCAATCTAAATAAAAACTAAATTCATAACTAATGATAGAAAAAGATACATAA 5460

Db 5401 GTAATGTTCCCAATCTAAATAAAAACTAAATTCATAACTAATGATAGAAAAAGATACATAA 5460

QY 5461 AGCAATGTGAAAGTT 5475

Db 5461 AGCAATGTGAAAGTT 5475

RESULT 2
US-10-005-338B-1
; Sequence 1, Application US/10005338B
; Publication No. US20030044895A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, Patrice

; APPLICANT: ROSTER-MONTUS, Marie-Francoise
; APPLICANT: PRADES, Catherine
; APPLICANT: ARNOULD-REGUIGNE, Isabelle
; APPLICANT: DUVBERGER, Nicolas
; APPLICANT: ALLIKMETS, Rando
; APPLICANT: DEAN, Michael
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENE
; TITLE OF INVENTION: CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
; FILE REFERENCE: ABCA5, 6, 9, 10
; CURRENT APPLICATION NUMBER: US/10/005,338B
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/263,231
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: FR 00403440.1
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4449
; OTHER INFORMATION: n=unknown, may be a or g or c or t
US-10-005-338B-1

Query Match 94.6%; Score 5181; DB 14; Length 6525;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5331; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 97 AGGTTTATTCAGAAAAACATGTCCTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 156

Db 994 AGGTTTATTCAGAAAAACATGTCCTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 1053

QY 157 GAACACTTCTACTGAAGAATTACTTAATTAATGCGAGAACCAAAAGAGTAGTGTTCAG 216

Db 1054 GAACACTTCTACTGAAGAATTACTTAATTAATGCGAGAACCAAAAGAGTAGTGTTCAG 1113

QY 217 AAATTCCTTTTCCACTATTTTTTTTATTTTGGTTAATAATTAATAGCATGATGCATCCAA 276

Db 1114 AAATTCCTTTTCCACTATTTTTTTTATTTTGGTTAATAATTAATAGCATGATGCATCCAA 1173

QY 277 ATAAGAAATATGAAGAAGTGCCTAATATATAGAACTCAATCTATGGACAAAGTTTACTCTTT 336

Db 1174 ATAAGAAATATGAAGAAGTGCCTAATATATAGAACTCAATCTATGGACAAAGTTTACTCTTT 1233

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Db 1234 CTAATCTAATTTCTTGGATATATCTCCAGTGACTAATATTACAAGCAGCATCATGCGAGAAAG 1293

QY 397 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAAGAAA 456

Db 1294 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAAGAAA 1353

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Db 1354 TGTTAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGGTGTCTTCAAAGACTCCA 1413

QY 517 TGTCCCTATGAACCTTCGTTTTTTTCTCTGATATGATTCAGTATCTTCTATTATATGGATT 576

Db 1414 TGTCCCTATGAACCTTCGTTTTTTTCTCTGATATGATTCAGTATCTTCTATTATATGGATT 1473

QY 577 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 636

Db 1474 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 1533

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Db 1534 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA 1593

QY 697 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGAGAAACTGCTGTGTAGAAATAGATA 756

Db 1594 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAAAGCTGCTGTTGTAGAAATAGATA 1653

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Db 1654 CCTTTCCTCCGAGGAGTAATTTTAATATATACCTAGTTATAGCAATTTTCACCTTTTGGATACT 1713

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Db 1714 TTTTGGCAATTCTATCGTAGCAGAAAAAGAAAAAATAAAAGAAATTTTAAAGATAA 1773

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Db 1774 TGGGACTTCATGAFACCTGCTTTTGGCTTTTCCCTTTATGGATTATCATCTGTATTTTGTCTT 1833

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Db 1834 TTCTTATGTCCTTCTTATGGCAGTCAATGGACAGCTTCTTTGTATTTTCCCAAGTA 1893

Qy 997 GCAGCAATGTGATATTTCTGCTTTTTCCTTTATGGATTATCATCTGTATTTTGTCTT 1056

Db 1894 GCAGCAATGTGATATTTCTGCTTTTTCCTTTATGGATTATCATCTGTATTTTGTCTT 1953

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Db 1954 TAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTGTA 2013

Qy 1117 CTGTGGCTTTTGGATTTATTTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAATCGT 1176

Db 2014 CTGTGGCTTTTGGATTTATTTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAATCGT 2073

Qy 1177 TAGTGTGGCTTTTTCAGTCTTTCTGTCTACCTGTAATTTTGTGATTTGGTATGTCACAGGTCA 1236

Db 2074 TAGTGTGGCTTTTTCAGTCTTTCTGTCTACCTGTAATTTTGTGATTTGGTATGTCACAGGTCA 2133

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Db 2134 TGCATTTAGAAAGATTTTAATGAAGGTGCTTCATTTTCAAATTTTGACTGCAGGCCCATATC 2193

Qy 1297 CTCTAATTATTACAATTATCATGCTCACACITTAATAGTATATTTCTATGTCCTCTTGGCTG 1356

Db 2194 CTCTAATTATTACAATTATCATGCTCACACITTAATAGTATATTTCTATGTCCTCTTGGCTG 2253

Qy 1357 TCTATCTTGATCAAGTCAATCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1416

Db 2254 TCTATCTTGATCAAGTCAATCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 2313

Qy 1417 TGAAGCCTTCATATTGGTCAAAGAGCAAAAGAAATTAATGAGGAGTTATCAGAGGGCAATG 1476

Db 2314 TGAAGCCTTCATATTGGTCAAAGAGTAAAGAAATTAATGAGGAGTTATCAGAGGGCAATG 2373

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Db 2374 TTAATGGAAATATTAGTTTATGTGAATTAATGAGCCAGTTTCTTCAGAAATTTGTAGGAA 2433

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Db 2434 AAGAAGCCATAAGAAATTAAGTGGTATTTCAGAGACATACAGAAAGAGGTGAAAATGTGG 2493

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Db 2614 ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAA 2673

Qy 1777 GAAAAATGATTGGCATTTTGTCCACAGTTAGATATACACTTTTGTATGTTTTGACAGTAGAAG 1836

Db 2674 GAAAAATGATTGGCATTTTGTCCACAGTTAGATATACACTTTTGTATGTTTTGACAGTAGAAG 2733

Qy 1837 AAAATTTTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCAAACAATATATACAAGAAG 1896

Db 2734 AAAATTTTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCAAACAATATATACAAGAAG 2793

Qy 1897 TGCAGAAAGGTTTACTAGATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAAT 1956

Db 2794 TGCAGAAAGGTTTACTAGATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAAT 2853

Qy 1957 TAAAGTGGTGGTCAAAAAAGAAAAGCTGTCAATTAGGAATTTGCTGTTCTTGGGAACCCAAAAGA 2016

Db 2854 TAAAGTGGTGGTCAAAAAAGAAAAGCTGTCAATTAGGAATTTGCTGTTCTTGGGAACCCAAAAGA 2913

Qy 2017 TACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTTGTATGGA 2076

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Db 3094 GTTCTTCAATGTTCCITCAAAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAG 3153

Qy 2257 ACAAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTA 2316

Db 3154 ACAAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTA 3213

Qy 2317 CTTTATTACAACAGAAATGACCCAACTTGTGTATAGCTTGCCCTTCAAGGACATGGACA 2376

Db 3214 CTTTATTACAACAGAAATGACCCAACTTGTGTATAGCTTGCCCTTCAAGGACATGGACA 3273

Qy 2377 AATTTTCAGGTTTGTGTTTCTGCCCTAGACAGTCATTCAAAATTTGGGTGTCTTTCTTATG 2436

Db 3274 AATTTTCAGGTTTGTGTTTCTGCCCTAGACAGTCATTCAAAATTTGGGTGTCTTTCTTATG 3333

Qy 2437 GTGTTTCCATGACGACTTTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAAATG 2496

Db 3334 GTGTTTCCATGACGACTTTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAAATG 3393

Qy 2497 ACCAAGCAGATTATAGTGATTTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT 2556

Db 3394 ACCAAGCAGATTATAGTGATTTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAT 3453

Qy 2557 CTTTGTGATGAAATGGAAACAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGA 2616

Db 3454 CTTTGTGATGAAATGGAAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGA 3513

Qy 2617 GCACCATGAGCCTTTGGAAAAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCT 2676

Db 3514 GCACCATGAGCCTTTGGAAAAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCT 3573

Qy 2677 TGAACCGTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG 2736

Db 3574 TGAACCGTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG 3633

Qy 2737 TTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAAATGCTGTGTTCCCATCAAAC 2796

Db 3634 TTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAAATGCTGTGTTCCCATCAAAC 3693

Qy 2797 TTGTTCCAGACTTATATTTTCTAAAAACCTGGAGACAAACCATATAAATACAAAAAAGTC 2856

Db 3694 TTGTTCCAGACTTATATTTTCTAAAAACCTGGAGACAAACCATATAAATACAAAAAAGTC 3753

Qy 2857 TGCTTCTTCAAAAATTTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTTCAAGCC 2916

Db 3754 TGCTTCTTCAAAAATTTCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTTCAAGCC 3813


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Db 5974 TTCTTTTCACTTAATTTTAACTTTGGTTTAAAAAGTTTTTTTATTTGGAATGGAAGTGGGAA 6033
Qy 5137 GAACCAAGAACGCACCTTGAAATTTTCTAAGCTCCTTAATTTGAAATGCTGTGGTTGTGTG 5196
Db 6034 GAACCAAGAACGCACCTTGAAATTTTCTAAGCTCCTTAATTTGAAATGCTGTGGTTGTGTG 6093
Qy 5197 TTTTGTCTTTCTTTAAATAAAACGATGTATATAATTAAGTGAAGCTGCATGTTTGTATTGA 5256
Db 6094 TTTTGTCTTTCTTTAAATAAAACGATGTATATAATTAAGTGAAGCTGCATGTTTGTATTGA 6153
Qy 5257 AGTATATTGAACATATATAGTTTGTATGTATCATCTTTTTCACCATTCAGAAACAGTCTTCT 5316
Db 6154 AGTATATTGAACATATATAGTTTGTATGTATCATCTTTTTCACCATTCAGAAACAGTCTTCT 6213
Qy 5317 GAATTTGTGATTTAAAGGAATTGPAATAGAAATAGTTTATTTTAAAGTTATCTTTAAAGTT 5376
Db 6214 GAATTTGTGATTTAAAGGAATTGPAATAGAAATAGTTTATTTTAAAGTTATCTTTAAAGTT 6273
Qy 5377 TATGCCATCTTCTTAAATAAGTACGTAATGTTCCAAATCTAAATAAAAAACTAAT 5430
Db 6274 TATGCCATCTTCTTAAATAAGTACGTAATGTTCCAAATCTAAATAAAAAACTAAT 6327

RESULT 3
US-09-971-121-5
; Sequence 5, Application US/09971121
; Patent No. US20020111477A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: No. US20020111477A1 Human Transporter Proteins and Polynucleot
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5262
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-971-121-5

Query Match 85.2%; Score 4664; DB 9; Length 5262;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5014; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 97 AGGTTTATTCAGAAAAACATGTCCTACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 156
Db 238 AGGTTTATTCAGAAAAACATGTCCTACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 297
Qy 157 GAACACTTCTACTGAAGAAATTACTTTAAATTAATGCAGAACCAAAAGAGTAGTGTTCAGG 216
Db 298 GAACACTTCTACTGAAGAAATTACTTTAAATTAATGCAGAACCAAAAGAGTAGTGTTCAGG 357
Qy 217 AAATCTTTTCCACTATTTTTTTTATTTTGGTTAATTAATTAATAGCATGATGCATCCAA 276
Db 358 AAATCTTTTCCACTATTTTTTTTATTTTGGTTAATTAATTAATAGCATGATGCATCCAA 417
Qy 277 ATAAGAAATATGAAGAAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 336
Db 418 ATAAGAAATATGAAGAAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 477
Qy 337 CTAATCTAATCTTGGATATACTCCAGTGACTAATATTACAAGCAGCATCATGCGAAAG 396
Db 478 CTAATCTAATCTTGGATATACTCCAGTGACTAATATTACAAGCAGCATCATGCGAAAG 537
Qy 397 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAA 456
Db 538 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAA 597
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Qy 457 TGTTAAACATCCAGTCTCTCTAAGCGGAGCAAACTTTGTAGTGTGGTTTTTCAAAGACTCCA 516
Db 598 TGTTAAACATCCAGTCTCTCTAAGCGGAGCAAACTTTGTAGTGTGGTTTTTCAAAGACTCCA 657
Qy 517 TGTCCATGAAACTTCGTTTTTTTCTGATATGATCCAGTATCTTCTATTTATATGGATT 576
Db 658 TGTCCATGAAACTTCGTTTTTTTCTGATATGATCCAGTATCTTCTATTTATATGGATT 717
Qy 577 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 636
Db 718 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 777
Qy 637 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA 696
Db 778 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA 837
Qy 697 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATA 756
Db 838 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATA 897
Qy 757 CCTTCCCGGAGGAGTAATTTTAAATATACCTAGTTATAGCAATTTTCACTTTTGGATACT 816
Db 898 CCTTCCCGGAGGAGTAATTTTAAATATACCTAGTTATAGCAATTTTCACTTTTGGATACT 957
Qy 817 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAAAAATTTTAAAGATAA 876
Db 958 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAAAAATTTTAAAGATAA 1017
Qy 877 TGGGACTTCATGATACTGCCCTTTTGGCTTTTCTCTGGGTTCTTCTATATACAAAGTTTAAAT 936
Db 1018 TGGGACTTCATGATACTGCCCTTTTGGCTTTTCTCTGGGTTCTTCTATAWACAAGTTTAAAT 1077
Qy 937 TTCTTATGTCCCTTCTTATGGCAGTCATTCGACAGCTTCTTTGTTATTTCTCCTCAAAGTA 996
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Qy 997 GCAGCATGTGATATTTCTGCTTTTTTCTTTTATGGAATATCATCTGTATTTTGTCTT 1056
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Qy 1057 TAATGCTGACACCTCTTTTAAAAAATCAAAACATGCGGAATAGTTGAATTTTGTGTTA 1116
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Qy 1117 CTGTGGCTTTTGGATTTATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAATCGT 1176
Db 1258 CTGTGGCTTTTGGATTTATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAATCGT 1317
Qy 1177 TAGTGTGGCTTTTTCAGTCCCTTTCTGTCACTGTACTTTTGTGATTTGGTATTCACAGGTCA 1236
Db 1318 TAGTGTGGCTTTTTCAGTCCCTTTCTGTCACTGTACTTTTGTGATTTGGTATTCACAGGTCA 1377
Qy 1237 TGCATTTAGAAGATTTTAAATGAAGTCTTTCATTTTCAAATTTGACTGCAGGCCCATATC 1296
Db 1378 TGCATTTAGAAGATTTTAAATGAAGTCTTTCATTTTCAAATTTGACTGCAGGCCCATATC 1437
Qy 1297 CTCTAATTATTAACAATATCATGCTCACACTTAATAGTATATCTATGTCTCTTGGCTG 1356
Db 1438 CTCTAATTATTAACAATATCATGCTCACACTTAATAGTATATCTATGTCTCTTGGCTG 1497
Qy 1357 TCTATCTTGATCAAGTCATTCAGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1416
Db 1498 TCTATCTTGATCAAGTCATTCAGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1557
Qy 1417 TGAAGCCTTCATATTTGGTCAAAGAGCAAAAGAAATTAAGAGGATTCAGAGGGCAATG 1476
Db 1558 TGAAGCCTTCATATTTGGTCAAAGAGCAAAAGAAATTAAGAGGATTCAGAGGGCAATG 1617
Qy 1477 TTAATGGAAATATAGTTTGTAGTGAATTTATGAGCCAGTTTCTTCAAGAAATTTGTAGGAA 1536
Db 1618 TTAATGGAAATATAGTTTGTAGTGAATTTATGAGCCAGTTTCTTCAAGAAATTTGTAGGAA 1677
Qy 1537 AAGAAGCCATAAGAAATTAGTGGTATTTCAGAAGACATACAGAAAGAGGTGAAAATGTGG 1596
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Db 1678 AAGAACCATAAAGAAATTAGTGGTATTTCAGAAGACATACAGAAAAGAGGGTGAATAATGTGG 1737
Qy 1597 AGGCTTTGAGAAAATTTGTCATTGTGACATATATGAGGGTCAGATTACTGCCTTACTTTGGCC 1656
Db 1738 AGGCTTTGAGAAAATTTGTCATTGTGACATATATGAGGGTCAGATTACTGCCTTACTTTGGCC 1797
Qy 1657 ACAGTGGAAACAGGAAGAGTACATTGATGAATATTCTTTGTGGACTCTGCCACCTTCTG 1716
Db 1798 ACAGTGGAAACAGGAAGAGTACATTGATGAATATTCTTTGTGGACTCTGCCACCTTCTG 1857
Qy 1717 ATGGGTTTGCATCTATATATGGAACACAGAGTCTCAGAAAATAGATGAAATGTTTGAAGCAA 1776
Db 1858 ATGGGTTTGCATCTATATATGGAACACAGAGTCTCAGAAAATAGATGAAATGTTTGAAGCAA 1917
Qy 1777 GAAAATGATTGGCAATTTGTCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAG 1836
Db 1918 GAAAATGATTGGCAATTTGTCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAG 1977
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Db 1978 AAAATTTATCAATTTTGGCTTTCAATCAAAGGGATACCAGCCCAACAATATATATACAAGAAG 2037
Qy 1897 TGCAGAAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAAT 1956
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Qy 1957 TAAGTGGTGGTCAAAAAAGAAAGCTGTCAATTAGGAATGCTGTTCTTGGGAACCCAAAGA 2016
Db 2098 TAAGTGGTGGTCAAAAAAGAAAGCTGTCAATTAGGAATGCTGTTCTTGGGAACCCAAAGA 2157
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Qy 2077 ATCTTTTAAAAATACAGAAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG 2136
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Qy 2197 GTTCTTCAATGTTCTCCTCAAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAG 2256
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Qy 2377 AATTTTCAGGTTTGTGTTCTGCCCTAGACAGTCAATTCAAAATTTGGGTGTCATTTCTTATG 2436
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QY 4498 GAATAACACATGCACCTTGATTTTAAAGAACATCTTCAGAGACCTGTAAGAAACTACCTG 4557
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Db |||

RESULT 4
US-09-971-121-1
; Sequence 1, Application US/09971121
; Patent No. US20020111477A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: No. US20020111477A1 Human Transporter Proteins and Polynucleot
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4929
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-971-121-1

Query Match 83.5%; Score 4572; DB 9; Length 4929;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4922; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 61 AATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGAAAATTTCTTTTCCACTA 120
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QY 294 GTGCCTAATATAGAACTCAATCCCTATGGACAAGTTTACTCTTTCTTAATCTAATTTCTTGA 353
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QY 181 GTGCCTAATATAGAACTCAATCCCTATGGACAAGTTTACTCTTTCTTAATCTAATTTCTTGA 240
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QY 354 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 413
Db |||
QY 241 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 300
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QY 414 CCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAAGAAATGTTAACATCCAGTCTC 473
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QY 301 CCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAAGAAATGTTAACATCCAGTCTC 360
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QY 474 TCTAAGCCGAGCAACTTTGTAGTGTGGTTTTTCAAAGACTCCATGTCCTATGAACTTCTG 533
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RESULT 5
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; Sequence 3, Application US/09971121
; Patent No. US20020111477A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: No. US20020111477A1 Human Transporter Proteins and Polynucleotides
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4785
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-971-121-3

Query Match      80.5%; Score 4408; DB 9; Length 4785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4758; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 114 ATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 173
Db 1 ATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 60

QY 174 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCACTA 233
Db 61 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCACTA 120

QY 234 TTTTCTTATTTTGGTTAATTAATTAGCATGTGCATCCAAATAAGAAATATGAAGAA 293
Db 121 TTTTCTTATTTTGGTTAATTAATTAGCATGTGCATCCAAATAAGAAATATGAAGAA 180

QY 294 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTGGGA 353
Db 181 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTGGGA 240

QY 354 TATACTCCAGTGACTAATATTAACAAGCAGCATCATGCAGAAAGTGCTACTGATCATCTA 413
Db 241 TATACTCCAGTGACTAATATTAACAAGCAGCATCATGCAGAAAGTGCTACTGATCATCTA 300

QY 414 CCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC 473
Db 301 CCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC 360

QY 474 TCTAAGCCGAGCAACTTTTGTAGGTGTGGTTTTTCAAAGACTCCCATGTCTCATGAACCTTCGT 533
Db 361 TCTAAGCCGAGCAACTTTTGTAGGTGTGGTTTTTCAAAGACTCCCATGTCTCATGAACCTTCGT 420

QY 534 TTTTCTTCTGATGATGATCCAGTATCTTCTATTTATATGATTCAAGAGCTGGCTGTTCA 593
Db 421 TTTTCTTCTGATGATGATCCAGTATCTTCTATTTATATGATTCAAGAGCTGGCTGTTCA 480
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QY 594 AAATCATGTGAGGCTGCTCAGTACTGCTCAGGTTCTCAGGTTTTCACAGTTTTCACAGCATCCATA 653
Db 481 AAATCATGTGAGGCTGCTCAGTACTGCTCAGGTTCTCAGGTTTTCACAGTTTTCACAGCATCCATA 540
QY 654 GATGCTGCCATTATACAGTTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 713
Db 541 GATGCTGCCATTATACAGTTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 600
QY 714 AAAGCTGTTTATATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGGAGGAGTA 773
Db 601 AAAGCTGTTTATATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGGAGGAGTA 660
QY 774 ATTTTAATATACCTAGTTATAGCATTTTACCTTTTGGATACCTTTTGGCAATTCATATC 833
Db 661 ATTTTAATATACCTAGTTATAGCATTTTACCTTTTGGATACCTTTTGGCAATTCATATC 720
QY 834 GTAGCAAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT 893
Db 721 GTAGCAAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT 780
QY 894 GCCTTTTGGCTTTTCCCTGGTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTT 953
Db 781 GCCTTTTGGCTTTTCCCTGGTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTT 840
QY 954 ATGCAGTCATTCGACAGCTTCTTGTATTTTCTCAAGTAGCAGCATTTGTGATATTT 1013
Db 841 ATGCAGTCATTCGACAGCTTCTTGTATTTTCTCAAGTAGCAGCATTTGTGATATTT 900
QY 1014 CTGCTTTTCTTCTTATGGAATATCATCTGTATTTTGTCTTAAATGCTGACACCTCTT 1073
Db 901 CTGCTTTTCTTCTTATGGAATATCATCTGTATTTTGTCTTAAATGCTGACACCTCTT 960
QY 1074 TTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTGTACTGTGGCTTTTGGATTT 1133
Db 961 TTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTGTACTGTGGCTTTTGGATTT 1020
QY 1134 ATTCGCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCACT 1193
Db 1021 ATTCGCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCACT 1080
QY 1194 CTTTCTGTCTCAGTGTACTTTTGTGATTGTTGATTTGCACAGGTCATGCATTTAGAAATTTT 1253
Db 1081 CTTTCTGTCTCAGTGTACTTTTGTGATTGTTGATTTGCACAGGTCATGCATTTAGAAATTTT 1140
QY 1254 AATGAAGGTGCTTTCATTTTCAAAATTTGACTGCAGSCCATATCCTCTAATTTATACAAT 1313
Db 1141 AATGAAGGTGCTTTCATTTTCAAAATTTGACTGCAGSCCATATCCTCTAATTTATACAAT 1200
QY 1314 ATCATGCTCACACTTAATAGTATATTTCTATGTCCTTGGCTGTCTATCTTGTCAAGTC 1373
Db 1201 ATCATGCTCACACTTAATAGTATATTTCTATGTCCTTGGCTGTCTATCTTGTCAAGTC 1260
QY 1374 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATATTTTCTGAAGCCTTCATATTGG 1433
Db 1261 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATATTTTCTGAAGCCTTCATATTGG 1320
QY 1434 TCAAAGAGCAAAAGAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAATATATTAGT 1493
Db 1321 TCAAAGAGCAAAAGAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAATATATTAGT 1380
QY 1494 TTTAGTGAAATTTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAACCAATAAGAAAT 1553
Db 1381 TTTAGTGAAATTTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAACCAATAAGAAAT 1440
QY 1554 AGTGGTATTCAGAAGACATACAGAAAGAGGGTGAAATGTGGAGGCTTTGAGAAATTTG 1613
Db 1441 AGTGGTATTCAGAAGACATACAGAAAGAGGGTGAAATGTGGAGGCTTTGAGAAATTTG 1500
QY 1614 TCATTTGACATATATGAGGTCAGATTACTGCTTACTCTTGGCCACAGTGGAAACAGGAAAG 1673
Db 1501 TCATTTGACATATATGAGGTCAGATTACTGCTTACTCTTGGCCACAGTGGAAACAGGAAAG 1560
QY 1674 AGTACATTGATGAATATCTTTTGTGGACTCTGCCCCACCCTTCTGTATGGGTTTGCATCTATA 1733
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Db 1561 ||||| AGTACATTGATGAATATTTCTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATA 1620
Qy 1734 TATGCACACAGAGTCTCAGAAATAGATGAAATGTTGAAGCAAGAAATGATTTGGCATT 1793
Db 1621 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTGAAGCAAGAAATGATTTGGCATT 1680
Qy 1794 TGTCCACAGTTAGATATACACTTTTGATGTTTTGACAGTAGAAGAAATTTATCAATTTTG 1853
Db 1681 TGTCCACAGTTAGATATACACTTTTGATGTTTTGACAGTAGAAGAAATTTATCAATTTTG 1740
Qy 1854 GCTTCAATCAAAGGGATACAGCCCAACAATATAATACAAGAAATTAAGTGGTGGTCAAAAA 1913
Db 1741 GCTTCAATCAAAGGGATACAGCCCAACAATATAATACAAGAAATTAAGTGGTGGTCAAAAA 1800
Qy 1914 GATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 1973
Db 1741 GCTTCAATCAAAGGGATACAGCCCAACAATATAATACAAGAAATTAAGTGGTGGTCAAAAA 1800
Qy 1914 GATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 1973
Db 1801 GATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 1860
Qy 1974 AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 2033
Db 1861 AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 1920
Qy 2034 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTTGATGGAATCTTTAAAAATACAGA 2093
Db 1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTTGATGGAATCTTTAAAAATACAGA 1980
Qy 2094 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTCAATTCATGGATGAAGTGACATTTCTTGCA 2153
Db 1981 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTCAATTCATGGATGAAGTGACATTTCTTGCA 2040
Qy 2154 GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGGTCTTCAATGTTCCCTC 2213
Db 2041 GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGGTCTTCAATGTTCCCTC 2100
Qy 2214 AAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTTGTGCCACA 2273
Db 2101 AAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTTGTGCCACA 2160
Qy 2274 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAAACAGAAT 2333
Db 2161 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAAACAGAAT 2220
Qy 2334 GACCAACAACTTGTGTATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAGGTTTGT 2393
Db 2221 GACCAACAACTTGTGTATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAGGTTTGT 2280
Qy 2394 TCTGCCCTAGACAGICATTCAAATTTGGGTGTCATTTCTTATGGTGTTCATGACGACT 2453
Db 2281 TCTGCCCTAGACAGICANTCAAATTTGGGTGGCATTTCTTATGGGTTTCCATGACGACT 2340
Qy 2454 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTATAGT 2513
Db 2341 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTATAGT 2400
Qy 2514 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTATGAAATGGAA 2573
Db 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTATGAAATGGAA 2460
Qy 2574 CAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 2633
Db 2461 CAGAGCTTACTTATTTCTGAAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTGG 2520
Qy 2634 AAAACAACAGATGTAFACAATAGCAAAAGTTTCATTTCTTTACCTTGAAACCGTGAAAGTAAA 2693
Db 2521 AAAACAACAGATGTAFACAATAGCAAAAGTTTCATTTCTTTACCTTGAAACCGTGAAAGTAAA 2580
Qy 2694 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2753
Db 2581 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2640
Qy 2754 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACCTGTTCCAGACTTATAT 2813

Db 2641 TTGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCTCATCAAACTTGTTCAGACTTATAT 2700
Qy 2814 TTTCTAAAAACCTGGAGACAAACCACATATAAATACAAAAAAGTCTGCTTCTTCAAATTTCT 2873
Db 2701 TTTCTAAAAACCTGGAGACAAACCACATATAAATACAAAAAAGTCTGCTTCTTCAAATTTCT 2760
Qy 2874 GCTGACTCAGATATCAGTGTATCTTATTAGCTTTTTTCAAGCCAGAACATAATGGTGACG 2933
Db 2761 GCTGACTCAGATATCAGTGTATCTTATTAGCTTTTTTCAAGCCAGAACATAATGGTGACG 2820
Qy 2934 ATGATTAATGACAGTGTATGATCCGTGGCTCCCCATAGTGGGCTTTAAATGTGATG 2993
Db 2821 ATGATTAATGACAGTGTATGATCCGTGGCTCCCCATAGTGGGCTTTAAATGTGRTG 2880
Qy 2994 CATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTTATTCTTTA 3053
Db 2881 CATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTTCAACAGTACTATGGTTTTATTCTTTA 2940
Qy 3054 CCTATATTAGTGAATATCATTAGTAACACTACTATCTTTTATCATTTAAATGTGACTGAAACC 3113
Db 2941 CCTATATTAGTGAATATCATTAGTAACACTACTATCTTTTATCATTTAAATGTGACTGAAACC 3000
Qy 3114 ATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATTAATGATATAGTTTTTAAATTTGAG 3173
Db 3001 ATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATTAATGATATAGTTTTTAAATTTGAG 3060
Qy 3174 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCAATGTTACTGCAATGCCACCTTACTTTGCC 3233
Db 3061 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCAATGTTACTGCAATGCCACCTTACTTTGCC 3120
Qy 3234 ATGGAAAAATGCAGAGAAATCAATAAGATCAAAGCTTATTACTCAACTTAAACCTTTCAGGTCTT 3293
Db 3121 ATGGAAAAATGCAGAGAAATCAATAAGATCAAAGCTTAYACTCAACTTAAACCTTTCAGGTCTT 3180
Qy 3294 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTT 3353
Db 3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTT 3240
Qy 3354 CTTATTTTGATGCTAGGAAGCTTATTGGCATTTCAATTTATGGATTATATTTTATACTGTA 3413
Db 3241 CTTATTTTGATGCTAGGAAGCTTATTGGCATTTCAATTTATGGATTATATTTTATACTGTA 3300
Qy 3414 AAGTTCTTGTGCTGGTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCGTTCACT 3473
Db 3301 AAGTTCTTGTGCTGGTTTTTGCCTTATTGGTTATGTTCCATCAGTTATTCGTTCACT 3360
Qy 3474 TATATTGCTTCTTTCACTTTAAGAAAAATTTTAAATACCAAGAAATTTTGGTCATTTATC 3533
Db 3361 TATATTGCTTCTTTCACTTTAAGAAAAATTTTAAATACCAAGAAATTTTGGTCATTTATC 3420
Qy 3534 TATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTTCTTTATGGGATAC 3593
Db 3421 TATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTTCTTTATGGGATAC 3480
Qy 3594 ACAATTGCAACTATTCTTTCATTAATGCTTTTGTATCATCATTTCCATCTATCCACTTCTA 3653
Db 3481 ACAATTGCAACTATTCTTTCATTAATGCTTTTGTATCATCATTTCCATCTATCCACTTCTA 3540
Qy 3654 GGTGGCCTGATTTCTTTCATAAAGATTTTCTTGGAAAGAAATGTACGAAAAAATGTGGACACC 3713
Db 3541 GGTGGCCTGATTTCTTTCATAAAGATTTTCTTGGAAAGAAATGTACGAAAAAATGTGGACACC 3600
Qy 3714 TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCCTTACCTGCAAGTGTGACTG 3773
Db 3601 TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCCTTACCTGCAAGTGTGACTG 3660
Qy 3774 TGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGAT 3833
Db 3661 TGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGAT 3720
Qy 3834 CCCTTTTTCAGAAACCTTTTCAACGAAGTCTTAAATAATAGGAAGCTTCCAGAACCCAGAC 3893
Db 3721 CCCTTTTTCAGAAACCTTTTCAACGAAGTCTTAAATAATAGGAAGCTTCCAGAACCCAGAC 3780

QY 721 TTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAATTTTAA 780
Db 721 TTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAATTTTAA 780
QY 781 TATACCTAGTTATAGCATTTTCACTTTTGGATACCTTTTGGCAATTCATATCGTAGCAG 840
Db 781 TATACCTAGTTATAGCATTTTCACTTTTGGATACCTTTTGGCAATTCATATCGTAGCAG 840
QY 841 AAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACCTCTTTT 900
Db 841 AAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACCTCTTTT 900
QY 901 GGCCTTCCTGGGTTCTTCTATATACAAGTTTAAATTTTCTTATGTCCCTTCTTATGGCAG 960
Db 901 GGCCTTCCTGGGTTCTTCTATATACAAGTTTAAATTTTCTTATGTCCCTTCTTATGGCAG 960
QY 961 TCATTGGGACAGCTTCTTTTGTATTTCCTCAAAGTAGCAGCATTTGTGATATTCTGCTTT 1020
Db 961 TCATTGGGACAGCTTCTTTTGTATTTCCTCAAAGTAGCAGCATTTGTGATATTCTGCTTT 1020
QY 1021 TTTTTCCTTTATGGATTATCATCTGTATTTTTTCCTCAAAGTAGCAGCATTTGTGATATTCTGCTTT 1080
Db 1021 TTTTTCCTTTATGGATTATCATCTGTATTTTTTCCTCAAAGTAGCAGCATTTGTGATATTCTGCTTT 1080
QY 1081 AATCAAAACATGTGGGAATAGTTGAAATTTTGTGTTACTGTGGCTTTTGGATTTATTTGGCC 1140
Db 1081 AATCAAAACATGTGGGAATAGTTGAAATTTTGTGTTACTGTGGCTTTTGGATTTATTTGGCC 1140
QY 1141 TTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCTTTCT 1200
Db 1141 TTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCTTTCT 1200
QY 1201 GTCAGTGTACTTTTGTGATTGGTATTGACAGGTCATGCATTTAGAAAGATTTAATGAAG 1260
Db 1201 GTCAGTGTACTTTTGTGATTGGTATTGACAGGTCATGCATTTAGAAAGATTTAATGAAG 1260
QY 1261 GTGCTTCATTTTCAAATTTGACTGCAGGCCCAATATCCTCTAATTTATACAAATATCATGC 1320
Db 1261 GTGCTTCATTTTCAAATTTGACTGCAGGCCCAATATCCTCTAATTTATACAAATATCATGC 1320
QY 1321 TCACACTTAATAGTATATTCTATGTCTCTTGGCTGTCTATCTTGATCAAGTCATTCAG 1380
Db 1321 TCACACTTAATAGTATATTCTATGTCTCTTGGCTGTCTATCTTGATCAAGTCATTCAG 1380
QY 1381 GGGAAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTTGGTCAAAGA 1440
Db 1381 GGGAAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTTGGTCAAAGA 1440
QY 1441 GCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATTTAATGGAAATATTAGTTTAGTG 1500
Db 1441 GCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATTTAATGGAAATATTAGTTTAGTG 1500
QY 1501 AAATTATTGAGCCAGTTTCTCAGAAATTTGTAGGAAAGAGCCATAAGAAATTAGTGGTA 1560
Db 1501 AAATTATTGAGCCAGTTTCTCAGAAATTTGTAGGAAAGAGCCATAAGAAATTAGTGGTA 1560
QY 1561 TTCAGAAGACATACAGAAAGAGGGTGAAAATGTGGAGGCTTTGAGAAATTTGTCAATTTG 1620
Db 1561 TTCAGAAGACATACAGAAAGAGGGTGAAAATGTGGAGGCTTTGAGAAATTTGTCAATTTG 1620
QY 1621 ACATATATGAGGGTCAGATTACTGCCCTTACTTGGCCAAGAGAGAGTACAT 1680
Db 1621 ACATATATGAGGGTCAGATTACTGCCCTTACTTGGCCAAGAGAGAGTACAT 1680
QY 1681 TGATGAATATTCTTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATATATGGAC 1740
Db 1681 TGATGAATATTCTTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATATATGGAC 1740
QY 1741 ACAGAGTCTCAGAAATAGATGAAATGTTGAAGCAAGAAAAATGATTGGCAATTTGTCCAC 1800
Db 1741 ACAGAGTCTCAGAAATAGATGAAATGTTGAAGCAAGAAAAATGATTGGCAATTTGTCCAC 1800
QY 1801 AGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAA 1860

RESULT 7

Db 1801 AGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAA 1860
QY 1861 TCAAAGGGATACCAGCCCAACAATAATAACAAGAAGTGCAGAAGTTTACTAGATTAG 1920
Db 1861 TCAAAGGGATACCAGCCCAACAATAATAACAAGAAGTGCAGAAGTTTACTAGATTAG 1920
QY 1921 ACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTCAAAAAAGAAAGC 1980
Db 1921 ACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTCAAAAAAGAAAGC 1980
QY 1981 TGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAACCAACAG 2040
Db 1981 TGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAACCAACAG 2040
QY 2041 CTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAAAGCCA 2100
Db 2041 CTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAAAGCCA 2100
QY 2101 ATCGGTGACAGTGTTCAGTACTCATTTTATGGATGAAGCTGACATTTCTTGCAGATAGGA 2160
Db 2101 ATCGGTGACAGTGTTCAGTACTCATTTTATGGATGAAGCTGACATTTCTTGCAGATAGGA 2160
QY 2161 AAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGGTCTTCAATGTTCTCAAAAAGTA 2220
Db 2161 AAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGGTCTTCAATGTTCTCAAAAAGTA 2220
QY 2221 AATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACAGAAATCTC 2280
Db 2221 AATGGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACAGAAATCTC 2280
QY 2281 TTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAATGACCAAC 2340
Db 2281 TTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAATGACCAAC 2340
QY 2341 AACTTGTGTATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAAGTTTGTCTGCCC 2400
Db 2341 AACTTGTGTATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAAGTTTGTCTGCCC 2400
QY 2401 TAGACAGTCATTCAAATTTGGGTGTCAATTTCTTATGGTGTCTTCCATGACGACTTTGGAAG 2460
Db 2401 TAGACAGTCATTCAAATTTGGGTGTCAATTTCTTATGGTGTCTTCCATGACGACTTTGGAAG 2460
QY 2461 ACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTCACCAAGCAGATTATAGTGTATTTA 2520
Db 2461 ACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTCACCAAGCAGATTATAGTGTATTTA 2520
QY 2521 CTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTATGAAATGGAACAGAGCT 2580
Db 2521 CTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTATGAAATGGAACAGAGCT 2580
QY 2581 TACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTTGGAAACAAC 2640
Db 2581 TACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTTGGAAACAAC 2640
QY 2641 AGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAACCGTGAAGTAAATCAGTGA 2700
Db 2641 AGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAACCGTGAAGTAAATCAGTGA 2700
QY 2701 GATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTTGGTTC 2760
Db 2701 GATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTTGGTTC 2760
QY 2761 ATCACTCTTTTAAAAATGCTGTGGTTCCTCATCAAACTGTTCCAGACTTATATTTCTAA 2820
Db 2761 ATCACTCTTTTAAAAATGCTGTGGTTCCTCATCAAACTGTTCCAGACTTATATTTCTAA 2820
QY 2821 AACCTGGAGACAAACCACATAAATACAAAACAAGTCTGCTTCTTCAAAATTTCTGCTG 2877
Db 2821 AACCTGGAGACAAACCACATAAATACAAAACAAGTCTGCTTCTTCAAAATTTCTGCTG 2877

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US-10-094-749-984
; Sequence 984, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 984
; LENGTH: 3268
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-984

Query Match      50.0%; Score 2739; DB 15; Length 3268;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3039; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2386 GTTTGTTTCTGCCCTAGACAGTCATTCAAATTTGGGTGTCAATTTCTTATGGTGTTCCTCA 2445
Db 220 GTTTGTTTCTGCCCTAGACAGTCATTCAAATTTGGGTGTCAATTTCTTATGGTGTTCCTCA 279

QY 2446 TGACGACTTTGGAAGACGTAATTTTAAAGCTAGAAGTTGAAGCAGAAATGACCAAGCAG 2505
Db 280 TGACGACTTTGGAAGACGTAATTTTAAAGCTAGAAGTTGAAGCAGAAATGACCAAGCAG 339

QY 2506 ATTATAGTGATTTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATG 2565
Db 340 ATTATAGTGATTTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATG 399

QY 2566 AAATGGAACAGAGCTTACTTAATCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGA 2625
Db 400 AAATGGAACAGAGCTTACTTAATCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGA 459

QY 2626 GCCTTTGGAAACAACAGATGTATACAAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGTG 2685
Db 460 GCCTTTGGAAACAACAGATGTATACAAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGTG 519

QY 2686 AAAGTAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTT 2745
Db 520 AAAGTAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTT 579

QY 2746 TTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCTCCATCAAACTGTTCCAG 2805
Db 580 TTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCTCCATCAAACTGTTCCAG 639

QY 2806 ACTTATATTTTCTAAACCTGGAGACAAACACATATAAATACAAACAAAGTCTGCTTCTTC 2865
Db 640 ACTTATATTTTCTAAACCTGGAGACAAACACATATAAATACAAACAAAGTCTGCTTCTTC 699
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QY 2866 AAAATTCTGCTGACTCAGATATCAGTGATCTTTATTAGCTTTTTCACAAGCCAGACATAA 2925
Db 700 AAAATTCTGCTGACTCAGATATCAGTGATCTTTATTAGCTTTTTCACAAGCCAGACATAA 759

QY 2926 TGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTCCGGCTTTAA 2985
Db 760 TGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTCCGGCTTTAA 819

QY 2986 ATGTGATGCATTCAGAAAAGGACTATGTTTTTGGCAGCTGTTTTCAACAGTACTATGTTTT 3045
Db 820 ATGTGATGCATTCAGAAAAGGACTATGTTTTTGGCAGCTGTTTTCAACAGTACTATGTTTT 879

QY 3046 ATTCTTTACCTATATTAGTGAATATCATTAGTAACCTACTATCTTTTATCATTTAAATGTGA 3105
Db 880 ATTCTTTACCTATATTAGTGAATATCATTAGTAACCTACTATCTTTTATCATTTAAATGTGA 939

QY 3106 CTGAAACCATCCAGATCTGGAGTACCCCATTTCTTTCAAGAAATTAAGTATAGTTTTTA 3165
Db 940 CTGAAACCATCCAGATCTGGAGTACCCCATTTCTTTCAAGAAATTAAGTATAGTTTTTA 999

QY 3166 AAATGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAATGCCACCTT 3225
Db 1000 AAATGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAATGCCACCTT 1059

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QY 3346 TTATCATTTCTTATTTTGTGCTAGGAAGCTTTATTGGCATTTTCATTATGGATTATATTTT 3405
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QY 3526 CATTTATCTATTCTGTGCGACGTTGGCTTGATTGCAATCACTGAAATAAATCTTCTTTA 3585
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QY 4066 ACATCTCTTTCTGTGTGAAAAGGAGAGATCTTAGGACTATTTGGTCCAAATGGTGTCTG 4125
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Db 2920 ACTTAATTTTAACTTTGGTTTAAAAAGTTTTTTTATTGGAAATGGTAACTGGAGAACCAAGA 2979
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RESULT 8
US-10-090-458-3
; Sequence 3, Application US/10090458
; Publication No. US20020123107A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Killinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090,458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4917
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2775, 2776
; OTHER INFORMATION: n = A,T,C or G
US-10-090-458-3

Query Match 49.6%; Score 2713; DB 13; Length 4917;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2763; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 174 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA 233
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QY 294 GTGCCTAATATAGAACTCAATCCATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGA 353
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QY 354 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 413

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QY 414 CCTGATGTCATAAATTACTGAAGAATAATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC 473
Db 301 CCTGATGTCATAAATTACTGAAGAATAATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC 360
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QY 594 AAATCATGTGAGGCTGCTCAGTACTGGTCCCTCAGGTTTACAGTTTTCACAGTTTTCACATCCATA 653
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QY 654 GATGCTGCCATTATACAGTTGAAGCAACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 713
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QY 714 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCGGAGGAGTA 773
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QY 1254 AATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATATTACAATTT 1313
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QY 1374 ATTCCAGGGGAATTTGGCTTACGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1433
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QY 1434 TCAAAGAGCAAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAATATTAGT 1493

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QY 1854 GCTTCAATCAAAGGGATACCAGCCCAACAATATATAAACAAGAGTGACAGAAAGGTTTACTA 1913
Db 1741 GCTTCAATCAAAGGGATACCAGCCCAACAATATATAAACAAGAGTGACAGAAAGGTTTACTA 1800
QY 1914 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 1973
Db 1801 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 1860
QY 1974 AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGBACCCAAAGATACTGCTGCTAGATGAA 2033
Db 1861 AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGBACCCAAAGATACTGCTGCTAGATGAA 1920
QY 2034 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA 2093
Db 1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA 1980
QY 2094 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTTGCA 2153
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QY	2574	CAGAGCTTACTTATCTCTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG	2633
Db	2461		
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Db	2521	AAACAACAGATGTATACAAATAGCAAAAGTTTCAATTTCTTTACCTTGAAACGTAAGTAAA	2580
QY	2694	TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT	2753
Db	2581	TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT	2640
QY	2754	TTGGTTTCATCACTCTTTTAAATAGCTGTGGTTCCCATCAAACTTGTTCAGACTTATAT	2813
Db	2641	TTGGTTTCATCACTCTTTTAAATAGCTGTGGTTCCCATCAAACTTGTTCAGACTTATAT	2700
QY	2814	TTTCTAAAACCTGGAGACAAACACATATAATACAAAACAAGTCTGCTTCTTCAAAATCT	2873
Db	2701	TTTCTAAAACCTGGAGACAAACACATATAATACAAAACAAGTCTGCTTCTTCAAAATCT	2760
QY	2874	GCTG 2877	
Db	2761	GCTG 2764	
RESULT 9			
US-10-108-260A-160			
; Sequence 160, Application US/10108260A			
; Publication No. US20040005560A1			
; GENERAL INFORMATION:			
; APPLICANT: HELIX RESEARCH INSTITUTE			
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA			
; FILE REFERENCE: H1-A0106			
; CURRENT APPLICATION NUMBER: US/10/108,260A			
; CURRENT FILING DATE: 2002-03-27			
; NUMBER OF SEQ ID NOS: 5458			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 160			
; LENGTH: 3347			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-108-260A-160			
Query Match 36.4%; Score 1991; DB 15; Length 3347;			
Best Local Similarity 99.9%; Pred. No. 0;			
Matches 2141; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
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QY	3347	TATCATCTTATTTTGAGCTAGGAAGCTTATTGGCAATTCATTTATGGATTATTTTA	3406
Db	1231	TATCATCTTATTTTGAGCTAGGAAGCTTACTGGCAATTCATTTATGGATTATTTTA	1290
QY	3407	TACTGTAAAGTTCCTTGTGCTGCTTTTTCCTTATTGGTTATGTTCCATCAGTTATCT	3466
Db	1291	TACTGTAAAGTTCCTTGTGCTGCTTTTTCCTTATTGGTTATGTTCCATCAGTTATCT	1350
QY	3467	GTTCACTTATATGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAAAGAAATTTGGTC	3526
Db	1351	GTTCACTTATATGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAAAGAAATTTGGTC	1410
QY	3527	ATTTATCTATCTGTGGCAGCGTTGGCTGTATTGCAATCACTGAAATACCTTTCTTTAT	3586
Db	1411	ATTTATCTATCTGTGGCAGCGTTGGCTGTATTGCAATCACTGAAATACCTTTCTTTAT	1470
QY	3587	GGGATACACAATTCGAATATCTTTCATTTATGCCCTTTTGTATCATCATTCCTCAATCC	3646
Db	1471	GGGATACACAATTCGAATATCTTTCATTTATGCCCTTTTGTATCATCATTCCTCAATCC	1530
QY	3647	ACTTCTAGTTGCCCTGATTTCTTTCATAAAGATTTCTTGGAGAAGTGTACGAAAAATGT	3706

Db	1531	ACCTTCTAGGTTGCCTGATTTCTTTTATAAAAAATTTCTTGGAGAATGTACGAAAAATGT	1590
QY	3707	GGACACCTATAATCCATGGGATAGGCTTTTCACTAGTAGCTGTATATCGCCTTACCTGCACTG	3766
Db	1591	GGACACCTATAATCCATGGGATAGGCTTTTCACTAGTAGCTGTATATCGCCTTACCTGCACTG	1650
QY	3767	TGTACTGTGGATTTTCCCTTTACAAATACTATGAGAAAAAATATGGAGGCAGATCAATAAG	3826
Db	1651	TGTACTGTGGATTTTCCCTTTACAAATACTATGAGAAAAAATATGGAGGCAGATCAATAAG	1710
QY	3827	AAAAAGATCCCTTTTTCAGAAAACTTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACC	3886
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Db	1771	ACCAGACAATGAGGATGAAGATGAAGATGTCAAAAGCTGAAAGACTAAAGGTCAAAAGAGCT	1830
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Db	1831	GATGGGTTGCCAGTGTGTGAGGAGAAAAACCATCCATTATGGTTCAGCAATTTGCATAAAGA	1890
QY	4007	ATATGATGACAAAGAAAGATTTTCTTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATA	4066
Db	1891	ATATGATGACAAAGAAAGATTTTCTTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATA	1950
QY	4067	CATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGG	4126
Db	1951	CATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGG	2010
QY	4127	CAAAAGCACAAATTATTAAATATTCTGTTGGTGATATTGAACCAACTTCAGGCCAGGTATT	4186
Db	2011	CAAAAGCACAAATTATTAAATATTCTGTTGGTGATATTGAACCAACTTCAGGCCAGGTATT	2070
QY	4187	TTTAGGAGATTTATCTTCAGAGACAAGTGAAGATGATGATCTCACTGAAGTGATGGTTA	4246
Db	2071	TTTAGGAGATTTATCTTCAGAGACAAGTGAAGATGATGATCTCACTGAAGTGATGGTTA	2130
QY	4247	CTGTCTCTCAGATAAAACCCCTTTTGTGCCCAGATACTACATTCAGGAAACATTTTGAAATTTA	4306
Db	2131	CTGTCTCTCAGATAAAACCCCTTTTGTGCCCAGATACTACATTCAGGAAACATTTTGAAATTTA	2190
QY	4307	TGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAAGAGTCAATAAGTCAATAACACA	4366
Db	2191	TGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAAGAGTCAATAAGTCAATAACACA	2250
QY	4367	TGCACCTGATTTAAAGAAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAA	4426
Db	2251	TGCACCTGATTTAAAGAAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAA	2310
QY	4427	ACGAAAGTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTAATTTGCTAGATGA	4486
Db	2311	ACGAAAGTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTAATTTGCTAGATGA	2370
QY	4487	ACCATCTACAGGTATGGATCCCAAGCCCAACAGCACATGTGGCGAGCAATTCGAACCTGC	4546
Db	2371	ACCATCTACAGGTATGGATCCCAAGCCCAACAGCACATGTGGCGAGCAATTCGAACCTGC	2430
QY	4547	ATTTAAAAACAGAAAAGCGGGTCTGCTATTCTGACCACCTACTATATGGAGGAGGAGGC	4606
Db	2431	ATTTAAAAACAGAAAAGCGGGTCTGCTATTCTGACCACCTACTATATGGAGGAGGAGGC	2490
QY	4607	TGCTCTGATCGAGTAGCTATCATATGGTGTCTGGGAGTTAAGATGTATCGGAACAGTACA	4666
Db	2491	TGCTCTGATCGAGTAGCTATCATATGGTGTCTGGGAGTTAAGATGTATCGGAACAGTACA	2550
QY	4667	ACATCTAAAGAGTAAATTTTGGAAAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGAT	4726
Db	2551	ACATCTAAAGAGTAAATTTTGGAAAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGAT	2610
QY	4727	AGAAAAACCTAGAAAGTAGACCGCTTCAAAAGAGAAATTCAGTATATTTTCCCAATGCAAG	4786

Db 2611 AGAAACCTAGAAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCAAATGCAAG 2670
QY 4787 CCGTCAGGAAAGTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTC 4846
Db 2671 CCGTCAGGAAAGTTTTCTTCTATTTTGGCTCATATAAATTCCTAAGGAAGATGTTTCAGTC 2730
QY 4847 CCTTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAATA 4906
Db 2731 CCTTTCACAATCTTTTTTAAGCTGGAAGAAGCTAAACATGCTTTTGCCATTGAAGAATA 2790
QY 4907 TAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCACAATAAGAACCAAGAGGA 4966
Db 2791 TAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCACAATAAGAACCAAGAGGA 2850
QY 4967 GGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAACACAAGAAGA 5026
Db 2851 GGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAACACAAGAAGA 2910
QY 5027 TAGAGTAGTATTTTGAATTTGTATTTGTCGGTCTGCTTACTGGGACTTCTTTCTTTTCA 5086
Db 2911 TAGAGTAGTATTTTGAATTTGTATTTGTCGGTCTGCTTACTGGGACTTCTTTCTTTTCA 2970
QY 5087 CTTAATTTTAACTTTTGGTTTAAAAAGTTTTTTTATTTGGAATGGTAACTGGGAACCAAGAA 5146
Db 2971 CTTAATTTTAACTTTTGGTTTAAAAAGTTTTTTTATTTGGAATGGTAACTGGGAACCAAGAA 3030
QY 5147 CGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTGTTTGTCTTTT 5206
Db 3031 CGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTGTTTGTCTTTT 3090
QY 5207 CTTTAAATAAAACGATGATATAAATTAAGTGAAGCTGATGTTTGTATTTGAAGTATATTGA 5266
Db 3091 CTTTAAATAAAACGATGATATAAATTAAGTGAAGCTGATGTTTGTATTTGAAGTATATTGA 3150
QY 5267 ACTATATAGTTTGTATGTCATCTTTTTCACCAATTCAGAAACAGTGCTTCTGAAATTTGTGA 5326
Db 3151 ACTATATAGTTTGTATGTCATCTTTTTCACCAATTCAGAAACAGTGCTTCTGAAATTTGTGA 3210
QY 5327 TTTTAAAGGAATTTGTAATAGAAATGTTTATTTTAAAGTATCTTTTAAAGTTATGCCATCT 5386
Db 3211 TTTTAAAGGAATTTGTAATAGAAATGTTTATTTTAAAGTATCTTTTAAAGTTATGCCATCT 3270
QY 5387 TCTTAAATAAGTACGTAATGTTCCAAATCTAATAAATAAACTAAT 5430
Db 3271 TCTTAAATAAGTACGTAATGTTCCAAATCTAATAAATAAACTAAT 3314

RESULT 10
US-09-822-846-97
; Sequence 97, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fehchel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6400

; CURRENT APPLICATION NUMBER: US/09/822,846
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 97
; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-846-97

Query Match 27.3%; Score 1497; DB 10; Length 1548;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2489 AGAATTGACCAAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGA 2548
Db 1 AGAATTGACCAAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGA 60
QY 2549 TTCAAAATCTTTTGATGAAATGGAACAGAGCTTACTTATTTCTTGAAACCAAGGCTTC 2608
Db 61 TTCAAAATCTTTTGATGAAATGGAACAGAGCTTACTTATTTCTTGAAACCAAGGCTTC 120
QY 2609 TCTAGTGAGCACCATGAGCCTTTGGAACAACAGATGTATACAATAGCAAAAGTTTCATTT 2668
Db 121 TCTAGTGAGCACCATGAGCCTTTGGAACAACAGATGTATACAATAGCAAAAGTTTCATTT 180
QY 2669 CTTTACCTTGAAACGTTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTT 2728
Db 181 CTTTACCTTGAAACGTTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTT 240
QY 2729 TTTTACAGTTTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGTGTTCC 2788
Db 241 TTTTACAGTTTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGTGTTCC 300
QY 2789 CATCAAACTTGTTCAGACTTATATTTTCTAAACCTGGAGACAAACCAACATAAATACAA 2848
Db 301 CATCAAACTTGTTCAGACTTATATTTTCTAAACCTGGAGACAAACCAACATAAATACAA 360
QY 2849 AACAACTGCTCTTCTTCAAAATTTCTGCTGACTCAGATATCAGTGATCTTTATAGCTTTT 2908
Db 361 AACAACTGCTCTTCTTCAAAATTTCTGCTGACTCAGATATCAGTGATCTTTATAGCTTTT 420
QY 2909 CACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCC 2968
Db 421 CACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCC 480
QY 2969 CCATAGTGGCGCTTTAAATGTGATGCATTCAGAAAGGACTATGTTTTTGCAGCTGTTTT 3028
Db 481 CCATAGTGGCGCTTTAAATGTGATGCATTCAGAAAGGACTATGTTTTTGCAGCTGTTTT 540
QY 3029 CAACAGTACTATGGTTTTATCTTTTACCTATATTAGTGAATATCATTAGTAACACTATCT 3088
Db 541 CAACAGTACTATGGTTTTATCTTTTACCTATATTAGTGAATATCATTAGTAACACTATCT 600
QY 3089 TTATCATTTAAATGTGACTGAAACCATCCAGATCTGAGTACCCCATTTCTTTCAAGAAAT 3148
Db 601 TTATCATTTAAATGTGACTGAAACCATCCAGATCTGAGTACCCCATTTCTTTCAAGAAAT 660
QY 3149 TACTGATATAGTTTTTAAATGAGCTGTATTTTCAAGCAGCTTTTGGATCATTTGT 3208
Db 661 TACTGATATAGTTTTTAAATGAGCTGTATTTTCAAGCAGCTTTTGGATCATTTGT 720
QY 3209 TACTGCAATGCCACCTTACTTTGCCATGGAAATGCAGAGAATCATAGATCAAAGCTTA 3268
Db 721 TACTGCAATGCCACCTTACTTTGCCATGGAAATGCAGAGAATCATAGATCAAAGCTTA 780
QY 3269 TACTCAACTTAAACTTTTCAGGCTTTTGGCATCTGCATTTGGATTGGACAAGCTTGT 3328
Db 781 TACTCAACTTAAACTTTTTCAGGCTTTTGGCATCTGCATTTGGATTGGACAAGCTTGT 840
QY 3329 TGATATCCCTTATTTTTTATCATCTTATTTTGAIGTAGGAAGCTTATTGGCATTTCA 3388

||||| 841 TGATAATCCCTTATTTTATCATCTCTTATTTTATGTCAGGAAGCTTATTGGCAATTC A 900
QY 3389 TTATGGATATATTTTATACGTAAAGTTCTCTGCTGCGTGTCTTTTGCCTTATGTTA 3448
Db 901 TTATGGATATATTTTATACGTAAAGTTCTCTGCTGCGTGTCTTTTGCCTTATGTTA 960
QY 3449 TGTTCATCAGTTATTTCTGTTCACTATATTTGCTTCTTTCACCTTTAAGAAATTTTAAA 3508
Db 961 TGTTCATCAGTTATTTCTGTTCACTATATTTGCTTCTTTCACCTTTAAGAAATTTTAAA 1020
QY 3509 TACCAAGAATTTTGGTCATTTATCTATTTCTGCGCAGCGTTGGCTTGATTTGCAATCAC 3568
Db 1021 TACCAAGAATTTTGGTCATTTATCTATTTCTGCGCAGCGTTGGCTTGATTTGCAATCAC 1080
QY 3569 TGAATAAATCTTTTATGGGATACACAATTTGCAACTATTTCTTCAATATGCCCTTTGTAT 3628
Db 1081 TGAATAAATCTTTTATGGGATACACAATTTGCAACTATTTCTTCAATATGCCCTTTGTAT 1140
QY 3629 CATCATTCGAATCTATCCACTTCTAGGTTGCTGATTTCTTTCATAAAGATTTCTTGGAA 3688
Db 1141 CATCATTCGAATCTATCCACTTCTAGGTTGCTGATTTCTTTCATAAAGATTTCTTGGAA 1200
QY 3689 GAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTTAT 3748
Db 1201 GAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTTAT 1260
QY 3749 ATCGCCTTACCTGCAGTGTGTACTGTGGATTTTCTCTTACAAATACTATGAGAAAAATA 3808
Db 1261 ATCGCCTTACCTGCAGTGTGTACTGTGGATTTTCTCTTACAAATACTATGAGAAAAATA 1320
QY 3809 TGGAGGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAA 3868
Db 1321 TGGAGGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAA 1380
QY 3869 TAGGAAGCTTCCAGAACCCAGACAAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAG 3928
Db 1381 TAGGAAGCTTCCAGAACCCAGACAAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAG 1440
QY 3929 ACTAAAGTCAAAGAGCTGATGGGTGCCAGTGTGTGAGGAGAAACCATCCATTATGGT 3988
Db 1441 ACTAAAGTCAAAGAGCTGATGGGTGCCAGTGTGTGAGGAGAAACCATCCATTATGGT 1500
QY 3989 CAGCAATTTGCATAAAGAATATGATGACAAGAAAGATTTTCTTTCTTTC 4036
Db 1501 CAGCAATTTGCATAAAGAATATGATGACAAGAAAGATTTTCTTTCTTTC 1548

RESULT 11
US-09-822-846-98
; Sequence 98, Application US/09822846
; Publication No. US20030027139A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steininger II, Robert J.
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS

; FILE REFERENCE: GIN 6400
; CURRENT APPLICATION NUMBER: US/09/822,846
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,605
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 3928
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-822-846-98

Query Match 24.5%; Score 1343; DB 10; Length 3928;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1044 GTATTTTGTGCTTAAATGCTGACACCTCTTTTAAAAAATCAAAAACATGTGGGAATAGTT 1103
Db 1 GTATTTTGTGCTTAAATGCTGACACCTCTTTTAAAAAATCAAAAACATGTGGGAATAGTT 60
QY 1104 GAATTTTGTGCTTAAATGCTGACACCTCTTTTAAAAAATCAAAAACATGTGGGAATAGTT 1163
Db 61 GAATTTTGTGCTTAAATGCTGACACCTCTTTTAAAAAATCAAAAACATGTGGGAATAGTT 120
QY 1164 TTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCCTTTCTGTCACTGTACTTTTGTGATGGT 1223
Db 121 TTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCCTTTCTGTCACTGTACTTTTGTGATGGT 180
QY 1224 ATTGCACAGGTCATGCATTTTAGAAGATTTTAATGAAGGTGCTTCATTTTCAAAATTTGACT 1283
Db 181 ATTGCACAGGTCATGCATTTTAGAAGATTTTAATGAAGGTGCTTCATTTTCAAAATTTGACT 240
QY 1284 GCAGGCCCATATCCTCTAATTTATACAATTTATCATGCTCACACTTAATAGTATATTTCTAT 1343
Db 241 GCAGGCCCATATCCTCTAATTTATACAATTTATCATGCTCACACTTAATAGTATATTTCTAT 300
QY 1344 GTCTCTTGGCTGTCTATCTTGTCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGATCA 1403
Db 301 GTCTCTTGGCTGTCTATCTTGTCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGATCA 360
QY 1404 TCTTTATATTTTCTGAAGCCCTTCATATTTGGTCAAAGAGCAAAAAGAAATTTATGAGGAGTTA 1463
Db 361 TCTTTATATTTTCTGAAGCCCTTCATATTTGGTCAAAGAGCAAAAAGAAATTTATGAGGAGTTA 420
QY 1464 TCAGAGGGCAATGTTAATGGAATATTTAGTTTGTAGTGAATTTATGAGCCAGTTTCTTCA 1523
Db 421 TCAGAGGGCAATGTTAATGGAATATTTAGTTTGTAGTGAATTTATGAGCCAGTTTCTTCA 480
QY 1524 GAATTTGTAGAAAAAGAACCCATAAGAAATTTAGTGGTATTTCAAGACATACAGAAAGAG 1583
Db 481 GAATTTGTAGAAAAAGAACCCATAAGAAATTTAGTGGTATTTCAAGACATACAGAAAGAG 540
QY 1584 GGTGAAAAATGTGGAGGCTTTTGAGAAATTTGTCAATTTTGACATATATGAGGGTCAGATTACT 1643
Db 541 GGTGAAAAATGTGGAGGCTTTTGAGAAATTTGTCAATTTTGACATATATGAGGGTCAGATTACT 600
QY 1644 GCCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACATTTGATGAATATTTCTTTGTGGACTC 1703
Db 601 GCCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACATTTGATGAATATTTCTTTGTGGACTC 660
QY 1704 TGCCCCACCTTCTGATGGGTTTGCATCTATATATGGAACACAGTCTCAGAAATAGATGAA 1763
Db 661 TGCCCCACCTTCTGATGGGTTTGCATCTATATATGGAACACAGTCTCAGAAATAGATGAA 720
QY 1764 ATGTTTGAAGCAAGAAAAAATGATTTGGCATTGTGCCACAGTTAGATATACACTTTTGATGTT 1823
Db 721 ATGTTTGAAGCAAGAAAAAATGATTTGGCATTGTGCCACAGTTAGATATACACTTTTGATGTT 780
QY 1824 TTGACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAATCAAAGGATACCAGCCCAACAT 1883
Db 781 TTGACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAATCAAAGGATACCAGCCCAACAT 840

QY 1884 ATAATACAGAAGTGCAGAAGGTTTTTACTAGATTAGACATGCAGACTATCAAGATAAC 1943
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 ATAATACAGAAGTGCAGAAGGTTTTTACTAGATTAGACATGCAGACTATCAAGATAAC 900
QY 1944 CAAGCTAAAAAATAAGTGGTGCACAAAAAGAAAGCTGTCTATTAGGAATTGCTGTTCTT 2003
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
901 CAAGCTAAAAAATAAGTGGTGCACAAAAAGAAAGCTGTCTATTAGGAATTGCTGTTCTT 960
QY 2004 GGGAACCCCAAGATACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGA 2063
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
961 GGGAACCCCAAGATACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGA 1020
QY 2064 CATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACT 2123
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1021 CATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACT 1080
QY 2124 CATTTCATGGATGAAGCTGACATTCCTGCAGATAGGAAAGCTGTGATATCACAAGGAATG 2183
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1081 CATTTCATGGATGAAGCTGACATTCCTGCAGATAGGAAAGCTGTGATATCACAAGGAATG 1140
QY 2184 CTGAAATGTGTGGTCTTCAATGTTCTCAAAAGTAAATGGGGATCGGCTACCGCCTG 2243
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1141 CTGAAATGTGTGGTCTTCAATGTTCTCAAAAGTAAATGGGGATCGGCTACCGCCTG 1200
QY 2244 AGCATGTACATACACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACAT 2303
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1201 AGCATGTACATACACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACAT 1260
QY 2304 ATACCTGGAGCTACTTTATTACACAGAAATGACCAACAACTTGTGTATAGCTTGCCCTTC 2363
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 ATACCTGGAGCTACTTTATTACACAGAAATGACCAACAACTTGTGTATAGCTTGCCCTTC 1320
QY 2364 AAGGACATGGACAAATTTTCAGG 2386
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1321 AAGGACATGGACAAATTTTCAGG 1343

RESULT 12
US-10-204-887-32
; Sequence 32, Application US/10204887
; Publication No. US20030124569A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PANZER, Scott R.
; APPLICANT: SPIRO, Peter A.
; APPLICANT: BANVILLE, Steven C.
; APPLICANT: SHAH, Purvi
; APPLICANT: CHALUP, Michael S.
; APPLICANT: CHANG, Simon C.
; APPLICANT: CHEN, Alice
; APPLICANT: D'SA, Steven A.
; APPLICANT: AMSHEY, Stefan
; APPLICANT: DAHL, Christopher R.
; APPLICANT: DAM, Tam C.
; APPLICANT: DANIELS, Susan E.
; APPLICANT: DUFOUR, Gerard E.
; APPLICANT: FLORES, Vincent
; APPLICANT: FONG, Willy T.
; APPLICANT: GREENAWALT, Lila B.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: JONES, Anissa L.
; APPLICANT: LIU, Tommy F.
; APPLICANT: ROSEBERRY, Ann M.
; APPLICANT: ROSEN, Bruce H.
; APPLICANT: RUSSO, Frank D.
; APPLICANT: STOCKDREHER, Theresa K.
; APPLICANT: DAFFO, Abel
; APPLICANT: WRIGHT, Rachel J.
; APPLICANT: YAP, Pierre E.
; APPLICANT: YU, Jimmy Y.
; APPLICANT: BRADLEY, Diana L.
; APPLICANT: BRATCHER, Shawn R.
; APPLICANT: CHEN, Wensheng

; APPLICANT: COHEN, Howard J.
; APPLICANT: HODGSON, David M.
; APPLICANT: LINCOLN, Stephen E.
; TITLE OF INVENTION: SECRETORY MOLECULES
; FILE REFERENCE: PT-1134 PCT
; CURRENT APPLICATION NUMBER: US/10/204,887
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/185,215; 60/185,216; 60/205,232; 60/205,323; 60/205,287
; 60/205,324; 60/205,286
; PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-05-16; 2000-05-17; 2000-05-17;
; 2000-05-17; 2000-05-17
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 1818
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030124569A1 LI:445188.1:2000MAY01
US-10-204-887-32

Query Match 13.6%; Score 744; DB 14; Length 1818;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 744; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 AGGTTTATTTCAGAAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 156
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1075 AGGTTTATTTCAGAAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 1134
QY 157 GAACACCTTCTACTGAAGAATTACTTAAATTAATTAATGCAGAACCAAAAAAGAGTAGTGTTCAGG 216
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1135 GAACACCTTCTACTGAAGAATTACTTAAATTAATTAATGCAGAACCAAAAAAGAGTAGTGTTCAGG 1194
QY 217 AAATCTTTTTCCACTATTTTTTTTTTTTATTTTGGTTAAATATTAAATAGCATGATGCCAA 276
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1195 AAATCTTTTTCCACTATTTTTTTTTTTTATTTTGGTTAAATATTAAATAGCATGATGCCAA 1254
QY 277 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGCAAGTTTACTCTTT 336
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1255 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGCAAGTTTACTCTTT 1314
QY 337 CTAATCTAATTTCTGGATATACTCCAGTGAATAATATTACAAGCAGCATCATGCAGAAAG 396
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1315 CTAATCTAATTTCTGGATATACTCCAGTGAATAATATTACAAGCAGCATCATGCAGAAAG 1374
QY 397 TGTCTACTGATCATCTACCTGATGTCTAATTAATTAATGAAGAATATACAAATGAAAAAGAAA 456
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1375 TGTCTACTGATCATCTACCTGATGTCTAATTAATTAATGAAGAATATACAAATGAAAAAGAAA 1434
QY 457 TGTAAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAAGACTCCA 516
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1435 TGTAAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAAGACTCCA 1494
QY 517 TGTCTATGAACCTTCGTTTTTTTCTGATATGATTCAGTATCTTCTATTTATATGGATT 576
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1495 TGTCTATGAACCTTCGTTTTTTTCTGATATGATTCAGTATCTTCTATTTATATGGATT 1554
QY 577 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 636
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1555 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 1614
QY 637 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA 696
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1615 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA 1674
QY 697 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGAGAAACTGCTGTTGTAGAAATAGATA 756
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1675 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGAGAAACTGCTGTTGTAGAAATAGATA 1734
QY 757 CCTTTCCCGAGGAGTAATTTTAATATACCTAGTTATAGCATTTTACCTTTGGATACT 816
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1735 CCTTTCCCGAGGAGTAATTTTAATATACCTAGTTATAGCATTTTACCTTTGGATACT 1794

Search completed: April 12, 2004, 21:29:49
Job time : 1252 sec

Db 1802 AGGAGTGGAGTCAACTAAAGCTGTATTATGGGAGAAACTGCTGTTGTAGAAATAGATA 1861
QY 757 CCTTCCCGGAGGAGTAATTTTAATATACCTAGTTATAGCATTTTCACCTTTTGGTACT 816
Db 1862 CCTTCCCGGAGGAGTAATTTTAATATACCTAGTTATAGCATTTTCACCTTTTGGTACT 1921
QY 817 TTTTGGCAATTTCATATCGTAGC 838
Db 1922 TTTTGGCAATTTCATATCGTAGC 1943

RESULT 15
US-10-085-783A-44227
; Sequence 44227, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44227
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-44227

Query Match 8.4%; Score 459; DB 12; Length 465;
Best Local Similarity 100.0%; Pred. No. 8.8e-209;
Matches 459; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4648 GATGTATCGGAACAGTACAACTCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAA 4707
Db 7 GATGTATCGGAACAGTACAACTCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAA 66
QY 4708 TTAATTTGAAGACTGGATAGAAAACCTAGAACCGCTTCAAAGAGAAATTCAGT 4767
Db 67 TTAATTTGAAGACTGGATAGAAAACCTAGAACCGCTTCAAAGAGAAATTCAGT 126
QY 4768 ATATTTTCCCAATGCAAGCCGTCAGGAAAGTTTTCTCTATTTTGGCTTATAAAATTC 4827
Db 127 ATATTTTCCCAATGCAAGCCGTCAGGAAAGTTTTCTCTATTTTGGCTTATAAAATTC 186
QY 4828 CTAAGGAAGATGTTTCAGTCCCTTTTCACAATCTTTTAAAGCTGGAAGAGCTAAACATG 4887
Db 187 CTAAGGAAGATGTTTCAGTCCCTTTTCACAATCTTTTAAAGCTGGAAGAGCTAAACATG 246
QY 4888 CTTTGTCCATTGAAGATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTGTGTAGAAC 4947
Db 247 CTTTGTCCATTGAAGATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTGTGTAGAAC 306
QY 4948 TCACTAAAGAACAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGT 5007
Db 307 TCACTAAAGAACAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGT 366
QY 5008 GGGAAACGAACACAGAAGATAGAGTAGTATTTTGAATTTGTATTTTGGTCTGCTTACT 5067
Db 367 GGGAAACGAACACAGAAGATAGAGTAGTATTTTGAATTTGTATTTTGGTCTGCTTACT 426
QY 5068 GGGACTTCTTTCTTTTCACTTAATTTTAACTTTGGTTT 5106
Db 427 GGGACTTCTTTCTTTTCACTTAATTTTAACTTTGGTTT 465

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OM nucleic - nucleic search, using sw model

Run on: April 12, 2004, 11:03:41 ; Search time 252 Seconds
(without alignments)
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Perfect score: 5475
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Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	743	13.6	974	US-09-833-381-1085	Sequence 1085, Ap
2	318	5.8	485	US-09-621-976-409	Sequence 409, App
3	21	0.4	2198	US-09-620-312D-852	Sequence 852, App
4	20	0.4	693	US-09-328-352-3244	Sequence 3244, Ap
C 5	20	0.4	837	US-09-891-641-36	Sequence 36, Appl
C 6	20	0.4	970	US-09-016-434-1416	Sequence 1416, Ap
C 7	20	0.4	1100	US-08-196-350-2	Sequence 2, Appli
8	20	0.4	2433	US-09-540-824-24	Sequence 24, Appl
9	20	0.4	4079	US-09-016-434-1247	Sequence 1247, Ap
10	20	0.4	112132	US-09-741-150-3	Sequence 3, Appli
11	20	0.4	112132	US-10-160-187-3	Sequence 3, Appli
12	20	0.4	1664976	US-08-916-421B-1	Sequence 1, Appli
C 13	19	0.3	210	US-09-016-434-426	Sequence 426, App
C 14	19	0.3	369	US-09-621-976-8464	Sequence 8464, Ap
C 15	19	0.3	634	US-08-450-065-1	Sequence 1, Appli
C 16	19	0.3	634	US-08-450-595-1	Sequence 1, Appli
C 17	19	0.3	893	US-09-370-838-166	Sequence 166, App
C 18	19	0.3	2017	US-07-667-276A-3	Sequence 3, Appli
C 19	19	0.3	3001	US-09-539-333D-171	Sequence 171, App
C 20	19	0.3	7653	US-08-394-189B-1	Sequence 1, Appli
C 21	19	0.3	7653	US-08-258-287B-1	Sequence 1, Appli
C 22	19	0.3	7653	US-08-368-704C-1	Sequence 1, Appli
C 23	19	0.3	7653	PCT-US93-05701-18	Sequence 18, Appl
C 24	19	0.3	7653	PCT-US93-05705-1	Sequence 1, Appli
C 25	19	0.3	8312	US-09-620-312D-1048	Sequence 1048, Ap
C 26	19	0.3	9370	US-08-320-559-27	Sequence 27, Appl
C 27	19	0.3	9370	US-08-545-860D-27	Sequence 27, Appl

C 28	19	0.3	9370	5	PCT-US94-04496-27	Sequence 27, Appl
C 29	19	0.3	9391	1	US-08-320-559-25	Sequence 25, Appl
C 30	19	0.3	9391	3	US-08-545-860D-25	Sequence 25, Appl
C 31	19	0.3	9391	5	PCT-US94-04496-25	Sequence 25, Appl
C 32	19	0.3	46718	4	US-09-816-093-3	Sequence 3, Appli
33	19	0.3	148567	4	US-09-801-876B-3	Sequence 3, Appli
34	19	0.3	148567	4	US-10-254-869-3	Sequence 3, Appli
C 35	19	0.3	269223	4	US-09-596-002-41	Sequence 41, Appl
36	19	0.3	640681	4	US-09-790-988-1	Sequence 1, Appli
C 37	19	0.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
C 38	19	0.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
C 39	18	0.3	59	4	US-09-532-656-2	Sequence 2, Appli
40	18	0.3	163	2	US-08-611-757-78	Sequence 78, Appl
41	18	0.3	163	5	PCT-US95-05980-78	Sequence 78, Appl
42	18	0.3	231	4	US-09-134-001C-1450	Sequence 1450, Ap
C 43	18	0.3	387	4	US-09-134-001C-1867	Sequence 1867, Ap
44	18	0.3	474	4	US-09-328-352-39	Sequence 39, Appl
C 45	18	0.3	525	4	US-09-134-001C-1623	Sequence 1623, Ap

ALIGNMENTS

RESULT 1
US-09-833-381-1085
; Sequence 1085, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1085
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1085

Query Match	13.6%;	Score 743;	DB 4;	Length 974;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches	743;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	97	AGGTTTATTTCAGAAACATGTCCTGCAATTCAGGAGGTAGGAGTTTGGAGACAGACCA	156	
Db	216	AGGTTTATTTCAGAAACATGTCCTGCAATTCAGGAGGTAGGAGTTTGGAGACAGACCA	275	
Qy	157	GAACACTTCTACTGAAGAATTACTTAATTAATGCGAGAACCAAAAGAGTAGTGTTCAGG	216	
Db	276	GAACACTTCTACTGAAGAATTACTTAATTAATGCGAGAACCAAAAGAGTAGTGTTCAGG	335	
Qy	217	AAATTCTTTTCCACTATTTTTTTTATTTTGGTAAATTAATAGCATGCATGCCAA	276	
Db	336	AAATTCTTTTCCACTATTTTTTTTATTTTGGTAAATTAATAGCATGCATGCCAA	395	
Qy	277	ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT	336	
Db	396	ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT	455	
Qy	337	CTAATCTAATTTCTGGATATACCTCCAGTGACTTAATTAACAAGCAGCATGCAGAAAG	396	
Db	456	CTAATCTAATTTCTGGATATACCTCCAGTGACTTAATTAACAAGCAGCATGCAGAAAG	515	
Qy	397	TGCTACTGATCATCTACCTGATGTGCATTAATTAACAAGTAAATCAAAATGAAAAAGAAA	456	
Db	516	TGCTACTGATCATCTACCTGATGTGCATTAATTAACAAGTAAATCAAAATGAAAAAGAAA	575	
Qy	457	TGTTAACATCCAGTCTCTTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAAGACTCCA	516	

Db 576 TGTTACATCCAGTCTCTCTAAGCGGAGCAACTTTGTAGTGTGGTTTTTCAAGACTCCA 635
QY 517 TGTCCTATGAACCTTCGTTTTTTTCTCTGATATGATCCAGTATCTTCTATTATATGGATT 576
Db 636 TGTCCTATGAACCTTCGTTTTTTTCTCTGATATGATCCAGTATCTTCTATTATATGGATT 695
QY 577 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCCTCAGGTTTCACAG 636
Db 696 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCCTCAGGTTTCACAG 755
QY 637 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA 696
Db 756 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA 815
QY 697 AGGAGCTGGAGTCAACTAAAGCTGTTATTATATGGGAGAACTGCTGTTGTAGAAATAGATA 756
Db 816 AGGAGCTGGAGTCAACTAAAGCTGTTATTATATGGGAGAACTGCTGTTGTAGAAATAGATA 875
QY 757 CCTTCCCGGAGGAGTAATTTTAATATACCTAGTTATAGCAATTTTCACCTTTGGATACT 816
Db 876 CCTTCCCGGAGGAGTAATTTTAATATACCTAGTTATAGCAATTTTCACCTTTGGATACT 935
QY 817 TTTTGGCAATTCATATCGTAGCA 839
Db 936 TTTTGGCAATTCATATCGTAGCA 958

RESULT 2
US-09-621-976-409
; Sequence 409, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 409
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 185..484
US-09-621-976-409

Query Match 5.8%; Score 318; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.2e-140;
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 97 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 156
Db 168 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 227
QY 157 GAACACTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGG 216
Db 228 GAACACTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGG 287
QY 217 AAATCTTTTCCACTATTTTTTTTATTTTGGTTAATTAATTAATAGCATGATGCATCCAA 276
Db 288 AAATCTTTTCCACTATTTTTTTTATTTTGGTTAATTAATTAATAGCATGATGCATCCAA 347
QY 277 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 336
Db 348 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 407
QY 337 CTAATCTAATCTTGGATATATCTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAG 396
Db 408 CTAATCTAATCTTGGATATATCTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAG 467

QY 397 TGTCCTACTGATCATCTAC 414
Db 468 TGTCCTACTGATCATCTAC 485

RESULT 3
US-09-620-312D-852
; Sequence 852, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 852
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)..(1867)
US-09-620-312D-852

Query Match 0.4%; Score 21; DB 4; Length 2198;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3895 ATGAGGATGAAGATGAAGATG 3915
Db 1503 ATGAGGATGAAGATGAAGATG 1523

RESULT 4
US-09-328-352-3244
; Sequence 3244, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3244
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii


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US-09-328-352-3244
Query Match          0.4%; Score 20; DB 4; Length 693;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3901 ATGAAGATGAAGATGTCAA 3920
Db 497 ATGAAGATGAAGATGTCAA 516

RESULT 5
US-09-891-641-36/c
; Sequence 36, Application US/09891641
; Patent No. 6617148
; GENERAL INFORMATION:
; APPLICANT: Ye, Rick
; APPLICANT: Bedzyk, Laura
; APPLICANT: Wang, Tao
; TITLE OF INVENTION: NATURAL PROMOTERS FOR GENE EXPRESSION IN BACILLUS SPECIES
; FILE REFERENCE: CL1686 US NA
; CURRENT APPLICATION NUMBER: US/09/891,641
; CURRENT FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Microsoft 97
; SEQ ID NO 36
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-891-641-36

Query Match          0.4%; Score 20; DB 4; Length 837;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2752 TTTGGTTCATCACTCTTT 2771
Db 812 TTTGGTTCATCACTCTTT 793

RESULT 6
US-09-016-434-1416/c
; Sequence 1416, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
```

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; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1416:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9531102
US-09-016-434-1416

Query Match          0.4%; Score 20; DB 4; Length 970;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1747 TCTCAGAAATAGATGAATG 1766
Db 854 TCTCAGAAATAGATGAATG 835

RESULT 7
US-08-196-350-2/c
; Sequence 2, Application US/08196350
; Patent No. 5585099
; GENERAL INFORMATION:
; APPLICANT: Richards, Sue
; APPLICANT: Kaplan, Joanne
; APPLICANT: Moscicki, Richard
; TITLE OF INVENTION: PROLACTIN AS ADJUVANT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brad Salcedo
; STREET: One Kendall Square
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,350
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gosz, William G
; REGISTRATION NUMBER: 27,787
; REFERENCE/DOCKET NUMBER: GEN 4-1.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 6172527868
; TELEFAX: 6173747225
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-196-350-2

Query Match          0.4%; Score 20; DB 1; Length 1100;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1747 TCTCAGAAATAGATGAATG 1766
Db 984 TCTCAGAAATAGATGAATG 965
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RESULT 8
US-09-540-824-24
; Sequence 24, Application US/09540824
; Patent No. 6383753
; GENERAL INFORMATION:
; APPLICANT: Thiele, Dennis
; APPLICANT: Liu, Phillip
; TITLE OF INVENTION: No. 6383753el Yeast and Mammalian Regulators of Cell Proliferat
; FILE REFERENCE: UM-04266
; CURRENT APPLICATION NUMBER: US/09/540,824
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 2433
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-540-824-24
Query Match 0.4%; Score 20; DB 4; Length 2433;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1767 TTTGAAGCAAGAAAAATGAT 1786
Db 295 TTTGAAGCAAGAAAAATGAT 314
RESULT 9
US-09-016-434-1247
; Sequence 1247, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1247:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g190037
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2778 GCTGTGGTCCCATCAAACT 2797
Db 2590 GCTGTGGTCCCATCAAACT 2609
RESULT 10
US-09-741-150-3
; Sequence 3, Application US/09741150
; Patent No. 6436689
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000968
; CURRENT APPLICATION NUMBER: US/09/741,150
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 112132
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3
Query Match 0.4%; Score 20; DB 4; Length 112132;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 788 AGTTATAGCATTTTCACCTT 807
Db 55116 AGTTATAGCATTTTCACCTT 55135
RESULT 11
US-10-160-187-3
; Sequence 3, Application US/10160187
; Patent No. 6620607
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al.
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000968DIV
; CURRENT APPLICATION NUMBER: US/10/160,187
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/252,410
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 09/741,150
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
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; TYPE: DNA
; ORGANISM: Homo sapien
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n = A,T,C or G
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US-10-160-187-3

Query Match 0.4%; Score 20; DB 4; Length 112132;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 AGTATAGCATTTTCACCTT 807
Db 55116 AGTATAGCATTTTCACCTT 55135

RESULT 12

US-08-916-421B-1
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus jannaschii
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
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LOCATION: (1569020)..(1569020)
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Query Match 0.4%; Score 20; DB 4; Length 1664976;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4938 TTTGTAGAACTCACTAAAGA 4957
Db 201642 TTTGTAGAACTCACTAAAGA 201661

RESULT 13
US-09-016-434-426/c
; Sequence 426, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 426:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: STOMNOT01
CLONE: 215814
US-09-016-434-426

Query Match 0.3%; Score 19; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1821 GTTTTGACAGTAGAAGAAA 1839
Db 20 GTTTTGACAGTAGAAGAAA 2

RESULT 14
US-09-621-976-8464/c
; Sequence 8464, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 8464
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8464

Query Match 0.3%; Score 19; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2709 TTGCTTCTGCTTTTAATTT 2727
Db 211 TTGCTTCTGCTTTTAATTT 193

RESULT 15
US-08-450-065-1/c
; Sequence 1, Application US/08450065
; Patent No. 5798105
; GENERAL INFORMATION:
; APPLICANT: Schoenmakers, Johannes G
; APPLICANT: Konings, Rudolph NH

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2004, 07:56:11 ; Search time 13649 Seconds
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Title: US-10-090-458-4
Perfect score: 5475
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	5181	94.6	6525	6	AX473847	AX473847 Sequence
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4	5086	92.9	6369	6	AX392931	AX392931 Sequence
5	4935	90.1	5096	9	HSA275973	AJ275973 Homo sapi
6	4664	85.2	5262	6	AX417828	AX417828 Sequence
7	4572	83.5	4929	6	AX417824	AX417824 Sequence
8	4408	80.5	4785	6	AX417826	AX417826 Sequence
9	2826	51.6	5463	6	AX537470	AX537470 Sequence
10	2739	50.0	3268	6	AX714300	AX714300 Sequence
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13	2617	47.8	2845	9	HSA512612	AJ512612 Homo sapi
14	2597	47.4	3112	9	AB067475	AB067475 Homo sapi
15	2294	41.9	5243	9	HSM807592	BX647447 Homo sapi
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17	1991	36.4	3347	9	AK094416	AK094416 Homo sapi
18	1758	32.1	1964	9	AK122803	AK122803 Homo sapi
19	1601	29.2	4078	9	HSM806823	BX640746 Homo sapi
20	1560	28.5	1560	9	AK058170	AK058170 Homo sapi
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22	744	13.6	1818	6	AX576092	AX576092 Sequence
23	742	13.6	1943	6	AX834300	AX834300 Sequence
24	742	13.6	1943	9	AK096664	AK096664 Homo sapi
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26	639	11.7	735	9	BC054480	BC054480 Homo sapi
27	548	10.0	548	6	AX778667	AX778667 Sequence
28	543	9.9	163229	9	AC115085	AC115085 Homo sapi
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38	242	4.4	341	6	BD071308	BD071308 Secreted
39	233	4.3	71794	2	AC023647	AC023647 Homo sapi
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ALIGNMENTS

RESULT 1
AX537473
LOCUS AX537473
DEFINITION Sequence 4 from Patent WO02070690.
ACCESSION AX537473
VERSION AX537473.1 GI:25269282
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Chen,H., Kilinski,L. and le Bihan,S.
TITLE Abca5 transporter and uses thereof
JOURNAL Patent: WO 02070690-A 4 12-SEP-2002;

AX537473 5475 bp DNA linear PAT 23-NOV-2002
Sequence 4 from Patent WO02070690.
AX537473
AX537473.1 GI:25269282
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Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Chen,H., Kilinski,L. and le Bihan,S.
Abca5 transporter and uses thereof
Patent: WO 02070690-A 4 12-SEP-2002;

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RESULT 2
AX473847
LOCUS AX473847 6525 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 1 from Patent WO0246458.
ACCESSION AX473847
VERSION AX473847.1 GI:22208006
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Denefle,P., Rosier-Montus,M.F., Prades,C., Arnould-Reguigne,I.,
Duverger,N., Allikmets,R. and Dean,M.
TITLE Nucleic acids of the human abca5, abca6, abca9, and abca10 genes,
vectors containing such nucleic acids and uses thereof
JOURNAL Patent: WO 0246458-A 1 13-JUN-2002;
Aventis Pharma S.A. (FR) ; The Secretary, Department of Health and
Human Services (US)
FEATURES
Source 1. 6525
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RESULT 3					
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LOCUS	Homo sapiens	ATP-binding cassette A5 mRNA, complete cds.			
DEFINITION	AY028897				
ACCESSION	AY028897.1	GI:17223619			
VERSION					
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 6525)				
AUTHORS	Schriml, L.M., Arnould, I., Prades, C., Lachtermacher-Rocha, M., Schneider, T., Maintoux, C., Lemoine, C., Debono, D., Devaud, C., Naudin, L., Bauche, S., Annat, M., Alikmets, R., Denefle, P., Rosier, M. and Dean, M.				
TITLE	Identification and characterization of a cluster of five new ATP-binding cassette transporter genes on human chromosome 17q24: a novel sub-group within the ABCA sub-family				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 6525)				
AUTHORS	Schriml, L.M., Arnould, I., Prades, C., Lachtermacher-Rocha, M., Schneider, T., Maintoux, C., Lemoine, C., Debono, D., Devaud, C., Naudin, L., Bauche, S., Annat, M., Alikmets, R., Denefle, P., Rosier, M. and Dean, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-MAR-2001) Evry Genomics Center, Aventis Pharma, 2 Rue Gaston Cremieux, Evry 91057, France				
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```

ORIGIN

Query Match	94.6%;	Score 5181;	DB 9;	Length 6525;
Best Local Similarity	99.9%;	Pred. No. 0;		
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QY	157	GAACACTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGG	216	
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QY	217	AAATCTTTTCCACTATTTTATTTTGGTTAATATTAATTAGCATGATGCATCCAA	276	
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QY	277	ATAAGAAATATGAAGAAAGTCCTAATAATAGAACTCAATCCTATGGACAAGTTTACTCTTT	336	
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QY 1237 TGCATTTAGAAGATTTTAAATGAAGTGTCTTCATTTTCAAAATTTGACTGCGAGGCCATATC 1296
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Db 2194 CTCTAAATPATACAATATCATGTCTCACACTTAATAGTATATTTCTATGTCTCTTGGCTG 2253
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Db 2614 ATGGGTTTGCACTCTATATATGGAACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA 2673
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Db 2794 TGCAGAAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAAGATAACCAAGCTTAAAAAT 2853
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QY 2557 CTTTGTGATGAAATGGAAACAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGA 2616
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Db 3694 TTGTTCCAGACTTATATTTTCTAAACCTGGAGACAAACACATATAAATACAAAACAAGTC 3753
Qy 2857 TGCTTCTTCAAAATCTGCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAAGCC 2916
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RESULT 4
AX392931
LOCUS AX392931 6369 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 33 from Patent WO0212340.
ACCESSION AX392931
VERSION AX392931.1 GI:19700978
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Yue,H., Thornton,M., Ramkumar,J., Tang,Y.T., Azimzai,Y., Baughn,M.R., Yang,J., Yao,M.G., Lal,P., Wallia,N.K., Gandhi,A.R., Hafalia,A.J., Nguyen,D.B., Patterson,C., Elliott,V.S., Tribouley,C.M., Lu,D.A., Xu,Y., Reddy,R., Hernandez,R., Borowsky,M.L., Lo,T.P., Lu,Y., Policky,J.L., Greene,B.D., Sanjanwala,M.S., Raumann,B.E., Burford,N., Ison,C.H., Lee,E.A., Ding,L., Das,D., Kallick,D.A., Khan,F.A. and Seilhamer,J.J.
JOURNAL Patent: WO 0212340-A 33 14-FEB-2002;
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/db_xref="taxon:9606"
/note="Incyte ID No: 2798241CB1"

ORIGIN
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Matches 5136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 157 GAACACTTCTACTGAAGAATTACTTAATTAATGCAAGACCAAAAGAGTAGTGTTCAGG 216
DB 1281 GAACACTTCTACTGAAGAATTACTTAATTAATGCAAGACCAAAAGAGTAGTGTTCAGG 1340

QY 217 AAATCTTTTCCACTATTTTATTTTATTTTGGTTAATTAATTAGCATGATCCAA 276
DB 1341 AAATCTTTTCCACTATTTTATTTTATTTTGGTTAATTAATTAGCATGATCCAA 1400
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DB 1461 CTAATCTAATTTCTTGGATATACTCCAGTGAATAATTAACAAGCAGCATGCAGAAAG 1520
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DEFINITION Homo sapiens mRNA for ATP-binding cassette protein of the (ABCA subfamily).
ACCESSION AJ275973
VERSION AJ275973.3 GI:22080663
KEYWORDS ABCA subfamily; ATP-binding cassette protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Petry, F., Kotthaus, A. and Hirsch-Ernst, K.I.
TITLE Molecular cloning and tissue distribution of a novel ATP-binding cassette (ABC) transporter belonging to the subfamily ABCA Unpublished
JOURNAL 2
REFERENCE Hirsch-Ernst, K.I.
AUTHORS Direct Submission
TITLE Submitted (02-MAR-2000) Hirsch-Ernst K.I., Department of Toxicology, University of Goettingen, Robert-Koch-Strasse 40, Lowery Saxony, D-37075, GERMANY
JOURNAL revised by [3]
REMARK 3 (bases 1 to 5096)
REFERENCE Hirsch-Ernst, K.I.
AUTHORS Direct Submission
TITLE Submitted (20-NOV-2001) Hirsch-Ernst K.I., Department of

Toxicology, University of Goettingen, Robert-Koch-Strasse 40,
Lower Saxony, D-37075, GERMANY
On Aug 1, 2002 this sequence version replaced gi:17046099.

COMMENT
FEATURES

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ORIGIN

Query Match 90.1%; Score 4935; DB 9; Length 5096;
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Matches 5085; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db	729	TTAATATACCTAGTTATAGCAATTTACCTTTTGGATACTTTTGGCAATTTCATATCGTA	788
Qy	837	GCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACTGCC	896
Db	789	GCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACTGCC	848
Qy	897	TTTTGGCTTTCCTGGGTTCTCTATATACAAGTTTAAATTTTCTTATGTCCTCTTATG	956
Db	849	TTTTGGCTTTCCTGGGTTCTCTATATACAAGTTTAAATTTTCTTATGTCCTCTTATG	908
Qy	957	GCAGTCATTGCGACAGCTTCTTTGTTATTTCTCCTCAAAGTAGCAGCATTTGTGATATTCTG	1016
Db	909	GCAGTCATTGCGACAGCTTCTTTGTTATTTCTCCTCAAAGTAGCAGCATTTGTGATATTCTG	968
Qy	1017	CTTTTCTTCTTTATGGAATATCATCTGTATTTTCTGTTTAAATGCTGACACCTCTTTT	1076
Db	969	CTTTTCTTCTTTATGGAATATCATCTGTATTTTCTGTTTAAATGCTGACACCTCTTTT	1028
Qy	1077	AAAAAATCAAAACATGTGGGAATAGTTGAAATTTTGTGTACTGTGGCTTTTGGATTTATT	1136
Db	1029	AAAAAATCAAAACATGTGGGAATAGTTGAAATTTTGTGTACTGTGGCTTTTGGATTTATT	1088
Qy	1137	GGCCTTATGATAATCCTCATAGAAAAGTTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCCT	1196
Db	1089	GGCCTTATGATAATCCTCATAGAAAAGTTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCCT	1148
Qy	1197	TTCTGTCACTGTACTTTTGTGATTTGGTATTTGCACAGGTCATGCATTTAGAGATTTTAAT	1256
Db	1149	TTCTGTCACTGTACTTTTGTGATTTGGTATTTGCACAGGTCATGCATTTAGAGATTTTAAT	1208
Qy	1257	GAAGGTGCTTCAATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAAATTATTACAATATC	1316
Db	1209	GAAGGTGCTTCAATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAAATTATTACAATATC	1268
Qy	1317	ATGCTCACACTTAATAGTATATTTCTATGTCCTCTTGGCTGTCTATCTTGATCAAGTCATT	1376
Db	1269	ATGCTCACACTTAATAGTATATTTCTATGTCCTCTTGGCTGTCTATCTTGATCAAGTCATT	1328
Qy	1377	CCAGGGGAATTTGGCTTACGGAGATCATCTTTTATATTTTCTGAAGCCTTTCATATTGGTCA	1436
Db	1329	CCAGGGGAATTTGGCTTACGGAGATCATCTTTTATATTTTCTGAAGCCTTTCATATTGGTCA	1388
Qy	1437	AAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGTTTT	1496

Db 1389 AAGAGCAAAAGAAATATAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGTTTT 1448
QY 1497 AGTGAATATTAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAGCCATAAGAAATTAGT 1556
Db 1449 AGTGAATATTAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAGCCATAAGAAATTAGT 1508
QY 1557 GGTATTCAGAGACATACAGAAAGAGGGTGAAAATGTGGAGGCTTTTGAGAAATTTGTCA 1616
Db 1509 GGTATTCAGAGACATACAGAAAGAGGGTGAAAATGTGGAGGCTTTTGAGAAATTTGTCA 1568
QY 1617 TTTGACATATATAGGGTCAGATTACTGCCTTACTTTGGCCACAGTGGAAACAGGAAAGAGT 1676
Db 1569 TTTGACATATATAGGGTCAGATTACTGCCTTACTTTGGCCACAGTGGAAACAGGAAAGAGT 1628
QY 1677 ACATTGATGAATATTCTTTGTGGACTCTGCCCCACCTTCTGATGGGTTTGCAATCTATATAT 1736
Db 1629 ACATTGATGAATATTCTTTGTGGACTCTGCCCCACCTTCTGATGGGTTTGCAATCTATATAT 1688
QY 1737 GGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCAATTTGT 1796
Db 1689 GGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCAATTTGT 1748
QY 1797 CCACAGTTAGATATACACTTTTGATGTTTGGACGTAGAGAAAAATTTATCAATTTTGGCT 1856
Db 1749 CCACAGTTAGATATACACTTTTGATGTTTGGACGTAGAGAAAAATTTATCAATTTTGGCT 1808
QY 1857 TCAATCAAAGGGATACCAGCCAAACAATATAAACAAGAGTGCAGAAAGTTTACTAGAT 1916
Db 1809 TCAATCAAAGGGATACCAGCCAAACAATATAAACAAGAGTGCAGAAAGTTTACTAGAT 1868
QY 1917 TTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAATTAAGTGGTGGTCAAAAAAGA 1976
Db 1869 TTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAATTAAGTGGTGGTCAAAAAAGA 1928
QY 1977 AAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGACTGCTGCTAGATGAACCA 2036
Db 1929 AAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGACTGCTGCTAGATGAACCA 1988
QY 2037 ACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAA 2096
Db 1989 ACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAA 2048
QY 2097 GCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCAGAT 2156
Db 2049 GCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCAGAT 2108
QY 2157 AGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTGGTCTTTCATGTTCTCTCAA 2216
Db 2109 AGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTGGTCTTTCATGTTCTCTCAA 2168
QY 2217 AGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCCACAGAA 2276
Db 2169 AGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCCACAGAA 2228
QY 2277 TCTCTTTCTTCACTGGTTAAACACACATATACCTGGAGCTACTTTATTACAACAGAAATGAC 2336
Db 2229 TCTCTTTCTTCACTGGTTAAACACACATATACCTGGAGCTACTTTATTACAACAGAAATGAC 2288
QY 2337 CAACAACCTTGTGTATAGCTTGGCTTTCAAGGACATGGACAAAATTTTCAGGTTTGTCTTCT 2396
Db 2289 CAACAACCTTGTGTATAGCTTGGCTTTCAAGGACATGGACAAAATTTTCAGGTTTGTCTTCT 2348
QY 2397 GCCCTAGACAGTCATTCAAAATTTGGGTGTCATTTCTTATGGTGTGTTCCATGACACTTTG 2456
Db 2349 GCCCTAGACAGTCATTCAAAATTTGGGTGTCATTTCTTATGGTGTGTTCCATGACACTTTG 2408
QY 2457 GAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGTA 2516
Db 2409 GAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGTA 2468
QY 2517 TTTACTCAGCAGCCACTGGAGGAAAGAAATGGATTCAAATCTTTTGATGAATGGAAACAG 2576

Db 2469 TTTACTCAGCAGCCACTGGAGGAGAAATGGATTCAAATCTTTTGATGAAATGGAAACAG 2528
QY 2577 AGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCAACCATGAGCCTTTTGAAA 2636
Db 2529 AGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCAACCATGAGCCTTTTGAAA 2588
QY 2637 CAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAACCGTGAAAGTAAATCA 2696
Db 2589 CAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAACCGTGAAAGTAAATCA 2648
QY 2697 GTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTTG 2756
Db 2649 GTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTTG 2708
QY 2757 GTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATATTT 2816
Db 2709 GTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATATTT 2768
QY 2817 CTAAAACTGGAGACAAACCCACATAAAATACAAAAACAAGTCTGCTTCTTCAAAATTCGCT 2876
Db 2769 CTAAAACTGGAGACAAACCCACATAAAATACAAAAACAAGTCTGCTTCTTCAAAATTCGCT 2828
QY 2877 GACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAAATGGTGACGATG 2936
Db 2829 GACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAAATGGTGACGATG 2888
QY 2937 ATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGGCTTTTAAATGTGATGCAT 2996
Db 2889 ATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGGCTTTTAAATGTGATGCAT 2948
QY 2997 TCAGAAAAAGGACTATGTTTTTGGCAGCTGTTTTTCAACAGTACTATGGTTTTATTTCTTTACCT 3056
Db 2949 TCAGAAAAAGGACTATGTTTTTGGCAGCTGTTTTTCAACAGTACTATGGTTTTATTTCTTTACCT 3008
QY 3057 ATATTAGTGAATATCATTTAGTAACTACTATCTTTTATCATTTAAATGTGACTGAAACCATC 3116
Db 3009 ATATTAGTGAATATCATTTAGTAACTACTATCTTTTATCATTTAAATGTGACTGAAACCATC 3068
QY 3117 CAGATCTGGAGTACCCCATTTCTTCAAGAAATTAAGTATAGTTTTTAAAAATGAGCTG 3176
Db 3069 CAGATCTGGAGTACCCCATTTCTTCAAGAAATTAAGTATAGTTTTTAAAAATGAGCTG 3128
QY 3177 TATTTTCAAGCAGCTTTGCTTGGAAATCATTTACTGCAATGCCACCTTACTTTTGGCATG 3236
Db 3129 TATTTTCAAGCAGCTTTGCTTGGAAATCATTTACTGCAATGCCACCTTACTTTTGGCATG 3188
QY 3237 GAAATGCAGAGAAATCATAAAGTCAAAGCTTATATCTCAACTTAACTTTTCAGGTCTTTTG 3296
Db 3189 GAAATGCAGAGAAATCATAAAGTCAAAGCTTATATCTCAACTTAACTTTTCAGGTCTTTTG 3248
QY 3297 CCATCTGCATATTGGATTGGACAGCTGTTGTTGATATCCCTTATTTTTTATCATCTT 3356
Db 3249 CCATCTGCATATTGGATTGGACAGCTGTTGTTGATATCCCTTATTTTTTATCATCTT 3308
QY 3357 ATTTTGATGTAGGAAGCTTATTTGGCATTTCAATTATGGAATATATTTTTTATCTGTAAAG 3416
Db 3309 ATTTTGATGTAGGAAGCTTATTTGGCATTTCAATTATGGAATATATTTTTTATCTGTAAAG 3368
QY 3417 TTCCCTGCTGTGGTTTTTTTGCCTTATTTGGTTATGTTCCATCAGTTATTTCTGTTCACTTAT 3476
Db 3369 TTCCCTGCTGTGGTTTTTTTGCCTTATTTGGTTATGTTCCATCAGTTATTTCTGTTCACTTAT 3428
QY 3477 ATTGCTTCTTTTCACTTTTAAAGAAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTAT 3536
Db 3429 ATTGCTTCTTTTCACTTTTAAAGAAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATCTAT 3488
QY 3537 TCTGTGCAGCGTTGGCTTGTATTGCAATCAGTGAATAAATCTTTCTTTATGGGATACACA 3596
Db 3489 TCTGTGCAGCGTTGGCTTGTATTGCAATCAGTGAATAAATCTTTCTTTATGGGATACACA 3548
QY 3597 ATTGCAACTATTTCTTCAATTAAGCTTTTGTATCATCATTCCTCAATCTATCCACTTCTAGGT 3656
Db 3549 ATTGCAACTATTTCTTCAATTAAGCTTTTGTATCATCATTCCTCAATCTATCCACTTCTAGGT 3608

QY	3657	TGCCTGATTTCTTTTCATAAAGATTTCTTTGGAAGAATGTACGAAAAAATGTGGACACCTAT	3711
Db	3609	TGCCTGATTTCTTTTCATAAAGATTTCTTTGGAAGAATGTACGAAAAAATGTGGACACCTAT	3668
QY	3717	AATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTGTGG	3776
Db	3669	AATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTGTGG	3728
QY	3777	ATTTTCCCTTTACAAATACTATGAGAAAAAATATGGAGCAGATCAATAAGAAAAAGATCCC	3836
Db	3729	ATTTTCCCTTTACAAATACTATGAGAAAAAATATGGAGCAGATCAATAAGAAAAAGATCCC	3788
QY	3837	TTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACCAGACAAT	3896
Db	3789	TTTTTTCAGAAACCTTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACCAGACAAT	3848
QY	3897	GAGGATGAAGATGAAGATGTCAAAGCTCAAAGACTAAAGGTCAAAGAGCTGATGGGTTGC	3956
Db	3849	GAGGATGAAGATGAAGATGTCAAAGCTCAAAGACTAAAGGTCAAAGAGCTGATGGGTTGC	3908
QY	3957	CAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGATATGATGAC	4016
Db	3909	CAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGATATGATGAC	3968
QY	4017	AAGAAAGATTTTCTTCTTCAAGAAAAAGTAAAGAAAGTGGCAACTTAAATACATCTCTTTC	4076
Db	3969	AAGAAAGATTTTCTTCTTCAAGAAAAAGTAAAGAAAGTGGCAACTTAAATACATCTCTTTC	4028
QY	4077	TGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGCACA	4136
Db	4029	TGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGCACA	4088
QY	4137	ATTATTAATATTCTGTTGGTGATATTGAACCACTTCAGGCCAGGTATTTTATGAGAGAT	4196
Db	4089	ATTATTAATATTCTGTTGGTGATATTGAACCACTTCAGGCCAGGTATTTTATGAGAGAT	4148
QY	4197	TATTCCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGTGTATGGGTTACTGTCTCTCAG	4256
Db	4149	TATTCCTTCAGAGTCAAGTGAAGATGATGATTCACCTGAAGTGTATGGGTTACTGTCTCTCAG	4208
QY	4257	ATAAACCCCTTTGTGGCCAGATACTACATTCGAGGAACATTTTGAATTTTATGGAGCTGTC	4316
Db	4209	ATAAACCCCTTTGTGGCCAGATACTACATTCGAGGAACATTTTGAATTTTATGGAGCTGTC	4268
QY	4317	AAAGGAATGAGTGCBAAGTGACATGAAAGAAAGTCATAAGTCGAATAACACATGCCACTTGAT	4376
Db	4269	AAAGGAATGAGTGCBAAGTGACATGAAAGAAAGTCATAAGTCGAATAACACATGCCACTTGAT	4328
QY	4377	TTAAAGAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAAGTTG	4436
Db	4329	TTAAAGAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAAGTTG	4388
QY	4437	TGTTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTTGCTAGATGAACCATCTACA	4496
Db	4389	TGTTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTTGCTAGATGAACCATCTACA	4448
QY	4497	GGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGCAATTTAAAAAC	4556
Db	4449	GGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGCAATTTAAAAAC	4508
QY	4557	AGAAAGCGGGTGTCTATTTCTGACCCTCCTATATGGAGGAGGCAGAGGCTGTCTGTGAT	4616
Db	4509	AGAAAGCGGGTGTCTATTTCTGACCCTCCTATATGGAGGAGGCAGAGGCTGTCTGTGAT	4568
QY	4617	CGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAAACATCTAAAG	4676
Db	4569	CGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAAACATCTAAAG	4628
QY	4677	AGTAAATTTGGAAAAGGCTACTTTTGTGAAATTTAAATTTGAAGGACTGGATAGAAAACCTA	4736
Db	4629	AGTAAATTTGGAAAAGGCTACTTTTGTGAAATTTAAATTTGAAGGACTGGATAGAAAACCTA	4688

Qy	4737	GAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAATATGCAAGCGTCAGGAA	4799
Db	4689	GAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAATATGCAAGCGTCAGGAA	4748
Qy	4797	AGTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTACAA	4856
Db	4749	AGTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTACAA	4808
Qy	4857	TCCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTTCT	4916
Db	4809	TCCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTTCT	4868
Qy	4917	CAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAAGAACCAAGAGGAGGAAGATAAT	4976
Db	4869	CAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAAGAACCAAGAGGAGGAAGATAAT	4928
Qy	4977	AGTTGTGGAACCTTTAAACAGCACACTTTGTGTGGAAACGAACACCAAGAAAGATAGTAGTA	5036
Db	4929	AGTTGTGGAACCTTTAAACAGCACACTTTGTGTGGAAACGAACACCAAGAAAGATAGTAGTA	4988
Qy	5037	TTTTGAATTTGTATTGTTCCGCTCTGCTTACTGGGACTTCTTTCTTTTTCACCTAAATTTTA	5096
Db	4989	TTTTGAATTTGTATTGTTCCGCTCTGCTTACTGGGACTTCTTTCTTTTTCACCTAAATTTTA	5048
Qy	5097	ACTTTGGTTTTAAAAAGTTTTTTTATTGGAATGGTAACTGGAGAACCAAG	5144
Db	5049	ACTTTGGTTTTAAAAAGTTTTTTTATTGGAATGGTAACTGGAGAACCAAG	5096
RESULT 6			
AX417828			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Matches 5014; Conservative			
85.2%; Score 4664; DB 6; Length 5262;			
99.9%; Pred. No. 0;			
0; Mismatches			
7; Indels			
0; Gaps			
Qy	97	AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA	156
Db	238	AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA	297
Qy	157	GAACACITCTACTGAAGAATTACTTAATTAATGCAGAACCCAAAAGAGTAGTGTTCAGG	216
Db	298	GAACACITCTACTGAAGAATTACTTAATTAATGCAGAACCCAAAAGAGTAGTGTTCAGG	357
Qy	217	AAATCTTTTCCACTATTTTTTTTTTATTTTGGTTAATATTATAGCATGATGCCAA	276
Db	358	AAATCTTTTCCACTATTTTTTTTTTATTTTGGTTAATATTATAGCATGATGCCAA	417
Qy	277	ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCCTATGGACAAGTTTACTCTTT	336
Db	418	ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCCTATGGACAAGTTTACTCTTT	477
Qy	337	CTAATCTTAATCTTTGGATATATCTCCAGTGACTAATATTACAGCAGCATCATGCAGAAAG	396

Db 478 CTAATCTAATTCCTGGATATACTCCAGTGACTAATATTAACAGCAGCATCATGCAGAAAG 537
Qy 397 TGCTACTGATCATCTACCTGATGTCTAATAATTACTGAAGAATATACAAATGAAAAAGAAA 456
Db 538 TGCTACTGATCATCTACCTGATGTCTAATAATTACTGAAGAATATACAAATGAAAAAGAAA 597
Qy 457 TGTTAACATCCAGTCTCTCTAAGCCGAGCAACCTTTGTAGGTGTGGTTTTCAAAGACTCCA 516
Db 598 TGTTAACATCCAGTCTCTCTAAGCCGAGCAACCTTTGTAGGTGTGGTTTTCAAAGACTCCA 657
Qy 517 TGTCCTATGAACCTTCGTTTTTTCCTGATATGATCCAGTATCTTCTATTTATATGGATT 576
Db 658 TGTCCTATGAACCTTCGTTTTTTCCTGATATGATCCAGTATCTTCTATTTATATGGATT 717
Qy 577 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTTCACAG 636
Db 718 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTTCACAG 777
Qy 637 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA 696
Db 778 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGA 837
Qy 697 AGGAGCTGGAGTCAACTAAAGCTGTTATTTATGGAGAAACTGCTGTTGTAGAAATAGATA 756
Db 838 AGGAGCTGGAGTCAACTAAAGCTGTTATTTATGGAGAAACTGCTGTTGTAGAAATAGATA 897
Qy 757 CCTTTCCTCCGAGGAGTAATTTAATATACCTAGTTATAGCATTTTCACTTTTGGATACT 816
Db 898 CCTTTCCTCCGAGGAGTAATTTAATATACCTAGTTATAGCATTTTCACTTTTGGATACT 957
Qy 817 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATAA 876
Db 958 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATAA 1017
Qy 877 TGGGACTTCATGATACTGCCTTTTGGCTTTTCCCTGGGTTCTTCTATAWACAAGTTTAAATTT 936
Db 1018 TGGGACTTCATGATACTGCCTTTTGGCTTTTCCCTGGGTTCTTCTATAWACAAGTTTAAATTT 1077
Qy 937 TTCTTATGTCCCTTCTTATGGCAGTCAATGCGACAGCTTCTTTGTTAATTTCTCAAAAGTA 996
Db 1078 TTCTTATGTCCCTTCTTATGGCAGTCAATGCGACAGCTTCTTTGTTAATTTCTCAAAAGTA 1137
Qy 997 GCAGCATGTGATATTTCTGCTTTTTTCCCTTATGGATTATCATCTGTAATTTTGTGCTT 1056
Db 1138 GCAGCATGTGATATTTCTGCTTTTTTCCCTTATGGATTATCATCTGTAATTTTGTGCTT 1197
Qy 1057 TAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTGTA 1116
Db 1198 TAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTGTA 1257
Qy 1117 CTGTGGCTTTTGGATTTATTTGGCCTTATGATAATCCTCATAGAAAGTTTTCCTCAAAATCGT 1176
Db 1258 CTGTGGCTTTTGGATTTATTTGGCCTTATGATAATCCTCATAGAAAGTTTTCCTCAAAATCGT 1317
Qy 1177 TAGTGTGGCTTTTCAAGTCCCTTCTGTCACTGTACTTTTGTGATTTGTAATGACAGGTCA 1236
Db 1318 TAGTGTGGCTTTTCAAGTCCCTTCTGTCACTGTACTTTTGTGATTTGTAATGACAGGTCA 1377
Qy 1237 TGCAATTTAGAAAGATTTTAAATGAAGGTGCTTCAATTTTCAAAATTTGACTGCAGGCCCATATC 1296
Db 1378 TGCAATTTAGAAAGATTTTAAATGAAGGTGCTTCAATTTTCAAAATTTGACTGCAGGCCCATATC 1437
Qy 1297 CTCTAATTTATTAACAATTCATGCTCACACTTTAATAGTATATTTCTATGTCCTTGGCTG 1356
Db 1438 CTCTAATTTATTAACAATTCATGCTCACACTTTAATAGTATATTTCTATGTCCTTGGCTG 1497
Qy 1357 TCTATCTTGATCAAGTCAATCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1416
Db 1498 TCTATCTTGATCAAGTCAATCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1557
Qy 1417 TGAAGCCTTCATATTGGTCAAAAGAGCAAAAGAAATATGAGGAGTTATCAGAGGGCAATG 1476

Db 1558 TGAAGCCTTCATATTGGTCAAAAGAGCAAAAGAAATATAGGAGTTATCAGAGGGCAATG 1617
Qy 1477 TTAATGGAATAATAGTTTGTAGTGAATATTATGAGCCAGTTTCTTTCAGAAATTTGTAGGAA 1536
Db 1618 TTAATGGAATAATAGTTTGTAGTGAATATTATGAGCCAGTTTCTTTCAGAAATTTGTAGGAA 1677
Qy 1537 AAGAAGCCATAAGAATTAGTGGTATTTCAGAAAGACATACAGAAAAGAGGTGAAATGTGG 1596
Db 1678 AAGAAGCCATAAGAATTAGTGGTATTTCAGAAAGACATACAGAAAAGAGGTGAAATGTGG 1737
Qy 1597 AGGCTTTGAGAAATTTGTCATTTGACATATATCAGGGGTGAGATTACTGCCTTACTTGGCC 1656
Db 1738 AGGCTTTGAGAAATTTGTCATTTGACATATATCAGGGGTGAGATTACTGCCTTACTTGGCC 1797
Qy 1657 ACAGTGGAAACAGGAAAGAGTACATTTGATGAATATCTTTGTGGACTCTGCCACCTTCTG 1716
Db 1798 ACAGTGGAAACAGGAAAGAGTACATTTGATGAATATCTTTGTGGACTCTGCCACCTTCTG 1857
Qy 1717 ATGGGTTTGCACTCTATATATATGGACACAGAGTCTCAGAAAATAGATGAATGTTTGAAGCAA 1776
Db 1858 ATGGGTTTGCACTCTATATATATGGACACAGAGTCTCAGAAAATAGATGAATGTTTGAAGCAA 1917
Qy 1777 GAAAAATGATTGGCAATTTGTCACAGTTTAGATATACACATTTTGATGTTTTCAGCAGTAGAAG 1836
Db 1918 GAAAAATGATTGGCAATTTGTCACAGTTTAGATATACACATTTTGATGTTTTCAGCAGTAGAAG 1977
Qy 1837 AAAATTTATCAATTTTGGCTTCAATCAAAAGGGATACCAGCCAAATATATATACAAAGAAG 1896
Db 1978 AAAATTTATCAATTTTGGCTTCAATCAAAAGGGATACCAGCCAAATATATATACAAAGAAG 2037
Qy 1897 TGCAGAAAGGTTTTTACTAGATTTTAGACATGACAGACTATCAAAAGATAACCAAGCTAAAAAAT 1956
Db 2038 TGCAGAAAGGTTTTTACTAGATTTTAGACATGACAGACTATCAAAAGATAACCAAGCTAAAAAAT 2097
Qy 1957 TAAAGTGGTGTCAAAAAAGAAAGCTGTCAATTAGGAATGCTGTTCTTGGGAACCCAAAGA 2016
Db 2098 TAAAGTGGTGTCAAAAAAGAAAGCTGTCAATTAGGAATGCTGTTCTTGGGAACCCAAAGA 2157
Qy 2017 TACTGCTGCTAGATGAACCAACAGCTGGAAATGGACCCCTGTTCTCGACATATTTGTATGGA 2076
Db 2158 TACTGCTGCTAGATGAACCAACAGCTGGAAATGGACCCCTGTTCTCGACATATTTGTATGGA 2217
Qy 2077 ATCTTTTAAAAATACAGAAAAAGCCAAATCGGGTGCAGTGTTCAGTACTCATTTTCATGGATG 2136
Db 2218 ATCTTTTAAAAATACAGAAAAAGCCAAATCGGGTGCAGTGTTCAGTACTCATTTTCATGGATG 2277
Qy 2137 AAGCTGACATTTCTTGCAGATAGGAAAGCTGTGATATACAAAGGAATGCTGAAATGTGTTG 2196
Db 2278 AAGCTGACATTTCTTGCAGATAGGAAAGCTGTGATATACAAAGGAATGCTGAAATGTGTTG 2337
Qy 2197 GTTCTTCAATGTTTCTCAAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAG 2256
Db 2338 GTTCTTCAATGTTTCTCAAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAG 2397
Qy 2257 ACAAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAAACATATACCTGGAGCTA 2316
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VERSION AX417824.1 GI:21522942
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Hu.Y. and Nepomnichy, B.
AUTHORS Human transporter proteins and polynucleotides encoding the same
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JOURNAL LEXICON GENETICS INC (US)
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DEFINITION Sequence 3 from Patent WO231147.
ACCESSION AX417826
VERSION AX417826.1 GI:21522943
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Hu, Y. and Nepomnichy, B.
TITLE Human transporter proteins and polynucleotides encoding the same
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LEXICON GENETICS INC (US)
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VERSION AX537470.1 GI:25269277
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Chen,H., Kilinski,L. and le Bihan,S.
TITLE Abcas transporter and uses thereof
JOURNAL Patent: WO 02070690-A 1 12-SEP-2002;
Active Pass Pharmaceuticals, Inc. (CA)
FEATURES
source
1. 5463
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 51.6%; Score 2826; DB 6; Length 5463;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2876; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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AX714300 3268 bp DNA linear PAT 15-APR-2003
LOCUS AX714300 Sequence 984 from Patent EP1293569.
DEFINITION AX714300
ACCESSION AX714300
VERSION AX714300.1 GI:29889252
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.
TITLE Full-length cDNAs
JOURNAL Patent: EP 1293569-A 984 19-MAR-2003;
Helix Research Institute (JP) ; Research Association for
Biotechnology (JP)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Query Match 50.0%; Score 2739; DB 6; Length 3268;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3039; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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RESULT 11
AK056533
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ACCESSION AK056533
VERSION AK056533.1 GI:16551960
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3268)
Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: RAB and
HRI.
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VERSION AX537472.1 GI:25269279
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ORGANISM Homo sapiens
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AUTHORS Chen,H., Kilinski,L. and le Bihan,S.
TITLE Abca5 transporter and uses thereof
JOURNAL Patent: WO 02070690-A 3 12-SEP-2002;
Active Pass Pharmaceuticals, Inc. (CA)
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LOCUS HSA512612 2845 bp mRNA linear PRI 06-JAN-2003
DEFINITION Homo sapiens mRNA for ABCA5 transporter (ABCA5 gene), V20+16 variant.
ACCESSION AJ512612
VERSION AJ512612.1 GI:27527021
KEYWORDS ABCA5 gene; ABCA5 transporter; alternative splicing.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petry,F., Kotthaus,A. and Hirsch-Ernst,K.I.
TITLE Molecular cloning and tissue distribution of a novel ATP-binding cassette (ABC) transporter belonging to the subfamily ABCA Unpublished
JOURNAL 2 (bases 1 to 2845)
AUTHORS Petry,F.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-2002) Petry F., Department of Toxicology, University of Goettingen, Robert-Koch-Strasse 40, Goettingen, Lower Saxony, D-37075, GERMANY
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ORIGIN

Query Match

47.8%; Score 2617; DB 9; Length 2845;

Best Local Similarity 99.9%; Pred. No. 0;									
Matches 2817; Conservative 0; Mismatches 4; Indels 0; Gaps 0;									
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QY	117	TCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAAT	176						
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QY	357	ACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGCTACTGATCATCTACCT	416						
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QY	477	AAGCCGAGCAACTTTGTAGGTGGTGTTCAAAGACTCCATGTCCTATGAACITCGTTTTT	536						
Db	427	AAGCCGAGCAACTTTGTAGGTGGTGTTCAAAGACTCCATGTCCTATGAACITCGTTTTT	486						
QY	537	TTTCCGTGATATGATCCAGTATCTTCTATTATATGGATTCAAGAGCTGGCTGTTCAAAA	596						
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QY	597	TCATGTGAGGCTGCTCAGTACTGGTCCCTCAGGTTTTCACAGTTTACAAACATCCATAGAT	656						
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QY	897	TTTTTGGCTTTCCTGGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCCTTCTTATG	956						
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QY	957	GCAGTCATTCGGACAGCTTCTTTTGTATTCTCCTCAAAGTAGCAGCATTTGTGATATTCTG	1016						
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QY	1017	CTTTTTTTCCTTTATGGATTATCATCTGTATTTTTTGTCTTTAATGCTGACACCTCTTTTT	1076						
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RESULT 14
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DEFINITION Homo sapiens mRNA for KIAA1888 protein, partial cds.
ACCESSION AB067475
VERSION AB067475.1 GI:15620834
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Nagase,T., Kikuno,R. and Ohara,O.
TITLE Prediction of the coding sequences of unidentified human genes.
XXI. The complete sequences of 60 new cDNA clones from brain which
code for large proteins
JOURNAL DNA Res. 8 (4), 179-187 (2001)
MEDLINE 21456161
PUBMED 11572484
REFERENCE 2 (bases 1 to 3112)
AUTHORS Ohara,O., Nagase,T. and Kikuno,R.
TITLE Direct Submission
JOURNAL Submitted (27-JUL-2001) Osamu Ohara, Kazusa DNA Research Institute,

Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
Fax:81-438-52-3914)

FEATURES
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Matches 2647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 15
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DEFINITION
ACCESSION      BX647447
VERSION        BX647447.1  GI:34366604
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 5243)
AUTHORS        Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
                Fobo,G., Han,M. and Wiemann,S.
CONSRMT        The German Human cDNA Consortium
TITLE          Direct Submission
JOURNAL        Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
                Neuherberg, GERMANY
COMMENT        Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
                Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                sequenced by BMFZ (Biomedical Research Center at the
                Heinrich-Heine-University, Duesseldorf/Germany) within the cDNA
                sequencing consortium of the German Genome Project. This clone
                (DKFZp451F117) is available at the RZPD in Berlin. Please contact
                the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
                information about the clone and the sequencing project is available
                at http://mips.gsf.de/proj/cDNA/.
FEATURES
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QY 3875 GCTTCCAGAACCCAGACCAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAA 3934
    841 GCTTCCAGAACCCAGACCAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAA 900
QY 3935 GGTCAAAGAGCTGATGGGTGCCAGTGTCTGTGAGGAGAAACCATCCATTATGCTCAGCAA 3994
    901 GGTCAAAGAGCTGATGGGTGCCAGTGTCTGTGAGGAGAAACCATCCATTATGCTCAGCAA 960
QY 3995 TTTGCATAAAGAAATATGATGACAAGAAAGATTTTCTTTCAAGAAAGTAAAGAAAGT 4054
    961 TTTGCATAAAGAAATATGATGACAAGAAAGATTTTCTTTCAAGAAAGTAAAGAAAGT 1020
QY 4055 GGCAACTAAATACATCTCTTCTGTGTGTAAGAAAGGAGAGATCTTAGGACTATTGGGTCC 4114
    1021 GGCAACTAAATACATCTCTTCTGTGTGTAAGAAAGGAGAGATCTTAGGACTATTGGGTCC 1080
QY 4115 AAATGGTGTGGCAAGCAAAAGCAAAATTAATATTCTTGGTGGTGATATTGAACCAACTTC 4174
    1081 AAATGGTGTGGCAAGCAAAAGCAAAATTAATATTCTTGGTGGTGATATTGAACCAACTTC 1140
QY 4175 AGGCCAGGTATTTTATGAGATTAATCTTTCAGAGACAAGTGAAGATGATGATTCACCTGAA 4234
    1141 AGGCCAGGTATTTTATGAGATTAATCTTTCAGAGACAAGTGAAGATGATGATTCACCTGAA 1200
QY 4235 GTGTATGGGTTACTGTCTCAGATAAAACCCCTTTGTGGCCAGATACATACATTGCAAGGAACA 4294
    1201 GTGTATGGGTTACTGTCTCAGATAAAACCCCTTTGTGGCCAGATACATACATTGCAAGGAACA 1260
QY 4295 TTTTGAAAATTTATGGAGCTGTCAAAGGAATGAGTGAAGTGAATGAAAGAGTCAATAAG 4354
    1261 TTTTGAAAATTTATGGAGCTGTCAAAGGAATGAGTGAAGTGAATGAAAGAGTCAATAAG 1320
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QY 4475 TTTGTAGATGAACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGC 4534
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Db 1501 AATTGGAACCTGCAATTTAAAAACAGAAAGCGGGCTGTATTCTGACCACTCACTATATGGA 1560

QY 4595 GGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTAAAGATGTAT 4654

Db 1561 GGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTAAAGATGTAT 1620

QY 4655 CGGAACAGTACAACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTTGGAAAATTAAATT 4714

Db 1621 CGGAACAGTACAACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTTGGAAAATTAAATT 1680

QY 4715 GAAGGACTGGATAGAAAACCTAGAAGTAGACCGCCTTCAAAGAGAAAATTCAGTATATTTT 4774

Db 1681 GAAGGACTGGATAGAAAACCTAGAAGTAGACCGCCTTCAAAGAGAAAATTCAGTATATTTT 1740

QY 4775 CCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGA 4834

Db 1741 CCCAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGA 1800

QY 4835 AGATGTTCAAGTCCCTTTTCACAATCTTTTTTAAGCTGGAAGAAAGCTAAACATGCTTTTTC 4894

Db 1801 AGATGTTCAAGTCCCTTTTCACAATCTTTTTTAAGCTGGAAGAAAGCTAAACATGCTTTTTC 1860

QY 4895 CATTGAAGAAATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTTTTGTAGAACTCACTAA 4954

Db 1861 CATTGAAGAAATATAGCTTTTCTCAAGCAACATTGGAACAGGTTTTTTGTAGAACTCACTAA 1920

QY 4955 AGAACAGAGGAGGAAGATAATAGTTGTGGAACITTTAAACAGCACACITTTGGTGGGAACG 5014

Db 1921 AGAACAGAGGAGGAAGATAATAGTTGTGGAACITTTAAACAGCACACITTTGGTGGGAACG 1980

QY 5015 AACACAAGAAAGATAGAGTAGTATTTTGAAATTTTGGTCTGCTGCTACTGGGACTT 5074

Db 1981 AACACAAGAAAGATAGAGTAGTATTTTGAAATTTTGGTCTGCTGCTACTGGGACTT 2040

QY 5075 CTTTCTTTTTTCACTTAATTTTAACTTTGGTTTAAAGTTTTTTTATTGGAAATGGTAACTG 5134

Db 2041 CTTTCTTTTTTCACTTAATTTTAACTTTGGTTTAAAGTTTTTTTATTGGAAATGGTAACTG 2100

QY 5135 GAGAACCAAGAACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTG 5194

Db 2101 GAGAACCAAGAACGCACTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTG 2160

QY 5195 TGTGTTGCTTTTCTTTAAATPAAAAAGTATGTATATAATTAAAGTGAAGCTGCAATGTTGTATT 5254

Db 2161 TGTGTTGCTTTTCTTTAAATPAAAAAGTATGTATATAATTAAAGTGAAGCTGCAATGTTGTATT 2220

QY 5255 GAAGTATATTGAACCTATATAGTTTGTATGTCATCTTTTTCACCAATTCAGAAAACAGTGCTT 5314

Db 2221 GAAGTATATTGAACCTATATAGTTTGTATGTCATCTTTTTCACCAATTCAGAAAACAGTGCTT 2280

QY 5315 CTGAATTTGTGATTTAAAGGAATGTAAAGAAAGTTTTTATTAAAGTATCTTTTAAG 5374

Db 2281 CTGAATTTGTGATTTAAAGGAATGTAAAGAAAGTTTTTATTAAAGTATCTTTTAAG 2340

QY 5375 TTTATGCGCATCTTCTTAAATPAAAGTACGTAATGTTCCAATCTAAATPAAAAACTAAT 5430

Db 2341 TTTATGCGCATCTTCTTAAATPAAAGTACGTAATGTTCCAATCTAAATPAAAAACTAAT 2396

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 60.0 , Gapext 60.0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5475	100.0	5475	7	ABs57751 cDNA enco
2	5181	94.6	6525	6	ABn89594 Human ATP
3	5086	92.9	6369	6	Ad33648 Human TRI
4	4664	85.2	5262	6	AAd37620 Human tra
5	4572	83.5	4929	6	AAd37618 Human tra
6	4408	80.5	4785	6	AAd37619 Human tra
7	2826	51.6	5463	7	ABs57749 cDNA enco
8	2739	50.0	3268	7	AdA53416 Human cod
9	2713	49.6	4917	7	ABs57750 Coding se
10	2633	48.1	2723	9	AdC51606 Human mac
11	1497	27.3	1548	6	ABK35706 cDNA sequ
12	1350	24.7	2481	7	ABz35938 Human sec
13	1343	24.5	3928	6	ABK35707 cDNA sequ
14	829	15.1	1632	7	ABz35926 Human sec
15	783	14.3	1506	3	AAC81717 Human sec
16	744	13.6	1818	5	AAs63176 Human pur
17	610	11.1	1677	5	AAS70746 DNA enco
18	448	8.2	477	6	ABl87826 Human ova
19	440	8.0	612	6	ABl99789 Human ova
20	376	6.9	1346	6	ABl64459 Stomach c
21	376	6.9	1346	6	ABl63763 Breast ca
22	376	6.9	1346	6	ABn96909 Gene #340
23	358	6.5	389	3	AAA42471 Human sec

24	331	6.0	476	6	ABL81384	Ab181384 Human ova
25	324	5.9	469	6	ABN95385	ABn95385 Gene #188
26	324	5.9	469	7	ABX74830	Abx74830 Human cDN
27	299	5.5	412	6	ABL81393	Ab181393 Human ova
28	286	5.2	1803	5	AAS71497	Aas71497 DNA enco
29	284	5.2	431	6	ABL89460	Ab189460 Human pol
30	277	5.1	1994	6	ABN85542	ABn85542 Human CBP
31	243	4.4	2079	4	AAF56391	Aaf56391 ABC trans
32	242	4.4	341	2	AAV89159	AAv89159 EST clone
33	227	4.1	252	2	AAV89430	AAv89430 EST clone
34	213	3.9	7838	4	AAI99209	AAi99209 Human exc
35	213	3.9	7838	4	AAK84993	AAk84993 Human imm
36	213	3.9	7838	5	AAI63559	AAi63559 Human kid
37	200	3.7	440	5	ABV61636	ABv61636 Human pro
38	193	3.5	1478	4	AAI99207	AAi99207 Human exc
39	193	3.5	1478	4	AAK84991	AAk84991 Human imm
40	193	3.5	1478	5	AAI63557	AAi63557 Human kid
41	178	3.3	474	4	ABA58572	ABa58572 Human foe
42	178	3.3	474	4	AAI38234	AAi38234 Probe #69
43	178	3.3	474	4	AAK32391	AAk32391 Human bon
44	178	3.3	474	4	AAK06692	AAk06692 Human bra
45	178	3.3	474	4	ABS32098	ABs32098 Human liv

ALIGNMENTS

RESULT 1
ABs57751
ID ABs57751 standard; cDNA; 5475 BP.
XX
AC ABs57751;
XX
DT 04-FEB-2003 (first entry)
XX
DE cDNA encoding novel human ATP binding cassette ABCA5 transporter #2.
XX
KW Human; ATP binding cassette; ABC; ABCA5; transporter;
KW neurotoxin transport; beta-amyloid peptide; chromosome mapping;
KW blood brain barrier transport; tissue typing; predictive medicine;
KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key
CDS Location/Qualifiers
FT 114..5042
FT /*tag= a
FT /product= "ABCA5"
FT /note= "ATP binding cassette (ABC) A5 transporter"

US2002123107-A1.
PN
XX
PD 05-SEP-2002.
XX
PF 01-MAR-2002; 2002US-00090458.
XX
PR 02-MAR-2001; 2001US-0272885P.
XX
PA (ACTI-) ACTIVE PASS PHARM INC.
XX
PI Chen H, Kilinski L, Le Bihan S;
XX
DR WPI; 2003-066798/06.
DR P-PSDB; ABG72424.

XX
PT Novel isolated ATP binding cassette transporter family polypeptide,
PT ABCA5, useful for treating disorders associated with aberrant or unwanted
PT ABCA5 transporter expression or activity.
XX
PS Claim 2; Page 39-42; 52pp; English.
XX
CC The invention describes an isolated ATP binding cassette (ABC)
CC transporter family polypeptide (I), designated ABCA5. (I) or the

CC polynucleotide encoding it (II) are useful as targets for developing
CC modulating agents to regulate a variety of cellular processes,
CC particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC (BBB), as targets for developing modulating agents of multi-drug
CC resistance, as diagnostic and therapeutic tools, or to treat disorders
CC associated with aberrant or unwanted ABCA5 transporter expression or
CC activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC screening assays, detection assays (e.g., chromosomal mapping, tissue
CC typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC (III) are useful as reagents or targets in assays applicable to treatment
CC and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC -hybrid or three-hybrid assay; and to identify other proteins which bind
CC to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC activity; to locate gene regions associated with genetic disease or to
CC associate ABCA5 with the disease, to identify an individual from a minute
CC biological sample (tissue typing), and to aid in forensic identification
CC of the biological sample. This sequence encodes a novel human ATP binding
CC cassette (ABC) A5 transporter
XX
SQ Sequence 5475 BP; 1705 A; 917 C; 1048 G; 1804 T; 0 U; 1 Other;

Query Match		100.0%;	Score 5475;	DB 7;	Length 5475;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 5475;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGGTCCGGCGCCTCGCACAGATCCNAGCTGGTCCACCGCGACTGAGTCAACAGACTCGAGC	60		
Db	1	GGGTCCGGCGCCTCGCACAGATCCNAGCTGGTCCACCGCGACTGAGTCAACAGACTCGAGC	60		
QY	61	GGGTCCAGGCTGACAGCTCTGCGGCTCGGCGCTGGGCTTATTCAGAAAACATGTCCA	120		
Db	61	GGGTCCAGGCTGACAGCTCTGCGGCTCGGCGCTGGGCTTATTCAGAAAACATGTCCA	120		
QY	121	CTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAATTACT	180		
Db	121	CTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAATTACT	180		
QY	181	TAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTATTTTTT	240		
Db	181	TAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTATTTTTT	240		
QY	241	TATTTTGGTTAATTAATTAATAGCATGATGCATCCAAATAGAAATATGAAGAAGTGCCTA	300		
Db	241	TATTTTGGTTAATTAATTAATAGCATGATGCATCCAAATAGAAATATGAAGAAGTGCCTA	300		
QY	301	ATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAATCTAATCTTGGATATATC	360		
Db	301	ATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAATCTAATCTTGGATATATC	360		
QY	361	CAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTACCTGATG	420		
Db	361	CAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTACCTGATG	420		
QY	421	TCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTCTCTAAGC	480		
Db	421	TCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTCTCTAAGC	480		
QY	481	CGAGCAACTTTGTAGGTGTGGTTTCAAAAGACTCCATGTCCTATGAACCTTCGTTTTTTC	540		
Db	481	CGAGCAACTTTGTAGGTGTGGTTTCAAAAGACTCCATGTCCTATGAACCTTCGTTTTTTC	540		
QY	541	CTGATATGATCCAGTATCTTCTATTATATGATTCAGAGCTGGCTGTTCAAAATCAT	600		
Db	541	CTGATATGATCCAGTATCTTCTATTATATGATTCAGAGCTGGCTGTTCAAAATCAT	600		
QY	601	GTGAGGCTGCTCAGTACTGGTCCCTCAGGTTTTCACAGTTTTCAGAGCATCCATAGATGCTG	660		

Db	601	GTGAGGCTGCTCAGTACTGGTCCCTCAGGTTTTCACAGTTTTCAGAGCATCCATAGATGCTG	660		
QY	661	CCATTATACAGTTGAAGACCAATGTTTCTCTTTTGAAGAGGAGCTGGAGTCAACTAAAGCTG	720		
Db	661	CCATTATACAGTTGAAGACCAATGTTTCTCTTTTGAAGAGGAGCTGGAGTCAACTAAAGCTG	720		
QY	721	TTATTATGGGAGAAAACCTGCTGTGTAGAAAATAGATACCTTCTCCCGAGGAGTAAATTTAA	780		
Db	721	TTATTATGGGAGAAAACCTGCTGTGTAGAAAATAGATACCTTCTCCCGAGGAGTAAATTTAA	780		
QY	781	TATACCTAGTTATAGCATTTTTCACCTTTTGGGATACCTTTTGGCAATTCATATCGTAGCAG	840		
Db	781	TATACCTAGTTATAGCATTTTTCACCTTTTGGGATACCTTTTGGCAATTCATATCGTAGCAG	840		
QY	841	AAAAAGAAAAAAATAAAAGAAATTTTAAAGATAATGGGACTTCATGATACCTGCTTTT	900		
Db	841	AAAAAGAAAAAAATAAAAGAAATTTTAAAGATAATGGGACTTCATGATACCTGCTTTT	900		
QY	901	GGCTTTCTGCGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCCTCTTATGGCAG	960		
Db	901	GGCTTTCTGCGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCCTCTTATGGCAG	960		
QY	961	TCATTGCGACAGCTTCTTTGTTTATTTCTCTCAAGTAGCAGANTGTGATATTTCTGCTTT	1020		
Db	961	TCATTGCGACAGCTTCTTTGTTTATTTCTCTCAAGTAGCAGANTGTGATATTTCTGCTTT	1020		
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Db	1021	TTTTCTTTTATGGATTATCATCTGTATTTTGTCTTAAATCTGACACCTCTTTTAAATAA	1080		
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QY	1201	GTCACTGTACTTTTGTGATTGGTATTCACAGGTTCATGCAATTTAGAAAGATTTTAAATGAAG	1260		
Db	1201	GTCACTGTACTTTTGTGATTGGTATTCACAGGTTCATGCAATTTAGAAAGATTTTAAATGAAG	1260		
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Db	1261	GTGCTTCATTTCAAATTTGACTGCAGGCCCATATCCTCTAATATTATACAATTTATCATGC	1320		
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Db	1321	TCACACTTAATAGTATATTCTATGTCTCTTGGCTGTCTATCTTGAAGCTTCATTCAG	1380		
QY	1381	GGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCTTCATATTTGGTCAAAGA	1440		
Db	1381	GGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCTTCATATTTGGTCAAAGA	1440		
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QY	1501	AAATTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAAATTAGTGTA	1560		
Db	1501	AAATTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAAATTAGTGTA	1560		
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Db	1621	ACATATATGAGGGTCAGATTACTGCTTACTTGGCCACAGTGGAAACAGGAAGAGTACAT	1680		
QY	1681	TGATGAATATTTTGTGGACTCTGCCCCACCTTCTGTGATGGGTTTGCATCTATATATGGAC	1740		
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Db |||||
1801 AGTTAGATATACACTTTTGATGTTTTGACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAA 1860
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Db |||||
1861 TCAAAAGGGATACCAGCCCAACAATATAATACAAGAGTGCAGAAAGTTTTTACTAGATTTAG 1920
QY 1921 ACATGCAGACTATCAAAAGATAACCAAGCTAAAAATTAAGTGGTGGTCAAAAAAGAAAGC 1980
Db |||||
1921 ACATGCAGACTATCAAAAGATAACCAAGCTAAAAATTAAGTGGTGGTCAAAAAAGAAAGC 1980
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Db |||||
1981 TGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAACCAACAG 2040
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Db |||||
2041 CTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAAAGCCA 2100
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QY 3001 AAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGTTTATTCTTTACCTATAT 3060
Db |||||
3001 AAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGTTTATTCTTTACCTATAT 3060
QY 3061 TAGTGAATATCATTTAGTAACTACTATCTTTTATCATTTTAAATGTGACTGAAACCATCCAGA 3120
Db |||||
3061 TAGTGAATATCATTTAGTAACTACTATCTTTTATCATTTTAAATGTGACTGAAACCATCCAGA 3120
QY 3121 TCTGAGTACCCCATTCCTTCAAGAAATTACTTGATATAGTTTTTAAATTTGAGCTGTATT 3180
Db |||||
3121 TCTGAGTACCCCATTCCTTCAAGAAATTACTTGATATAGTTTTTAAATTTGAGCTGTATT 3180
QY 3181 TTCAAGCAGCTTTGCTTTGGAATCATTTGTTACTGCAATGCCACCTTACTTTGCCATGGAAA 3240
Db |||||
3181 TTCAAGCAGCTTTGCTTTGGAATCATTTGTTACTGCAATGCCACCTTACTTTGCCATGGAAA 3240
QY 3241 ATGCAGAGAAATCATAAAGATCAAAGCTTATACTCAACTTAAACTTTTCAGGTCTTTTGCCAT 3300
Db |||||
3241 ATGCAGAGAAATCATAAAGATCAAAGCTTATACTCAACTTAAACTTTTCAGGTCTTTTGCCAT 3300
QY 3301 CTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTTTATCATTTCTTATT 3360
Db |||||
3301 CTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTTTATCATTTCTTATT 3360
QY 3361 TGATGCTAGGAAGCTTATTGGCATTTTCATTATGGATATATTTTTTATCTGTAAGTTCC 3420
Db |||||
3361 TGATGCTAGGAAGCTTATTGGCATTTTCATTATGGATATATTTTTTATCTGTAAGTTCC 3420
QY 3421 TTGCTGTGGTTTTTTGCTTATTTGGTTATGTTCCATCAGTTATTCTGTTCACTTATATTG 3480
Db |||||
3421 TTGCTGTGGTTTTTTGCTTATTTGGTTATGTTCCATCAGTTATTCTGTTCACTTATATTG 3480
QY 3481 CTTCTTTTCACTTTAAGAAAAATTTTAAATACCAAGAAATTTTGGTCATTTATCTATTCTG 3540
Db |||||
3481 CTTCTTTTCACTTTAAGAAAAATTTTAAATACCAAGAAATTTTGGTCATTTATCTATTCTG 3540
QY 3541 TGGCAGCGTTGGCTTGTTATGCAATCACTGAAATAAATCTTTTATGGGATACACAATTG 3600
Db |||||
3541 TGGCAGCGTTGGCTTGTTATGCAATCACTGAAATAAATCTTTTATGGGATACACAATTG 3600
QY 3601 CAACTATTCTTCAATTATGCTTTTGTATCATCATTTCAAATCTATCCACTTCTAGGTTGCC 3660
Db |||||
3601 CAACTATTCTTCAATTATGCTTTTGTATCATCATTTCAAATCTATCCACTTCTAGGTTGCC 3660
QY 3661 TGATTTCTTTTCAATAAAGATTTCTTGGAGAATGTACGAAAAAATGTGGACACCTATAATC 3720
Db |||||
3661 TGATTTCTTTTCAATAAAGATTTCTTGGAGAATGTACGAAAAAATGTGGACACCTATAATC 3720
QY 3721 CATGGATAGGCTTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTGTGGATTT 3780
Db |||||
3721 CATGGATAGGCTTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTGTGGATTT 3780
QY 3781 TCCTTTTACAATACTATGAAAAAATATGGAGGAGCTTCCAGAACCACAGACAAATGAGG 3840
Db |||||
3781 TCCTTTTACAATACTATGAAAAAATATGGAGGAGCTTCCAGAACCACAGACAAATGAGG 3840
QY 3841 TCAGAAACCTTTCAACGAGTCTAAAAATAGGAAGCTTCCAGAACCACAGACAAATGAGG 3900
Db |||||
3841 TCAGAAACCTTTCAACGAGTCTAAAAATAGGAAGCTTCCAGAACCACAGACAAATGAGG 3900
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Db 3901 ATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGTGCCAGT 3960
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Db 3961 GTTGTGAGAGAAACCATCCATTATGGTCAGCAATTTGCAATAAGAATATGATGACAAGA 4020
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Db 4021 AAGATTTTCTCTTTCAAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTG 4080
QY 4081 TGA AAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAAGCACAATTA 4140
Db 4081 TGA AAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAAGCACAATTA 4140
QY 4141 TTAATATTCTGGTTGGTGATATTGAACCAAACTTCAGGCCAGGTATTTTAGGAGATTATT 4200
Db 4141 TTAATATTCTGGTTGGTGATATTGAACCAAACTTCAGGCCAGGTATTTTAGGAGATTATT 4200
QY 4201 CTTTCAGAGACAAGTGAAGATGATGATTCACTGAAAGTGATGGTTACTGTCTCCAGATAA 4260
Db 4201 CTTTCAGAGACAAGTGAAGATGATGATTCACTGAAAGTGATGGTTACTGTCTCCAGATAA 4260
QY 4261 ACCCTTTGTGCCAGATACTACATTCAGTGCAGGAACATTTTGAAAATTTATGGAGCTGTCAAAG 4320
Db 4261 ACCCTTTGTGCCAGATACTACATTCAGTGCAGGAACATTTTGAAAATTTATGGAGCTGTCAAAG 4320
QY 4321 GAATGAGTGAAGTGACATGAAGAAGTCAATAAGTCGAATAACACATGCACATTGATTTAA 4380
Db 4321 GAATGAGTGAAGTGACATGAAGAAGTCAATAAGTCGAATAACACATGCACATTGATTTAA 4380
QY 4381 AAGAACAATCTTCAGAAGACTGTAAGAAAACACTACCTGCAGGAATCAAACGAAAGTTGTGTT 4440
Db 4381 AAGAACAATCTTCAGAAGACTGTAAGAAAACACTACCTGCAGGAATCAAACGAAAGTTGTGTT 4440
QY 4441 TTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCTACAGGTA 4500
Db 4441 TTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCTACAGGTA 4500
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QY 4621 TAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAAACATCTAAAGAGTA 4680
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QY 4681 AATTTGGAAAAGGCTACTTTTTTGGAATTAATAATTGAAGCACTGGATAGAAAACCTAGAAG 4740
Db 4681 AATTTGGAAAAGGCTACTTTTTTGGAATTAATAATTGAAGCACTGGATAGAAAACCTAGAAG 4740
QY 4741 TAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCAAATGCAAGCCGTCAGGAAAAGTT 4800
Db 4741 TAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCAAATGCAAGCCGTCAGGAAAAGTT 4800
QY 4801 TTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTTCAAAATCTT 4860
Db 4801 TTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTTCAAAATCTT 4860
QY 4861 TTTTAAAGCTGGAAGAAAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTTCTCAAG 4920
Db 4861 TTTTAAAGCTGGAAGAAAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTTCTCAAG 4920
QY 4921 CAACATTGGAACAGGTTTTTTGTAGAACTCACTAAAGAAACAAGAGGAGGAAGATAATAGTT 4980
Db 4921 CAACATTGGAACAGGTTTTTTGTAGAACTCACTAAAGAAACAAGAGGAGGAAGATAATAGTT 4980
QY 4981 GTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAAACAAGAAGATAGAGTAGTATTTT 5040

Db 4981 GTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAAACAAGAAGATAGAGTAGTATTTT 5040
QY 5041 GAAATTTGTATTGTTCCGGTCTGCTTACTGGGACTTCTTTCTTTTTCACCTAAATTTAACTT 5100
Db 5041 GAAATTTGTATTGTTCCGGTCTGCTTACTGGGACTTCTTTCTTTTTCACCTAAATTTAACTT 5100
QY 5101 TGGTTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGGAGAACCAAGAACGCACTTGAAATTT 5160
Db 5101 TGGTTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGGAGAACCAAGAACGCACTTGAAATTT 5160
QY 5161 TTCTAAGCTCCTTAATTGAATGCTGTGGTTGTGTGTTTGTCTTTTCTTTAAATAAAACG 5220
Db 5161 TTCTAAGCTCCTTAATTGAATGCTGTGGTTGTGTGTTTGTCTTTTCTTTAAATAAAACG 5220
QY 5221 TATGTATAATTAAAGTGAAGCTGCATGTTTGTATTGAAGTATATTGAACCTATATAGTTGT 5280
Db 5221 TATGTATAATTAAAGTGAAGCTGCATGTTTGTATTGAAGTATATTGAACCTATATAGTTGT 5280
QY 5281 ATGTCATCTTTTTCACCAATTCAGAAAACAGTGTCTTCTGAATTTGTGATTTAAAGGAATTGT 5340
Db 5281 ATGTCATCTTTTTCACCAATTCAGAAAACAGTGTCTTCTGAATTTGTGATTTAAAGGAATTGT 5340
QY 5341 AATAGAATAGTTTTTATTATTTTAAAGTTATCTTTAAAGTTATGCCATCTTCTTTAAATAAGTAC 5400
Db 5341 AATAGAATAGTTTTTATTATTTTAAAGTTATCTTTAAAGTTATGCCATCTTCTTTAAATAAGTAC 5400
QY 5401 GTAATGTTCCAACTCTAAATAAAAACTAATTCATACTAATGCATAGAAAAGATACATAA 5460
Db 5401 GTAATGTTCCAACTCTAAATAAAAACTAATTCATACTAATGCATAGAAAAGATACATAA 5460
QY 5461 AGCAATGTGAAAGTT 5475
Db 5461 AGCAATGTGAAAGTT 5475

RESULT 2
ABN89594
ID ABN89594 standard; cdna; 6525 BP.
XX
AC ABN89594;
XX
DT 18-SEP-2002 (first entry)
XX
DE Human ATP-binding cassette transporter ABCA5 cdna SEQ ID NO:1.
KW Human; ABCA5; ABCA6; ABCA9; ABCA10; ATP-binding cassette transporter;
KW chromosome 17; chromosome 17q; chromosome 17q24; antiarteriosclerotic;
KW gene therapy; cholesterol; lipophilic molecule; inflammation;
KW prostaglandin; prostacyclin; arteriosclerosis; transport; gene; ss.
OS Homo sapiens.
XX
PN WO200246458-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-EP015401.
XX
PR 07-DEC-2000; 2000EP-00403440.
PR 23-JAN-2001; 2001US-0263231P.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Denefle P, Rosier-Montus M, Prades C, Arnould-Reguigne I;
PI Duverger N, Allikmets R, Dean M;
XX
DR WPI; 2002-557584/59.
DR P-PSDB; ABB81574.
XX
PT A novel nucleic acid corresponding to ATP-binding cassette transporter
PT genes and the encoded polypeptide, useful for preventing or treating a
PT dysfunction in reverse transport of cholesterol.

XX Claim 1; Page 151-153; 216pp; English.

PS The present invention describes human ATP-binding cassette transporters

XX (ABC). Specifically described are the human ABCA5, ABCA6, ABCA9 and

CC ABCA10 genes (see ABN89594 to ABN89597) which encode the proteins given

CC in ABN81574 to ABN81577). ABN89598 to ABN89715 represent ABCA5, ABCA6,

CC ABCA9 and ABCA10 nucleotide fragments; and ABN89716 to ABN89806 represent

CC primers for ABCA5, ABCA6, ABCA9 and ABCA10 genes which are used in the

CC exemplification of the present invention. The ABC sequences have

CC antiarteriosclerotic activities and can be used in gene therapy. ABC

CC sequences can be used in the manufacture of a medicament intended for the

CC prevention and/or treatment of a subject affected by a dysfunction in the

CC reverse transport of cholesterol. The ABC proteins are involved in the

CC reverse transport of cholesterol, in membrane transport of lipophilic

CC molecules, in particular inflammation mediating substance such as

CC prostaglandins and prostacyclins, or in any pathology whose candidate

CC chromosomal region is situated on chromosome 17. They are also useful for

CC the manufacture of a medicament intended for prevention of

CC arteriosclerosis in various forms. The ABCA5, ABCA6, ABCA9 and ABCA10

CC genes are located to chromosome 17, more specifically to the 17q24 locus

XX

SQ Sequence 6525 BP; 1973 A; 1108 C; 1258 G; 2185 T; 0 U; 1 Other;

Query Match 94.6%; Score 5181; DB 6; Length 6525;

Best Local Similarity 99.9%; Pred.No. 0;

Matches 5331; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 97 AGGTTTATCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 156

DB 994 AGGTTTATCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 1053

QY 157 GAACACTTCTACTGAAGAAATTACTTAATTAATAATGCAGAACCAAAAGAGTAGTGTTCAGG 216

DB 1054 GAACACTTCTACTGAAGAAATTACTTAATTAATAATGCAGAACCAAAAGAGTAGTGTTCAGG 1113

QY 217 AAATCTTTTCCACTATTTTATTTTATTTTGGTTAATAATTAATAGCATGATGCATCCAA 276

DB 1114 AAATCTTTTCCACTATTTTATTTTATTTTGGTTAATAATTAATAGCATGATGCATCCAA 1173

QY 277 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 336

DB 1174 ATAAGAAATATGAAGAAGTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 1233

QY 337 CTAATCTAATCTTGGATATCTCCAGTGAATAATTAATTAACAAGCAGCATCATGCAGAAAG 396

DB 1234 CTAATCTAATCTTGGATATCTCCAGTGAATAATTAATTAACAAGCAGCATCATGCAGAAAG 1293

QY 397 TGTCTACTGATCATCTACCTGATGTCATAATTAATTAACAAGCAGCATCATGCAGAAAG 456

DB 1294 TGTCTACTGATCATCTACCTGATGTCATAATTAATTAACAAGCAGCATCATGCAGAAAG 1353

QY 457 TGTAAACATCCAGTCTCTAAGCCGAGCAACTTTGTAGTGTGGTTTCAAAAGACTCCA 516

DB 1354 TGTAAACATCCAGTCTCTAAGCCGAGCAACTTTGTAGTGTGGTTTCAAAAGACTCCA 1413

QY 517 TGTCCATGAACTTCGTTTTTTTCCCTGATATGATTCAGTATCTTCTATTTATATGGATT 576

DB 1414 TGTCCATGAACTTCGTTTTTTTCCCTGATATGATTCAGTATCTTCTATTTATATGGATT 1473

QY 577 CAAGAGCTGGTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 636

DB 1474 CAAGAGCTGGTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 1533

QY 637 TTTTCAAGCATCCATAGATGCTGCCATTATACAGTTGAACCAATGTTTCTCTTTGGA 696

DB 1534 TTTTCAAGCATCCATAGATGCTGCCATTATACAGTTGAACCAATGTTTCTCTTTGGA 1593

QY 697 AGGAGCTGGAGTCAACTAAAGCTGTATTATGGGAGAACTGCTGTTGTAGAAATAGATA 756

DB 1594 AGGAGCTGGAGTCAACTAAAGCTGTATTATGGGAGAACTGCTGTTGTAGAAATAGATA 1653

QY 757 CCTTTCCCGAGGAGTAATTTTAAATATACCTAGTTATAGCAATTTTCACTTTTGGATACT 816

DB 1654 CCTTTCCCGAGGAGTAATTTTAAATATACCTAGTTATAGCAATTTTCACTTTTGGATACT 1713

QY 817 TTTTGGCAATTCATATCGTAGCAAAAAAGAAAAATAAAGAAATTTTAAAGATAA 876

DB 1714 TTTTGGCAATTCATATCGTAGCAAAAAAGAAAAATAAAGAAATTTTAAAGATAA 1773

QY 877 TGGGACTTCATGATACTGCCCTTTTGGCTTTTCTGGGTTCTTCTATATACAAGTTTAAATTT 936

DB 1774 TGGGACTTCATGATACTGCCCTTTTGGCTTTTCTGGGTTCTTCTATATACAAGTTTAAATTT 1833

QY 937 TTCTTATGTCCTTCTTATGGCAGTCATTTGCGACAGCTTCTTTGTTATTTCTCAAAGTA 996

DB 1834 TTCTTATGTCCTTCTTATGGCAGTCATTTGCGACAGCTTCTTTGTTATTTCTCAAAGTA 1893

QY 997 GCAGCATTGTGATATTTCTGCTTTTCTTTTCTTTATGGAATTCATCTGTATTTTGTGCTT 1056

DB 1894 GCAGCATTGTGATATTTCTGCTTTTCTTTTCTTTATGGAATTCATCTGTATTTTGTGCTT 1953

QY 1057 TAAATGCTGACACCTCTTTTAAATAAATCAAAACATGTTGGGAATAGTTGAATTTTGTGTA 1116

DB 1954 TAAATGCTGACACCTCTTTTAAATAAATCAAAACATGTTGGGAATAGTTGAATTTTGTGTA 2013

QY 1117 CTGTGGCTTTTGGATTTATTTGGCTTTATGATAATCCTCATAGAAAGTTTTCCTCAAATCGT 1176

DB 2014 CTGTGGCTTTTGGATTTATTTGGCTTTATGATAATCCTCATAGAAAGTTTTCCTCAAATCGT 2073

QY 1177 TAGTGTGGCTTTTTCAGTCCCTTCTGTCACTGTACTTTTGTGATTTGGTATTGCACAGGTCA 1236

DB 2074 TAGTGTGGCTTTTTCAGTCCCTTCTGTCACTGTACTTTTGTGATTTGGTATTGCACAGGTCA 2133

QY 1237 TGCATTTAGAAAGATTTTAATGAAGTGTCTTCAATTTTCAATTTGACTGCAGGCCCATATC 1296

DB 2134 TGCATTTAGAAAGATTTTAATGAAGTGTCTTCAATTTTCAATTTGACTGCAGGCCCATATC 2193

QY 1297 CTCTAATTTATACAATTTATCATGCTCACACTTAATAGTATATTTCTATGTTCTCTTGGCTG 1356

DB 2194 CTCTAATTTATACAATTTATCATGCTCACACTTAATAGTATATTTCTATGTTCTCTTGGCTG 2253

QY 1357 TCTATCTTGATCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1416

DB 2254 TCTATCTTGATCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 2313

QY 1417 TGAAGCCTTCATATTTGGTCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG 1476

DB 2314 TGAAGCCTTCATATTTGGTCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG 2373

QY 1477 TTAATGGAAATATTAGTTTGTAGTAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA 1536

DB 2374 TTAATGGAAATATTAGTTTGTAGTAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA 2433

QY 1537 AAGAAGCCATAAGAAATTTAGTGGTATTCAGAAGACATACAGAAAGAGGTGAAATGTGG 1596

DB 2434 AAGAAGCCATAAGAAATTTAGTGGTATTCAGAAGACATACAGAAAGAGGTGAAATGTGG 2493

QY 1597 AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAAGTTACTGCCTTACTTTGGCC 1656

DB 2494 AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAAGTTACTGCCTTACTTTGGCC 2553

QY 1657 ACAGTGGAAACAGGAAAGAGTACATTGATGAATATTTCTTTGAGACTCTGCCCACTTCTG 1716

DB 2554 ACAGTGGAAACAGGAAAGAGTACATTGATGAATATTTCTTTGAGACTCTGCCCACTTCTG 2613

QY 1717 ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA 1776

DB 2614 ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA 2673

QY 1777 GAAAAATGATTTGGCATTGTGCCACAGTTAGATATACACTTTTGAATGTTTGTACAGTAGAAG 1836

DB 2674 GAAAAATGATTTGGCATTGTGCCACAGTTAGATATACACTTTTGAATGTTTGTACAGTAGAAG 2733

QY 1837 AAAATTTATCAATTTTGGCTTCAATCAAAAGGGATACCAGCCAAACAATATATACAAAGAG 1896

Db 2734 AAAATTATCAATTTTGGCTTCAATCAAAAGGGATACCAGCCAAACAATATATACAAGAAG 2793

Qy 1897 TGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAAT 1956

Db 2794 TGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAAT 2853

Qy 1957 TAAGTGGTGGTCAAAAAAGAAAGCTGTCAATTAGGAATTGCTGTTCTTTGGGBAACCCAAAGA 2016

Db 2854 TAAGTGGTGGTCAAAAAAGAAAGCTGTCAATTAGGAATTGCTGTTCTTTGGGBAACCCAAAGA 2913

Qy 2017 TACTGTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATGTATGGA 2076

Db 2914 TACTGTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATGTATGGA 2973

Qy 2077 ATCTTTTAAAAATACAGAAAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG 2136

Db 2974 ATCTTTTAAAAATACAGAAAAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG 3033

Qy 2137 AAGCTGACATTTCTTGCAGATAGGAAAGCTGTGATATACAAAGGAATGCTGAAATGTGTTG 2196

Db 3034 AAGCTGACATTTCTTGCAGATAGGAAAGCTGTGATATACAAAGGAATGCTGAAATGTGTTG 3093

Qy 2197 GTTCTTCAATGTTCTCTCAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAG 2256

Db 3094 GTTCTTCAATGTTCTCTCAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAG 3153

Qy 2257 ACAATATTTGTCACAGAAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAGCTA 2316

Db 3154 ACAATATTTGTCACAGAAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAGCTA 3213

Qy 2317 CTTTATTAACAACAGAAATGACCAACAACCTTGTGTATAGCTTGCCCTTTCAAGGACATGGACA 2376

Db 3214 CTTTATTAACAACAGAAATGACCAACAACCTTGTGTATAGCTTGCCCTTTCAAGGACATGGACA 3273

Qy 2377 AATTTTCAGGTTTTGTTTTCTGCCCTAGACAGTCATTCAAATTTGGGTGTCAATTTCTTTATG 2436

Db 3274 AATTTTCAGGTTTTGTTTTCTGCCCTAGACAGTCATTCAAATTTGGGTGTCAATTTCTTTATG 3333

Qy 2437 GTGTTTCCATGACGACTTTTGGAAAGACGTATTTTTTAAAGCTAGAAGTTGAAGCAGAAATTG 2496

Db 3334 GTGTTTCCATGACGACTTTTGGAAAGACGTATTTTTTAAAGCTAGAAGTTGAAGCAGAAATTG 3393

Qy 2497 ACCAAGCAGATTATAGTGATTTACTCAGCAGCCACTGGAGGAAAGAAATGGATTCAAAAT 2556

Db 3394 ACCAAGCAGATTATAGTGATTTACTCAGCAGCCACTGGAGGAAAGAAATGGATTCAAAAT 3453

Qy 2557 CTTTTCATGAAATGGAACAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGA 2616

Db 3454 CTTTTCATGAAATGGAACAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGA 3513

Qy 2617 GCACCATGAGCCTTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTTACCT 2676

Db 3514 GCACCATGAGCCTTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTTACCT 3573

Qy 2677 TGAACCGTGAAAGTAAATCAGTGAGATCAGTGTTCGCTTTTAAATTTTTCACAG 2736

Db 3574 TGAACCGTGAAAGTAAATCAGTGAGATCAGTGTTCGCTTTTAAATTTTTCACAG 3633

Qy 2737 TTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAAATGCTGGTTCCCATCAAAC 2796

Db 3634 TTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAAATGCTGGTTCCCATCAAAC 3693

Qy 2797 TTGTTCCAGACTTATATTTTCTAAAAACCTGGAGACAACCAACATATAACAAAAAAGTC 2856

Db 3694 TTGTTCCAGACTTATATTTTCTAAAAACCTGGAGACAACCAACATATAACAAAAAAGTC 3753

Qy 2857 TGCCTTCTCAAAAATCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTTTCACAAGCC 2916

Db 3754 TGCTTCTTCAAAAATCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTTTCACAAGCC 3813

Qy 2917 AGAACATTAATGGTGACGATGATTAATGACAGTGAATGTATCCGTGGCTCCCATAGTG 2976

Db 3814 AGAACATTAATGGTGACGATGATTAATGACAGTGAATGTATCCGTGGCTCCCATAGTG 3873

Qy 2977 CGGCTTTAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTTCAGCTGTTTTTCAACAGTA 3036

Db 3874 CGGCTTTAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTTCAGCTGTTTTTCAACAGTA 3933

Qy 3037 CTATGGTTTATTTCTTTACCTATATATTAGTGAATATCATATTAGTAACACTACTATCTTTATCAT 3096

Db 3934 CTATGGTTTATTTCTTTACCTATATATTAGTGAATATCATATTAGTAACACTACTATCTTTATCAT 3993

Qy 3097 TAAATGTGACTGAAACCAATCCAGATCTGGAGTACCCCATTTCTTTCAAGAAATTAAGTATA 3156

Db 3994 TAAATGTGACTGAAACCAATCCAGATCTGGAGTACCCCATTTCTTTCAAGAAATTAAGTATA 4053

Qy 3157 TAGTTTTTAAAAATTGAGCTGTATTTTCAAGCAGCTTTTGGAAATCATTTGTTACTGCAA 3216

Db 4054 TAGTTTTTAAAAATTGAGCTGTATTTTCAAGCAGCTTTTGGAAATCATTTGTTACTGCAA 4113

Qy 3217 TGCCACCTTACTTTGCCATGGAATAATGCAGAGATCATTAAGATCAAAAGCTTATACTCAAC 3276

Db 4114 TGCCACCTTACTTTGCCATGGAATAATGCAGAGATCATTAAGATCAAAAGCTTATACTCAAC 4173

Qy 3277 TTAACCTTTTCAAGTCTTTTGGCCATCTGCATATTGGAAATGGAAAGCTGTTGTTGATATCC 3336

Db 4174 TTAACCTTTTCAAGTCTTTTGGCCATCTGCATATTGGAAATGGAAAGCTGTTGTTGATATCC 4233

Qy 3337 CCTTATTTTATCATTTCTTATTTTGTATGCTAGGAAGCTTATTGGCAATTTCAATATGGAT 3396

Db 4234 CCTTATTTTATCATTTCTTATTTTGTATGCTAGGAAGCTTACTGGCAATTTCAATATGGAT 4293

Qy 3397 TATATTTTATACTGTAAAGTCTCTTGCTGTGGTTTTTTCCTTATTTGGTTATGTTCCAT 3456

Db 4294 TATATTTTATACTGTAAAGTCTCTTGCTGTGGTTTTTTCCTTATTTGGTTATGTTCCAT 4353

Qy 3457 CAGTTATTTCTGTTCACTTATATTTGCTTCTTTCACCTTTAAAGAAAAATTTTAAATACCAAG 3516

Db 4354 CAGTTATTTCTGTTCACTTATATTTGCTTCTTTCACCTTTAAAGAAAAATTTTAAATACCAAG 4413

Qy 3517 AATTTTGGTCAATTTATCTATTTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAA 3576

Db 4414 AATTTTGGTCAATTTATCTATTTCTGTGGCAGCGTTGCTTGTATTGCAATCACTGAAATAA 4473

Qy 3577 CTTTCTTTATGGGATACACAATTTGCAACTATTTCTTCATTTATGCTTTTGTATCATCATTC 3636

Db 4474 CTTTCTTTATGGGATACACAATTTGCAACTATTTCTTCATTTATGCTTTTGTATCATCATTC 4533

Qy 3637 CAATCTATCCACTTCTAGGTTGCTGATTTCTTTTCATAAAAGATTTCTTTGGAAGAAATGTAC 3696

Db 4534 CAATCTATCCACTTCTAGGTTGCTGATTTCTTTTCATAAAAGATTTCTTTGGAAGAAATGTAC 4593

Qy 3697 GAAAAAATGTGGACACCTTATATCCATGGGATAGGCTTTTCAGTAGCTGTTTATATCGCCTT 3756

Db 4594 GAAAAAATGTGGACACCTTATATCCATGGGATAGGCTTTTCAGTAGCTGTTTATATCGCCTT 4653

Qy 3757 ACCTGCAGTGTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAAGCA 3816

Db 4654 ACCTGCAGTGTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAAGCA 4713

Qy 3817 GATCAATAAGAAAAAGATCCCTTTTTCAGAAAAACCTTTCAACGAAGCTTAAAAAATAGGAAGC 3876

Db 4714 GATCAATAAGAAAAAGATCCCTTTTTCAGAAAAACCTTTCAACGAAGCTTAAAAAATAGGAAGC 4773

Qy 3877 TTCCAGAAACCAACAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAAGACTTAAAGG 3936

Db 4774 TTCCAGAAACCAACAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAAGACTTAAAGG 4833

Qy 3937 TCAAAGAGCTGATGGGTTGCCAGTGTGTTGAGGAGAAACCATCCATTATGGTCAGCAATT 3996

Db 4834 TCAAAGAGCTGATGGGTTGCCAGTGTGTTGAGGAGAAACCATCCATTATGGTCAGCAATT 4893

Qy 3997 TGCATAAAGAAATATGATGACAAGAAAGATTTTCTTTTCAAGAAAAAGTAAAGAAAGTGG 4056

Db 4894 TGCATAAAGAAATATGATGACAAGAAAGATTTTCTTTTCAAGAAAAAGTAAAGAAAGTGG 4953

QY 1537 AAGAACCCATAAGAAATTAGTGGTATTTCAGAAAGACATACAGAAAGAAGGGTGAAAATGTGG 1596
D6 2661 AAGAACCCATAAGAAATTAGTGGTATTTCAGAAAGACATACAGAAAGAAGGGTGAAAATGTGG 2720
QY 1597 AGGCTTTGAGAAAATTTGTCTATTGACATATATGAGGGTCAGATTACTGCGCTTACTTTGGCC 1656
D6 2721 AGGCTTTGAGAAAATTTGTCTATTGACATATATGAGGGTCAGATTACTGCGCTTACTTTGGCC 2780
QY 1657 ACAGTGAACAGGAAAGAGTACATTGATGAATATTCTTTGTGGACTCTGCGCCACCTTCTG 1716
D6 2781 ACAGTGAACAGGAAAGAGTACATTGATGAATATTCTTTGTGGACTCTGCGCCACCTTCTG 2840
QY 1717 ATGGGTTTGCATCTATATATGACACAGAGTCTCAGAAAATAGATGAAAATGTTTGAAGCAA 1776
D6 2841 ATGGGTTTGCATCTATATATGACACAGAGTCTCAGAAAATAGATGAAAATGTTTGAAGCAA 2900
QY 1777 GAAAATGATTGGCATTGTGCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAG 1836
D6 2901 GAAAATGATTGGCATTGTGCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAG 2960
QY 1837 AAAATTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCAAACAATATATATACAAGAAG 1896
D6 2961 AAAATTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCAAACAATATATATACAAGAAG 3020
QY 1897 TGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGTAAAAAAT 1956
D6 3021 TGCAGAAGGTTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGTAAAAAAT 3080
QY 1957 TAAGTGGTGGTCAAAAAAGAAAGCTGTCTATTAGGAATTGCTGTTCTTGGGAACCCAAAGA 2016
D6 3081 TAAGTGGTGGTCAAAAAAGAAAGCTGTCTATTAGGAATTGCTGTTCTTGGGAACCCAAAGA 3140
QY 2017 TACTGTGCTAGATGAACCAAAGCTGGAATGGACCGCTGTTCTCGACATATTGTATGGA 2076
D6 3141 TACTGTGCTAGATGAACCAAAGCTGGAATGGACCGCTGTTCTCGACATATTGTATGGA 3200
QY 2077 ATCTTTTAAAAATACAGAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG 2136
D6 3201 ATCTTTTAAAAATACAGAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG 3260
QY 2137 AAGCTGACATCTTGCAGATAGGAAAAGCTGTGATATACAAAGGAATGCTGAAATGTGTTG 2196
D6 3261 AAGCTGACATCTTGCAGATAGGAAAAGCTGTGATATACAAAGGAATGCTGAAATGTGTTG 3320
QY 2197 GTTCTTCAATGTTCTCTCAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAG 2256
D6 3321 GTTCTTCAATGTTCTCTCAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAG 3380
QY 2257 ACAAAATATTGTGCCACAGAAATCTCTTCTTCACTGGTTAAACAACAATATACCTGGAGCTA 2316
D6 3381 ACAAAATATTGTGCCACAGAAATCTCTTCTTCACTGGTTAAACAACAATATACCTGGAGCTA 3440
QY 2317 CTTTATTACAAACAGAAATGACCAACAACCTTGTGTATAGTTGCTTTCAGAGGACATGGACA 2376
D6 3441 CTTTATTACAAACAGAAATGACCAACAACCTTGTGTATAGTTGCTTTCAGAGGACATGGACA 3500
QY 2377 AATTTTCAGGTTTGTCTTCTGCGCTAGACAGTCAATTCAAAATTTGGGTGTCATTTCTTATG 2436
D6 3501 AATTTTCAGGTTTGTCTTCTGCGCTAGACAGTCAATTCAAAATTTGGGTGTCATTTCTTATG 3560
QY 2437 GTGTTTCCATGACGACTTTTGGAAAGACGTAATTTTAAAGCTAGAAGTTGAAGCAGAAATTG 2496
D6 3561 GTGTTTCCATGACGACTTTTGGAAAGACGTAATTTTAAAGCTAGAAGTTGAAGCAGAAATTG 3620
QY 2497 ACCAAGCAGATTATAGTGTATTACTCAGCAGCCACTGGAGGAAAGAAATGGATTCAAAAT 2556
D6 3621 ACCAAGCAGATTATAGTGTATTACTCAGCAGCCACTGGAGGAAAGAAATGGATTCAAAAT 3680
QY 2557 CTTTGTGATGAAATGGAAACAGAGTTACTTATCTTTCTGAAACCAAGGCTTCTCTAGTGA 2616
D6 3681 CTTTGTGATGAAATGGAAACAGAGTTACTTATCTTTCTGAAACCAAGGCTTCTCTAGTGA 3740
QY 2617 GCACCATGAGCCTTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTTACCT 2676

D6 3741 GCACCATGAGCCTTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTTACCT 3800
QY 2677 TGAACGCTGAAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTTTTTCACAG 2736
D6 3801 TGAACGCTGAAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTTTTTCACAG 3860
QY 2737 TTCAGATTTTATGTTTGTGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAAAC 2796
D6 3861 TTCAGATTTTATGTTTGTGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAAAC 3920
QY 2797 TTGTTCCAGACTTATATTTTCTAAAAACCTGGAGACAACACACATAAAATACAAAAACAAGTC 2856
D6 3921 TTGTTCCAGACTTATATTTTCTAAAAACCTGGAGACAACACACATAAAATACAAAAACAAGTC 3980
QY 2857 TGCTTCTTCAAAAATTCIGCTGACTCAGATATCAGTGAATCTTATTAGCTTTTTCACAAGCC 2916
D6 3981 TGCTTCTTCAAAAATTCIGCTGACTCAGATATCAGTGAATCTTATTAGCTTTTTCACAAGCC 4040
QY 2917 AGAACATAAATGGTGACGATGAATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTG 2976
D6 4041 AGAACATAAATGGTGACGATGAATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTG 4100
QY 2977 CGGCTTTAAAAATGTGATGCATTCAGAAAAAGGACTATGTTTTCAGCTGTGTTTCAACAGTA 3036
D6 4101 CGGCTTTAAAAATGTGATGCATTCAGAAAAAGGACTATGTTTTCAGCTGTGTTTCAACAGTA 4160
QY 3037 CTATGCTTTATTTCTTTACCTATATTAGTGAATATCAATTAGTAACTACTATCTTTATCATTT 3096
D6 4161 CTATGCTTTATTTCTTTACCTATATTAGTGAATATCAATTAGTAACTACTATCTTTATCATTT 4220
QY 3097 TAAATGTGACTGAAACCCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTACTGATA 3156
D6 4221 TAAATGTGACTGAAACCCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTACTGATA 4280
QY 3157 TAGTTTTTAAAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAA 3216
D6 4281 TAGTTTTTAAAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAA 4340
QY 3217 TGCCACCTTACTTTTGCCATGGAAAAATGCAGAGAAATCATAAAGATCAAAGCTTATACTCAAC 3276
D6 4341 TGCCACCTTACTTTTGCCATGGAAAAATGCAGAGAAATCATAAAGATCAAAGCTTATACTCAAC 4400
QY 3277 TTAACCTTTTCAAGGTCTTTTGGCATCTGCATATTGGATTTGGACAAGCTGTTGTTGATATCC 3336
D6 4401 TTAACCTTTTCAAGGTCTTTTGGCATCTGCATATTGGATTTGGACAAGCTGTTGTTGATATCC 4460
QY 3337 CCTATTTTATTCATTTCTTATTTTGTAGTGCTAGGAAGCTTATTTGGCATTTTCATTTATGGAT 3396
D6 4461 CCTATTTTATTCATTTCTTATTTTGTAGTGCTAGGAAGCTTATTTGGCATTTTCATTTATGGAT 4520
QY 3397 TATATTTTATACGTGAAAAGTTCCTTGTGCTGCTGCTTTTTCCTTATTTGCTTATGTTCCAT 3456
D6 4521 TATATTTTATACGTGAAAAGTTCCTTGTGCTGCTGCTTTTTCCTTATTTGCTTATGTTCCAT 4580
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D6 4581 CAGTTATTTCTGTTCACTTATATTGCTTTCACCTTTAAGAAAAATTTTAAATACCAAAG 4640
QY 3517 AATTTTGGTCATTTATCTATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAA 3576
D6 4641 AATTTTGGTCATTTATCTATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAA 4700
QY 3577 CTTTCTTTATGGGATACACAATTTGCAACTATTCTTCAATATGCTTTTGTATCATCATTC 3636
D6 4701 CTTTCTTTATGGGATACACAATTTGCAACTATTCTTCAATATGCTTTTGTATCATCATTC 4760
QY 3637 CAATCTATCCACTTCTAGTTGCTGATTTCTTTTCAFAAAGATTTCTTTGGAAGATGTAC 3696
D6 4761 CAATCTATCCACTTCTAGTTGCTGATTTCTTTTCAFAAAGATTTCTTTGGAAGATGTAC 4820
QY 3697 GAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCCTT 3756

Db 4821 GAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTT 4880
QY 3757 ACCTGCAGTGTGTACTGTGGATTTCCTCTCTTACAATACTATGAGAAAAAATATGGAGGCA 3816
Db 4881 ACCTGCAGTGTGTACTGTGGATTTCCTCTCTTACAATACTATGAGAAAAAATATGGAGGCA 4940
QY 3817 GATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAAGAAAGTCTAAAAATAGGAAGC 3876
Db 4941 GATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAAGAAAGTCTAAAAATAGGAAGC 5000
QY 3877 TTCCAGAACCCACAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAAGCTAAAGG 3936
Db 5001 TTCCAGAACCCACAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAAGCTAAAGG 5060
QY 3937 TCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 3996
Db 5061 TCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 5120
QY 3997 TGCATAAAGAAATATGATGACAAAGAAAGATTTCCTCTTCAAGAAAGTAAAGAAAGTGG 4056
Db 5121 TGCATAAAGAAATATGATGACAAAGAAAGATTTCCTCTTCAAGAAAGTAAAGAAAGTGG 5180
QY 4057 CAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 4116
Db 5181 CAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 5240
QY 4117 ATGGTGTGGCAAAAGCACAAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAG 4176
Db 5241 ATGGTGTGGCAAAAGCACAAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAG 5300
QY 4177 GCCAGGTATTTTAGGAGATTATCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGT 4236
Db 5301 GCCAGGTATTTTAGGAGATTATCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGT 5360
QY 4237 GTATGGGTTACTGTCTTCAGATAAAACCCCTTTGTGGCCAGATACATGATTCAGGAACATT 4296
Db 5361 GTATGGGTTACTGTCTTCAGATAAAACCCCTTTGTGGCCAGATACATGATTCAGGAACATT 5420
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Db 5421 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCACAGTACATGAAAGAAGTCAATAAGTC 5480
QY 4357 GAATAACACATGCACCTTGATTTTAAAGAAACATCTTCAGAAGACTGTAAAGAAACTACCTG 4416
Db 5481 GAATAACACATGCACCTTGATTTTAAAGAAACATCTTCAGAAGACTGTAAAGAAACTACCTG 5540
QY 4417 CAGGAATCAAAACGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTT 4476
Db 5541 CAGGAATCAAAACGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTT 5600
QY 4477 TGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAAACAGCACATGTGGCGAGCAA 4536
Db 5601 TGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAAACAGCACATGTGGCGAGCAA 5660
QY 4537 TTCGAACCTGCATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGG 4596
Db 5661 TTCGAACCTGCATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGG 5720
QY 4597 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCG 4656
Db 5721 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCG 5780
QY 4657 GAACAGTACAAACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATFAAATTGA 4716
Db 5781 GAACAGTACAAACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATFAAATTGA 5840
QY 4717 AGGACTGGATAGAAAACCTTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCC 4776
Db 5841 AGGACTGGATAGAAAACCTTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCC 5900
QY 4777 CAAATGCAAGCCGTGAGGAAAGTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAG 4836
Db 5901 CAAATGCAAGCCGTGAGGAAAGTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAG 5960

QY 4837 ATGTTCAGTCCCTTTTCACAATCTTTTAAAGCTGGAGAAGCTAAACATGCTTTTGCCA 4896
Db 5961 ATGTTCAGTCCCTTTTCACAATCTTTTAAAGCTGGAGAAGCTAAACATGCTTTTGCCA 6020
QY 4897 TTGAAGAATATAGCTTTTCTCAAGCAACATTGGAAACAGGTTTTTGTAGAACTCACTAAAG 4956
Db 6021 TTGAAGAATATAGCTTTTCTCAAGCAACATTGGAAACAGGTTTTTGTAGAACTCACTAAAG 6080
QY 4957 AACAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAA 5016
Db 6081 AACAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAA 6140
QY 5017 CACAAGAAGATAGAGTAGTATTTTGAATTTGTATTTGTTCCGTTCTGCTTACTGGGACTTCT 5076
Db 6141 CACAAGAAGATAGAGTAGTATTTTGAATTTGTATTTGTTCCGTTCTGCTTACTGGGACTTCT 6200
QY 5077 TTCCTTTTTCACCTTAATTTTAACTTTGGTTTAAAGTTTTTATTGGAATGTTAACTGGA 5136
Db 6201 TTCCTTTTTCACCTTAATTTTAACTTTGGTTTAAAGTTTTTATTGGAATGTTAACTGGA 6260
QY 5137 GAACCAAGAACGCACCTTGAAATTTTCTAAGCTCCCTAAATTGAAATGCTGTGGTTGTG 5196
Db 6261 GAACCAAGAACGCACCTTGAAATTTTCTAAGCTCCCTAAATTGAAATGCTGTGGTTGTG 6320
QY 5197 TTTTGCTTTTCTTTAAATAAAACGTATGTATAATTAA 5233
Db 6321 TTTTGCTTTTCTTTAAATAAAACGTATGTATAATTAA 6357

RESULT 4
AAD37620
ID AAD37620 standard; cDNA; 5262 BP.
XX
AC AAD37620;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human transporter protein cDNA #3.
XX
KW Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application;
KW cosmetic application; polymorphism; ss.
XX
OS Homo sapiens.
XX
PN WO200231147-A2.
XX
PD 18-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031113.
XX
PR 10-OCT-2000; 2000US-0239629P.
XX
PA (LEXI-) LEXICON GENETICS INC.
PI Hu Y, Nepomnichy B;
XX
XX WPI; 2002-454552/48.
DR
XX
PT Novel nucleic acid molecule encoding novel human proteins, useful for
PT therapeutic, diagnostic and pharmacogenomic applications.
XX
PS Disclosure; Page 45-46; 46pp; English.
XX
CC The present sequence is a cDNA coding for novel human protein (NHP),
CC human transporter protein. NHPs shares structural similarity with the
CC mammalian ATP-binding cassette (ABC) transporters and multidrug
CC resistance transporters. NHP polynucleotides are useful for the
CC therapeutic, diagnostic and pharmacogenomic applications. They are used
CC for detecting and treating mental disorders and cancers. They are also
CC used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and

CC	disorders, and cosmetic or nutraceutical applications									
XX										
SQ	Sequence 5262 BP; 1615 A; 888 C; 1012 G; 1743 T; 0 U; 4 Other;									
	Query Match 85.2%; Score 4664; DB 6; Length 5262;									
	Best Local Similarity 99.9%; Pred. No. 0;									
	Matches 5014; Conservative 0; Mismatches 7; Indels 0; Gaps 0;									
QY	97	AGGTTTATTTCAGAAAACATGTCCACTGCAATTAGGGAGGTPAGGAGTTTGGAGACAGACCA	156							
Db	238	AGGTTTATTTCAGAAAACATGTCCACTGCAATTAGGGAGGTPAGGAGTTTGGAGACAGACCA	297							
QY	157	GAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGG	216							
Db	298	GAACACTTCTACTGAAGAATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGG	357							
QY	217	AAATTCCTTTTCCACTATTTTCTTTTATTTTGGTTAAATTAATTAGCATGATGCATCCAA	276							
Db	358	AAATTCCTTTTCCACTATTTTCTTTTATTTTGGTTAAATTAATTAGCATGATGCATCCAA	417							
QY	277	ATAAGAAATATGAAGAAGTGCCTAAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT	336							
Db	418	ATAAGAAATATGAAGAAGTGCCTAAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT	477							
QY	337	CTAATCTAATTCTTGGATATATCTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAG	396							
Db	478	CTAATCTAATTCTTGGATATATCTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAG	537							
QY	397	TGTCFACATGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAA	456							
Db	538	TGTCFACATGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAA	597							
QY	457	TGTTAACATCCAGTCTCTTAAGCCGAGCAACTTTGAGGTGTGGTTTTCAAAGACTCCA	516							
Db	598	TGTTAACATCCAGTCTCTTAAGCCGAGCAACTTTGAGGTGTGGTTTTCAAAGACTCCA	657							
QY	517	TGTCCTATGAACCTTCGTTTTTTCCTGATATGATCCAGTATCTTCTATTATATATGGATT	576							
Db	658	TGTCCTATGAACCTTCGTTTTTTCCTGATATGATCCAGTATCTTCTATTATATATGGATT	717							
QY	577	CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCCTCAGGTTTCACAG	636							
Db	718	CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCCTCAGGTTTCACAG	777							
QY	637	TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTTGA	696							
Db	778	TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGA	837							
QY	697	AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAACTGCTGTTGTAGAAAATAGATA	756							
Db	838	AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAACTGCTGTTGTAGAAAATAGATA	897							
QY	757	CCTTTTCCCGAGGAGTAATTTTAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACT	816							
Db	898	CCTTTTCCCGAGGAGTAATTTTAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACT	957							
QY	817	TTTTTGGCAATTTCATATCGTAGCAGAAAAAGAAAAATAAAAGAAATTTTAAAGATAA	876							
Db	958	TTTTTGGCAATTTCATATCGTAGCAGAAAAAGAAAAATAAAAGAAATTTTAAAGATAA	1017							
QY	877	TGGGACTTCATGATACCTGCTTTTGGCTTTCCCTGGGTTCTTCTATATACAAGTTTAAATTT	936							
Db	1018	TGGGACTTCATGATACCTGCTTTTGGCTTTCCCTGGGTTCTTCTATAWACAAGTTTAAATTT	1077							
QY	937	TTCTTATGTCCTTCTTATGGCAGTCAATGGCAGAGCTTCTTTTGGTTATTTCTCTCAAAGTA	996							
Db	1078	TTCTTATGTCCTTCTTATGGCAGTCAATGGCAGAGCTTCTTTTGGTTATTTCTCTCAAAGTA	1137							
QY	997	GCAGCAATTGTGATATTTCTGCTTTTTTTCCTTATGGATTATCATCTGTATTTTTTGCCTT	1056							
Db	1138	GCAGCAATTGTGATATTTCTGCTTTTTTTCCTTATGGATTATCATCTGTATTTTTTGCCTT	1197							
QY	1057	TAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTTGTTA	1116							

Db	1198	TAATGCTGACACCTCTTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTGTTA	1257							
QY	1117	CTGTGGCTTTTGGATTTATTGGCCTTATGATAAATCCTCATAGAAAAGTTTTCCCAAATCGT	1176							
Db	1258	CTGTGGCTTTTGGATTTATTGGCCTTATGATAAATCCTCATAGAAAAGTTTTCCCAAATCGT	1317							
QY	1177	TAGTGTGGCTTTTCAGTCCCTTCTGTCACTGTACTCTTTTGTGATGGTATTGCACAGGTCA	1236							
Db	1318	TAGTGTGGCTTTTCAGTCCCTTCTGTCACTGTACTCTTTTGTGATGGTATTGCACAGGTCA	1377							
QY	1237	TGCATTTAGAAAGATTTTAATGAAGTGTCTTCAATTTTCAAAATTTGACTGCAGGCCCATATC	1296							
Db	1378	TGCATTTAGAAAGATTTTAATGAAGTGTCTTCAATTTTCAAAATTTGACTGCAGGCCCATATC	1437							
QY	1297	CTCTAATTATTACAATTATCATGTCTCACACTTAATAGTATATTTCTATGTCTCTTGGCTG	1356							
Db	1438	CTCTAATTATTACAATTATCATGTCTCACACTTAATAGTATATTTCTATGTCTCTTGGCTG	1497							
QY	1357	TCTATCTTGATCAAGTCATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC	1416							
Db	1498	TCTATCTTGATCAAGTCATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC	1557							
QY	1417	TGAAGCCTTCATATTGGTCAAAGAGCAAAAAGAAATTATGAGGAGTTATCAGAGGGCAATG	1476							
Db	1558	TGAAGCCTTCATATTGGTCAAAGAGCAAAAAGAAATTATGAGGAGTTATCAGAGGGCAATG	1617							
QY	1477	TTAATGGAAATATTAGTTTTAGTGAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA	1536							
Db	1618	TTAATGGAAATATTAGTTTTAGTGAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA	1677							
QY	1537	AAGAAGCCATAAGAAATTAGTGGTATTTCAGAAAGACATACAGAAAAGGGTGAAATGTGG	1596							
Db	1678	AAGAAGCCATAAGAAATTAGTGGTATTTCAGAAAGACATACAGAAAAGGGTGAAATGTGG	1737							
QY	1597	AGGCTTTGAGAAAATTTGTCACTTTGACATATATGAGGGTCAGATTACTGCCCTTACTTGGCC	1656							
Db	1738	AGGCTTTGAGAAAATTTGTCACTTTGACATATATGAGGGTCAGATTACTGCCCTTACTTGGCC	1797							
QY	1657	ACAGTGGAAACAGGAAAGATACATTGATGAATATTCTTTGTGGACTCTGCCCCACCTTCTG	1716							
Db	1798	ACAGTGGAAACAGGAAAGATACATTGATGAATATTCTTTGTGGACTCTGCCCCACCTTCTG	1857							
QY	1717	ATGGGTTTGCACTCTATATATGGAACAAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA	1776							
Db	1858	ATGGGTTTGCACTCTATATATGGAACAAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA	1917							
QY	1777	GAAAAATGATGGCAATTTGTCCACAGTTAGATATACATTTGATGTTTTGACAGTAGAAG	1836							
Db	1918	GAAAAATGATGGCAATTTGTCCACAGTTAGATATACATTTGATGTTTTGACAGTAGAAG	1977							
QY	1837	AAAAATTTATCAATTTTGGCTTCAATCAAAGGGATACAGCCCAACAATATAATACAAAG	1896							
Db	1978	AAAAATTTATCAATTTTGGCTTCAATCAAAGGGATACAGCCCAACAATATAATACAAAG	2037							
QY	1897	TGCAGAAAGGTTTTTACTAGATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAAT	1956							
Db	2038	TGCAGAAAGGTTTTTACTAGATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAAT	2097							
QY	1957	TAAGTGGTGGTCAAAAAAGAAAAGCTGTCAATTAGGAATTTGCTTCTTGGGAACCCAAAGA	2016							
Db	2098	TAAGTGGTGGTCAAAAAAGAAAAGCTGTCAATTAGGAATTTGCTTCTTGGGAACCCAAAGA	2157							
QY	2017	TACTGCTGTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTTGTATGGA	2076							
Db	2158	TACTGCTGTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTTGTATGGA	2217							
QY	2077	ATCTTTTAAAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG	2136							
Db	2218	ATCTTTTAAAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG	2277							
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DT 10-SEP-2002 (first entry)
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DE Human transporter protein cDNA #1.
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KW Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutritional application; gene;
KW cosmetic application; polymorphism; ss.
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FH Key Location/Qualifiers
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XX 18-APR-2002.
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XX 04-OCT-2001; 2001WO-US031113.
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XX 10-OCT-2000; 2000US-0239629P.
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XX (LEXI-) LEXICON GENETICS INC.
XX
XX Hu Y, Nepomnichy B;
XX
XX WPI; 2002-454552/48.
XX P-PSDB; AAE23656.
XX
XX Novel nucleic acid molecule encoding novel human proteins, useful for
XX therapeutic, diagnostic and pharmacogenomic applications.
XX
XX Claim 1; Page 34-35; 46pp; English.
XX
XX The present sequence is a cDNA coding for novel human protein (NHP),
XX human transporter protein. NHPs shares structural similarity with the
XX mammalian ATP-binding cassette (ABC) transporters and multidrug
XX resistance transporters. NHP polynucleotides are useful for the
XX therapeutic, diagnostic and pharmacogenomic applications. They are used
XX for detecting and treating mental disorders and cancers. They are also
XX used in gene therapy. NHP polypeptides are useful for diagnosis, drug
XX screening, clinical trial monitoring, treatment of diseases and
XX disorders, and cosmetic or nutraceutical applications.
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XX Sequence 4929 BP; 1544 A; 827 C; 950 G; 1604 T; 0 U; 4 Other;
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Query Match 83.5%; Score 4572; DB 6; Length 4929;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4922; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 4921 GTATTTTGA 4929

RESULT 6
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ID AAD37619 standard; cDNA; 4785 BP.
AC AAD37619;
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DT 10-SEP-2002 (first entry)
DE Human transporter protein cDNA #2.
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KW Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application; gene;
KW cosmetic application; polymorphism; ss.
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FH Key
FT CDS
FT Location/Qualifiers
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18-APR-2002.
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PF 04-OCT-2001; 2001WO-US031113.
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PR 10-OCT-2000; 2000US-0239629P.
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PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B;
XX
DR WPI; 2002-454552/48.
DR P-PSDB; AAB23657.
XX
XX Novel nucleic acid molecule encoding novel human proteins, useful for
PT therapeutic, diagnostic and pharmacogenomic applications.

XX Claim 1; Page 39-41; 46pp; English.
PS
XX
CC The present sequence is a cDNA coding for novel human protein (NHP),
CC human transporter protein. NHPs shares structural similarity with the
CC mammalian ATP-binding cassette (ABC) transporters and multidrug
CC resistance transporters. NHP polynucleotides are useful for the
CC therapeutic, diagnostic and pharmacogenomic applications. They are used
CC for detecting and treating mental disorders and cancers. They are also
CC used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and
CC disorders, and cosmetic or nutraceutical applications
XX
SQ Sequence 4785 BP; 1489 A; 807 C; 917 G; 1568 T; 0 U; 4 Other;
Query Match 80.5%; Score 4408; DB 6; Length 4785;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4758; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 114 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 173
Db 1 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 60
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Db 61 AATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTCCTTTCCACTA 120
QY 234 TTTTCTTATTTTGGTTAATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 293
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Db 1981 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCA 2040

QY 2154 GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAAATGTGTGGTTCTTCAATGTTCCCTC 2213

Db 2041 GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAAATGTGTGGTTCTTCAATGTTCCCTC 2100

QY 2214 AAAAGTAAATGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCCACA 2273

Db 2101 AAAAGTAAATGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCCACA 2160

QY 2274 GAATCTCTTTCTTCACTGGTTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAAT 2333

Db 2161 GAATCTCTTTCTTCACTGGTTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAAT 2220

QY 2334 GACCAACAACTTGTGTATAGCTTGCTTCAAGGACATGGACAAAATTTTCAGGTTTGTGTT 2393

Db 2221 GACCAACAACTTGTGTATAGCTTGCTTCAAGGACATGGACAAAATTTTCAGGTTTGTGTT 2280

QY 2394 TCTGCCCTAGACAGTCAATTCAAATTTGGGTGTCAATTTCTTATGTTGTTTCCATGACGACT 2453

Db 2281 TCTGCCCTAGACAGTCAATTCAAATTTGGGTGGCAATTTCTTATGGGTTTCCATGACGACT 2340

QY 2454 TTGGAAGACGTATTTTTTAAAGCTAGAAGTTGAAGCAGAAATTTGATGAAAATGGAA 2513

Db 2341 TTGGAAGACGTATTTTTTAAAGCTAGAAGTTGAAGCAGAAATTTGATGAAAATGGAA 2400

QY 2514 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTGAAAATGGAA 2573

Db 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTGAAAATGGAA 2460

QY 2574 CAGAGCTTACTTATTTCTTCTGAAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 2633

Db 2461 CAGAGCTTACTTATTTCTTCTGAAAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTGG 2520

QY 2634 AAACAACAGATGTATACAATAGCAAGTTTCATTTCTTTACCTTGAAACGTTGAAAGTAAA 2693

Db 2521 AAACAACAGATGTATACAATAGCAAGTTTCATTTCTTTACCTTGAAACGTTGAAAGTAAA 2580

QY 2694 TCAGTGAGATCAGTGTGTTCTGCTTTTAAATTTTTTTCACAGTTCAGATTTTATGTTT 2753

Db 2581 TCAGTGAGATCAGTGTGTTCTGCTTTTAAATTTTTTTCACAGTTCAGATTTTATGTTT 2640

QY 2754 TTGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATAT 2813

Db 2641 TTGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATAT 2700

QY 2814 TTTCTAAAACTGGAGACAAACCACATAFAAATACAAAACAAGTCTGCTTCTTCAAAATTTCT 2873

Db 2701 TTTCTAAAACTGGAGACAAACCACATAFAAATACAAAACAAGTCTGCTTCTTCAAAATTTCT 2760

QY 2874 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTTCAAGCCAGAACATAATGGTGACG 2933

Db 2761 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTTCAAGCCAGAACATAATGGTGACG 2820

QY 2934 ATGATTTAATGACAGTGACTATGTATCCGTGGCTCCCATATAGTGGGCTTTAAATGTGATG 2993

Db 2821 ATGATTTAATGACAGTGACTATGTATCCGTGGCTCCCATATAGTGGGCTTTAAATGTGRTG 2880

QY 2994 CATTCAAGAAAAGGACTATGTTTTTGCAGCTGTTTTTCAACAGTACTATGTTTATTTCTTTA 3053

Db 2881 CATTCAAGAAAAGGACTATGTTTTTGCAGCTGTTTTTCAACAGTACTATGTTTATTTCTTTA 2940

QY 3054 CCTATATTAGTGAATATCATTTAGTAACTACTATCTTTATCATTTTAAATGTGACTGAAACC 3113

Db 2941 CCTATATTAGTGAATATCATTTAGTAACTACTATCTTTATCATTTTAAATGTGACTGAAACC 3000

QY 3114 ATCCAGATCTGGAGTACCCCATCTCTTCAAGAAATTAACGATATAGTTTTTAAATTTGAG 3173
Dd |||||||
Dd 3001 ATCCAGATCTGGAGTACCCCATCTCTTCAAGAAATTAACGATATAGTTTTTAAATTTGAG 3060
QY 3174 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAATGCCACCTTACTTTGCC 3233
Dd |||||||
Dd 3061 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAATGCCACCTTACTTTGCC 3120
QY 3234 ATGGAATGAGAGAAATCATAGATCAAAAGCTTATATCTCAACTTAAACTTTCAGGTCTT 3293
Dd |||||||
Dd 3121 ATGGAATGAGAGAAATCATAGATCAAAAGCTTAYACTCAACTTAAACTTTCAGGTCTT 3180
QY 3294 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTT 3353
Dd |||||||
Dd 3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTT 3240
QY 3354 CTATATTTGATGCTAGGAAGCTTATTTGGCAATTTCAATATGGATTATATTTTATACGTGA 3413
Dd |||||||
Dd 3241 CTATATTTGATGCTAGGAAGCTTATTTGGCAATTTCAATATGGATTATATTTTATACGTGA 3300
QY 3414 AAGTTCCCTGCTGCTGTTTTTTTGGCTTATTTGGTTATGTTCCATCAGTTATTTCTGTTCACT 3473
Dd |||||||
Dd 3301 AAGTTCCCTGCTGCTGTTTTTTTGGCTTATTTGGTTATGTTCCATCAGTTATTTCTGTTCACT 3360
QY 3474 TATATTTGCTTTTCCACCTTTTAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC 3533
Dd |||||||
Dd 3361 TATATTTGCTTTTCCACCTTTTAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC 3420
QY 3534 TATTCTGTGGCAGCGTTGGCTTGTATTTGCAATCACTGAAATAACTTTCTTTATGGGATAC 3593
Dd |||||||
Dd 3421 TATTCTGTGGCAGCGTTGGCTTGTATTTGCAATCACTGAAATAACTTTCTTTATGGGATAC 3480
QY 3594 ACAATTTGCAACTATTCTTCATTTATGCTTTTGTATCATCATTTCCAACTATCCACTTCTA 3653
Dd |||||||
Dd 3481 ACAATTTGCAACTATTCTTCATTTATGCTTTTGTATCATCATTTCCAACTATCCACTTCTA 3540
QY 3654 GGTTCCTGATTTCTTTTCATAAAGATTTCTTTGGAAGAAATGACGAAAAAATGTGGACACC 3713
Dd |||||||
Dd 3541 GGTTCCTGATTTCTTTTCATAAAGATTTCTTTGGAAGAAATGACGAAAAAATGTGGACACC 3600
QY 3714 TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCCCTTACCTGCAGTGTGACTG 3773
Dd |||||||
Dd 3601 TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCCCTTACCTGCAGTGTGACTG 3660
QY 3774 TGGATTTTCTCTTCAATACATATGAGAAAAAATATGGAGGAGATCAATAAGAAAGAT 3833
Dd |||||||
Dd 3661 TGGATTTTCTCTTCAATACATATGAGAAAAAATATGGAGGAGATCAATAAGAAAGAT 3720
QY 3834 CCCTTTTTCAGAAACCTTTTCAACGAACTTAAAAATAGGAAGTTCCAGAACCCAGAC 3893
Dd |||||||
Dd 3721 CCCTTTTTCAGAAACCTTTTCAACGAACTTAAAAATAGGAAGTTCCAGAACCCAGAC 3780
QY 3894 AATGAGGATGAAGATGAAGATGTCAAGCTGAAAGACTAAAGGTCAAAAGAGCTGATGGGT 3953
Dd |||||||
Dd 3781 AATGAGGATGAAGATGAAGATGTCAAGCTGAAAGACTAAAGGTCAAAAGAGCTGATGGGT 3840
QY 3954 TGCCAGTGTGTGAGGAGAAACCATCCATTTATGCTCAGCAATTTGCATAAAGAATATGAT 4013
Dd |||||||
Dd 3841 TGCCAGTGTGTGAGGAGAAACCATCCATTTATGCTCAGCAATTTGCATAAAGAATATGAT 3900
QY 4014 GACAAGAAAGATTTCTTCTTTCAAGAAAGTAAAGAAAGTGCGCAACTAAATACATCTCT 4073
Dd |||||||
Dd 3901 GACAAGAAAGATTTCTTCTTTCAAGAAAGTAAAGAAAGTGCGCAACTAAATACATCTCT 3960
QY 4074 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTCTGGCAAAAGC 4133
Dd |||||||
Dd 3961 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTCTGGCAAAAGC 4020
QY 4134 ACAATTATTAATTTCTGGTTGGTGATATTGAACCAACTTCAGSCCAGGTATTTTITAGGA 4193
Dd |||||||
Dd 4021 ACAATTATTAATTTCTGGTTGGTGATATTGAACCAACTTCAGSCCAGGTATTTTITAGGA 4080
QY 4194 GATTATTTCTTCAGAGACAAGTGAAGATGATGATTTCACTGAAGTGATGGGTTACTGTCTT 4253

Dd |||||||
QY 4081 GATTATTTCTCAGAGACAAGTGAAGATGATGATTTCACTGAAGTGATGGTTACTGTCTT 4140
QY 4254 CAGATAAACCCCTTTGTGGCCAGATACTACATTTGCAGGAACATTTTGAATTTATGGAGCT 4313
Dd |||||||
Dd 4141 CAGATAAACCCCTTTGTGGCCAGATACTACATTTGCAGGAACATTTTGAATTTATGGAGCT 4200
QY 4314 GTCAAAAGGAATGAGTGTCAAGTGACATGAAAAGAGTCATAAGTCGAATAACACATGCACCT 4373
Dd |||||||
Dd 4201 GTCAAAAGGAATGAGTGTCAAGTGACATGAAAAGAGTCATAAGTCGAATAACACATGCACCT 4260
QY 4374 GATTTTAAAGAAACATCTTTCAGAAAGCTGTAAAGAACTTACCTGCAGGAATCAAACGAAAG 4433
Dd |||||||
Dd 4261 GATTTTAAAGAAACATCTTTCAGAAAGCTGTAAAGAACTTACCTGCAGGAATCAAACGAAAG 4320
QY 4434 TTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4493
Dd |||||||
Dd 4321 TTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4380
QY 4494 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTTAA 4553
Dd |||||||
Dd 4381 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTTAA 4440
QY 4554 AACAGAAAGCGGCTGCTATTCTTGACCACTCACTATATGGAGAGGCAGAGGCTGTCTGT 4613
Dd |||||||
Dd 4441 AACAGAAAGCGGCTGCTATTCTTGACCACTCACTATATGGAGAGGCAGAGGCTGTCTGT 4500
QY 4614 GATCGAGTAGCTATCATGTTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA 4673
Dd |||||||
Dd 4501 GATCGAGTAGCTATCATGTTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA 4560
QY 4674 AAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTTAAATTTGAAGGACTGGATAGAAAAC 4733
Dd |||||||
Dd 4561 AAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTTAAATTTGAAGGACTGGATAGAAAAC 4620
QY 4734 CTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAG 4793
Dd |||||||
Dd 4621 CTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAG 4680
QY 4794 GAAAGTTTTTCTTCTATTTTGGCTTATAAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA 4853
Dd |||||||
Dd 4681 GAAAGTTTTTCTTCTATTTTGGCTTATAAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA 4740
QY 4854 CAATCTTTTTTTTAAGCTGGAAGAG 4878
Dd |||||||
Dd 4741 CAATCTTTTTTTTAAGCTGGAAGAG 4765

RESULT 7

ABS57749

ID ABS57749 standard; cDNA; 5463 BP.

XX ABS57749;

XX AC ABS57749;

XX DT 04-FEB-2003 (first entry)

XX cDNA encoding novel human ATP binding cassette ABCA5 transporter #1.

DE Human; ATP binding cassette; ABC; ABCA5; transporter;

XX neurotoxin transport; beta-amyloid peptide; chromosome mapping;

KW blood brain barrier transport; tissue typing; predictive medicine;

KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 114..5030

FT /*tag= a

FT /product= "ABCA5"

FT /note= "ATP binding cassette (ABC) A5 transporter"

FT /transl_except= (pos:3273..3275, aa:Ser)

XX

PN US2002123107-A1.

XX 05-SEP-2002.
PD
XX
PF 01-MAR-2002; 2002US-00090458.
XX
PR 02-MAR-2001; 2001US-0272885P.
XX
PA (ACTI-) ACTIVE PASS PHARM INC.
XX
XX Chen H, Kilinski L, Le Bihan S;
PI
XX WPI; 2003-066798/06.
DR P-PSDB; ABG72423.
XX

PT Novel isolated ATP binding cassette transporter family polypeptide,
PT ABCA5, useful for treating disorders associated with aberrant or unwanted
PT ABCA5 transporter expression or activity.

XX Claim 2; Fig 1; 52pp; English.

CC The invention describes an isolated ATP binding cassette (ABC)
CC transporter family polypeptide (I), designated ABCA5. (I) or the
CC polynucleotide encoding it (II) are useful as targets for developing
CC modulating agents to regulate a variety of cellular processes,
CC particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC (BBB), as targets for developing modulating agents of multi-drug
CC resistance, as diagnostic and therapeutic tools, or to treat disorders
CC associated with aberrant or unwanted ABCA5 transporter expression or
CC activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC screening assays, detection assays (e.g., chromosomal mapping, tissue
CC typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC (III) are useful as reagents or targets in assays applicable to treatment
CC and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC -hybrid or three-hybrid assay; and to identify other proteins which bind
CC to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC activity; to locate gene regions associated with genetic disease or to
CC associate ABCA5 with the disease, to identify an individual from a minute
CC biological sample (tissue typing), and to aid in forensic identification
CC of the biological sample. This sequence encodes a novel human ATP binding
CC cassette (ABC) A5 transporter

XX SQ Sequence 5463 BP; 1699 A; 912 C; 1055 G; 1794 T; 0 U; 3 Other;

Query Match 51.6%; Score 2826; DB 7; Length 5463;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2876; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGTCCGGCCCTCGCACAGATCCNAGCTGGTCAACCGCACTGAGTCAACAGACTCGAGC 60
DB |||||||
QY 61 GCGTCCAGCCCTGACAGCTCTGCGGCTCGGGCCCTGAGGTTATTCAGAAAACATGTCCA 120
DB |||||||
QY 121 CTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAATTACT 180
DB |||||||
QY 181 TAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTATTTTTT 240
DB |||||||
QY 241 TATTTGGTAAATTAATTAGCATGATGCCAAATGAAGAAATATGAAGAAGTGCCTA 300
DB |||||||
QY 241 TATTTGGTAAATTAATTAGCATGATGCCAAATGAAGAAATATGAAGAAGTGCCTA 300
DB |||||||

QY 301 ATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGGATATATC 360
DB |||||||
QY 361 CAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTACCTGATG 420
DB |||||||
QY 421 TCATAATTACTGAAGAATATACAATGAAAAAGAAATGTTAAACATCCAGTCTCTCTAAGC 480
DB |||||||
QY 481 CGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCCATGCTCTATGAACCTTCGTTTTTTC 540
DB |||||||
QY 541 CTGATATGATCCAGTATCTTCTATTTATATGATTCAAGAGCTGGCTGTTCAAAAATCAT 600
DB |||||||
QY 601 GTGAGGCTGCTCAGTACTGCTCCTCAGGTTTTCACAGTTTTTACAAGCATCCATAGATCTG 660
DB |||||||
QY 661 CCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGTGGAGTCAACTAAAGCTG 720
DB |||||||
QY 721 TTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTAATTTAA 780
DB |||||||
QY 781 TATACCTAGTTATAGCATTTTACCTTTTGGATACCTTTTGGCAATTCATATCGTAGCAG 840
DB |||||||
QY 841 AAAAGAAAAAAATAAAGAAATTTTAAAGATAATGAGGACTTCATGATACTGCCTTT 900
DB |||||||
QY 901 GGCTTTCTGGGTTCTTCTATATACAAGTTTAAATTTTCTTATGTCCCTTCTTATGGCAG 960
DB |||||||
QY 961 TCATTGGCAGAGCTTCTTTGTTATTTCTCTCAAAGTAGCAGCATTTCTGCTTT 1020
DB |||||||
QY 1021 TTTTCTTTTATGGATTATCATCTGTATTTTGTCTTTAATGCTGACACCTCTTTTAAAA 1080
DB |||||||
QY 1081 AATCAAAACATGTGGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTTATTGGCC 1140
DB |||||||
QY 1141 TTATGATAATCCTCATAGAAAAGTTTCCCAAATCGTTAGTGGCTTTTTCAGTCCCTTTCT 1200
DB |||||||
QY 1201 GTCACCTGACTTTTGTGATTGGTATTCACAGGTTCATGCAATTAGAAGATTTTAAATGAG 1260
DB |||||||
QY 1261 GTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATATTACAATATCATGC 1320
DB |||||||
QY 1321 TCACACTTAATAGTATATTTCTATGCTCTTGGCTGTCTATCTTGATCAAGTCAATCCAG 1380
DB |||||||
QY 1381 GGGAAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGGTCAAAGA 1440
DB |||||||

Db 1381 GGGAAATTGGCTTACGGAGATCACTTTATATTTCTGAAGCCTTCATATTGGTCAAGA 1440
QY 1441 GCAAAAGAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGTTTAGTG 1500
Db 1441 GCAAAAGAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGTTTAGTG 1500
QY 1501 AAATTATTAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAGCCATAAGAATTAGTGGTA 1560
Db 1501 AAATTATTAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAGCCATAAGAATTAGTGGTA 1560
QY 1561 TTCAGAAGACATACAGAAAGAGGGGTGAAAATGTGGAGGTTTGAGAAAATTTGTCAATTTG 1620
Db 1561 TTCAGAAGACATACAGAAAGAGGGGTGAAAATGTGGAGGTTTGAGAAAATTTGTCAATTTG 1620
QY 1621 ACATATATGAGGGTCAGATTACTGCGCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACAT 1680
Db 1621 ACATATATGAGGGTCAGATTACTGCGCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACAT 1680
QY 1681 TGATGAATATCTTTTGTGGACTCTGCGCCACCTTCTGATGGGTTTGCATCTATATATGGAC 1740
Db 1681 TGATGAATATCTTTTGTGGACTCTGCGCCACCTTCTGATGGGTTTGCATCTATATATGGAC 1740
QY 1741 ACAGAGTCTCAGAAAATAGATGAATGTTTGAAGCAAGAAAATGATTGGCATTGTGCCAC 1800
Db 1741 ACAGAGTCTCAGAAAATAGATGAATGTTTGAAGCAAGAAAATGATTGGCATTGTGCCAC 1800
QY 1801 AGTTAGATATACACTTTTGATGTTTTTGACAGTAGAAGAAAATTTATCAATTTTGGCTTCAA 1860
Db 1801 AGTTAGATATACACTTTTGATGTTTTTGACAGTAGAAGAAAATTTATCAATTTTGGCTTCAA 1860
QY 1861 TCAAAGGGATACCAGCCCAACAATATAATACAAGAAGTGCAGAAGTTTTTACTAGATTAG 1920
Db 1861 TCAAAGGGATACCAGCCCAACAATATAATACAAGAAGTGCAGAAGTTTTTACTAGATTAG 1920
QY 1921 ACATGCAGACTATCAAAGATAACCAAGCTAAAAATTAAGTGGTGCATCAAAAAAGAAAGC 1980
Db 1921 ACATGCAGACTATCAAAGATAACCAAGCTAAAAATTAAGTGGTGCATCAAAAAAGAAAGC 1980
QY 1981 TGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACCTGCTAGATGAACCAACAG 2040
Db 1981 TGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACCTGCTAGATGAACCAACAG 2040
QY 2041 CTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGAAAAAGCCA 2100
Db 2041 CTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGAAAAAGCCA 2100
QY 2101 ATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCAGATAGGA 2160
Db 2101 ATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCAGATAGGA 2160
QY 2161 AAGCTGTGATATCAAGGAATGCTGAAATGTGTTGGTTCTTCAATGTTCTCCTCAAAGTA 2220
Db 2161 AAGCTGTGATATCAAGGAATGCTGAAATGTGTTGGTTCTTCAATGTTCTCCTCAAAGTA 2220
QY 2221 AATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACAGAAATCTC 2280
Db 2221 AATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACAGAAATCTC 2280
QY 2281 TTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATACAACAGAAATGACCAAC 2340
Db 2281 TTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATACAACAGAAATGACCAAC 2340
QY 2341 AACTTGTGTATGAGCTTGCCTTTCAGGACATGGACAAATTTTCAAGGTTTGTCTGCCCC 2400
Db 2341 AACTTGTGTATGAGCTTGCCTTTCAGGACATGGACAAATTTTCAAGGTTTGTCTGCCCC 2400
QY 2401 TAGACAGTCATTCAAATTTGGGTGTCAATTTCTTATGGTGTTCATGACGACTTTTGGAAAG 2460
Db 2401 TAGACAGTCATTCAAATTTGGGTGTCAATTTCTTATGGTGTTCATGACGACTTTTGGAAAG 2460
QY 2461 ACGTATTTTAAAGCTAGAAGTTGAAGCAGAAAATTGACCAAGCAGATTATAGTGTATTTA 2520

Db 2461 ACGTATTTTAAAGCTAGAAGTTGAAGCAGAAAATTGACCAAGCAGATTATAGTGTATTTA 2520
QY 2521 CTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTCATGAAATGGAACAGAGCT 2580
Db 2521 CTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTCATGAAATGGAACAGAGCT 2580
QY 2581 TACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTTGGAAACAAC 2640
Db 2581 TACTTATTTCTTTCTGAAACCAAGGCTGCTCTAGTGAGCACCATGAGCCTTTTGGAAACAAC 2640
QY 2641 AGATGTATACAATAGCAAAAGTTTCATTTTACCTTGAACGTTGAAAGTAAATCAGTGA 2700
Db 2641 AGATGTATACAATAGCAAAAGTTTCATTTTACCTTGAACGTTGAAAGTAAATCAGTGA 2700
QY 2701 GATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTGGTTC 2760
Db 2701 GATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTTTGGTTC 2760
QY 2761 ATCACTCTTTTAAAAATGCTGTGTTCCCATCAAACTTGTTCAGACTTATATTTCTAA 2820
Db 2761 ATCACTCTTTTAAAAATGCTGTGTTCCCATCAAACTTGTTCAGACTTATATTTCTAA 2820
QY 2821 AACCTGGAGACAAACCAACATAAATACAAAACAAGTCTGCTTCTTCAAAATTTCTGCTG 2877
Db 2821 AACCTGGAGACAAACCAACATAAATACAAAACAAGTCTGCTTCTTCAAAATTTCTGCTG 2877

RESULT 8

ADA53416
ID ADA53416 standard; cDNA; 3268 BP.

XX ADA53416;

XX AC

XX DT 20-NOV-2003 (first entry)

XX Human coding sequence, SEQ ID 984.

XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;

XX Gene Therapy; human; secretory protein; membrane proteins; cancer;

XX inflammatory disease; osteoporosis; neurological disease; gene; ss.

XX Homo sapiens.

XX EPI293569-A2.

XX PD 19-MAR-2003.

XX 21-MAR-2002; 2002EP-00006586.

XX 14-SEP-2001; 2001JP-00328381.

XX 24-JAN-2002; 2002US-0350435P.

XX (HELI-) HELIX RES INST.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-395539/38.

XX P-PSDB; ADA55055.

XX New polynucleotides encoding full-length polypeptides, e.g. secretory

XX and/or membrane proteins, useful for developing medicines for diseases in

XX which the gene is involved, or as target molecules for gene therapy.

XX Claim 1; SEQ ID NO 984; 205pp; English.

XX The present invention relates to novel human secretory or membrane

XX proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-

XX ADA54071). The coding sequences are useful in the gene therapy of

XX diseases caused by abnormalities of the proteins, e.g. cancer,

XX inflammatory diseases, osteoporosis or neurological disease.

QY 4486 AACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTG 4545
Dbb|||||
Dbb 2320 AACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTG 2379
QY 4546 CATTAAAAACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGAGGAGGCAGAGG 4605
Dbb|||||
Dbb 2380 CATTAAAAACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGAGGAGGCAGAGG 2439
QY 4606 CTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGCGAGTTAAGATGATATCGGAACAGTAC 4665
Dbb|||||
Dbb 2440 CTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGCGAGTTAAGATGATATCGGAACAGTAC 2499
QY 4666 AACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAAATTAATTAAGGACTGGA 4725
Dbb|||||
Dbb 2500 AACATCTAAAGAGTAGATTTGGAAAAGGCTACTTTTGGAAAATTAATTAAGGACTGGA 2559
QY 4726 TAGAAAACCTAGAAAGTAGACCGCCTTCAAAGAGAAAATTCAGTATATTTCCCAAATGCAA 4785
Dbb|||||
Dbb 2560 TAGAAAACCTAGAAAGTAGACCGCCTTCAAAGAGAAAATTCAGTATATTTCCCAAATGCAA 2619
QY 4786 GCCGTACAGGAAAGTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGT 4845
Dbb|||||
Dbb 2620 GCCGTACAGGAAAGTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGT 2679
QY 4846 CCCTTTCACAATCTTTTAAAGCTGGAAGAACTAAACATGCTTTTGCCATTGAAGAAT 4905
Dbb|||||
Dbb 2680 CCCTTTCACAATCTTTTAAAGCTGGAAGAACTAAACATGCTTTTGCCATTGAAGAAT 2739
QY 4906 ATAGCTTTTCTCAAGCAACATTGGGAACAGGTTTTGTAGAACTCTACTAAAGAAACAAGAGG 4965
Dbb|||||
Dbb 2740 ATAGCTTTTCTCAGGCAACATTGGGAACAGGTTTTGTAGAACTCTACTAAAGAAACAAGAGG 2799
QY 4966 AGGAAGATAATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAACGAAACAAGAG 5025
Dbb|||||
Dbb 2800 AGGAAGATAATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAACGAAACAAGAG 2859
QY 5026 ATAGAGTAGTATTTTGAATTTGTATTGTTCCGTCTGCTTACTGGGACTTCTTTCTTTTC 5085
Dbb|||||
Dbb 2860 ATAGAGTAGTATTTTGAATTTGTATTGTTCCGTCTGCTTACTGGGACTTCTTTCTTTTC 2919
QY 5086 ACTTAATTTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGGTAAGTGGAGAACCAAGA 5145
Dbb|||||
Dbb 2920 ACTTAATTTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGGTAAGTGGAGAACCAAGA 2979
QY 5146 ACGCACTTGAAATTTTCTAAGCTCCTTAATGAAATGCTGTGGTGTGTTTGTCTTT 5205
Dbb|||||
Dbb 2980 ACGCACTTGAAATTTTCTAAGCTCCTTAATGAAATGCTGTGGTGTGTTTGTCTTT 3039
QY 5206 TCTTTAAATAAAACGATGTATATAATTAAGTGAAGCTGCATGTTTGPATTAAGTATATTG 5265
Dbb|||||
Dbb 3040 TCTTTAAATAAAACGATGTATATAATTAAGTGAAGCTGCATGTTTGPATTAAGTATATTG 3099
QY 5266 AACTATATAGTTTGTATGTCATCTTTTTCACCAATTCAGAAACAGTGTCTTCTGAATTTGTG 5325
Dbb|||||
Dbb 3100 AACTATATAGTTTGTATGTCATCTTTTTCACCAATTCAGAAACAGTGTCTTCTGAATTTGTG 3159
QY 5326 ATTTAAAGGAATTCGTAATAGATAGTTTATTTTAAAGTTATCTTTAAAGTTTATGCCATC 5385
Dbb|||||
Dbb 3160 ATTTAAAGGAATTCGTAATAGATAGTTTATTTTAAAGTTATCTTTAAAGTTTATGCCATC 3219
QY 5386 TTCTTAAATAAGTACGTAATGTTCCAAATCTAAATAAAAACTAAT 5430
Dbb|||||
Dbb 3220 TTCTTAAATAAGTACGTAATGTTCCAAATCTAAATAAAAACTAAT 3264

RESULT 9
ABS57750
ID ABS57750 standard; cDNA; 4917 BP.
XX AC ABS57750;
XX DT 04-FEB-2003 (first entry)

XX Coding sequence of human ATP binding cassette ABCA5 transporter #1.
DE Human; ATP binding cassette; ABC; ABCA5; transporter;
XX neurotoxin transport; beta-amyloid peptide; chromosome mapping;
KW blood brain barrier transport; tissue typing; predictive medicine;
KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.
XX Homo sapiens.
OS
XX Location/Qualifiers
FH 1. .4917
FT /*tag= a
FT /product= "ABCA5"
FT /note= "ATP binding cassette (ABC) A5 transporter"
FT /transl_except= (pos:3160..3162, aa:Ser)
XX
PN US2002123107-A1.
XX
XX 05-SEP-2002.
PD
XX 01-MAR-2002; 2002US-00090458.
PF
XX 02-MAR-2001; 2001US-0272885P.
PR
XX (ACTI-) ACTIVE PASS PHARM INC.
PA Chen H, Kilinski L, Le Bihan S;
XX WPI; 2003-066798/06.
DR P-PSDB; ABG72423.
XX
PT Novel isolated ATP binding cassette transporter family polypeptide,
PT ABCA5, useful for treating disorders associated with aberrant or unwanted
PT ABCA5 transporter expression or activity.
XX
PS Claim 2; Fig 1; 52pp; English.
XX
CC The invention describes an isolated ATP binding cassette (ABC)
CC transporter family polypeptide (I), designated ABCA5. (I) or the
CC polynucleotide encoding it (II) are useful as targets for developing
CC modulating agents to regulate a variety of cellular processes,
CC particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC (BBB), as targets for developing modulating agents of multi-drug
CC resistance, as diagnostic and therapeutic tools, or to treat disorders
CC associated with aberrant or unwanted ABCA5 transporter expression or
CC activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC screening assays, detection assays (e.g., chromosomal mapping, tissue
CC typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC (III) are useful as reagents or targets in assays applicable to treatment
CC and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC -hybrid or three-hybrid assay; and to identify other proteins which bind
CC to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC activity; to locate gene regions associated with genetic disease or to
CC associate ABCA5 with the disease, to identify an individual from a minute
CC biological sample (tissue typing), and to aid in forensic identification
CC of the biological sample. This sequence encodes a novel human ATP binding
CC cassette (ABC) A5 transporter
XX
SQ Sequence 4917 BP; 1540 A; 821 C; 955 G; 1599 T; 0 U; 2 Other;

Query Match 49.6%; Score 2713; DB 7; Length 4917;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2763; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 114 ATGTCCTGCAATTAGGAGGTAGGAGTTGGAGACAGACACACTTCTACTGAAG 173
|||||

Db 1 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAAACACTTCTACTGAAG 60

QY 174 AATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAAATTCCTTTTCCACTA 233

Db 61 AATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAAATTCCTTTTCCACTA 120

QY 234 TTTTTTTTAAATTTGGTTAAATATTAAATTAGCATGATGCATCAAAATAAGAAAATATGAAGAA 293

Db 121 TTTTTTTTAAATTTGGTTAAATATTAAATTAGCATGATGCATCAAAATAAGAAAATATGAAGAA 180

QY 294 GTGCCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGGGA 353

Db 181 GTGCCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGGGA 240

QY 354 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAAGTGTCTACTGATCATCTA 413

Db 241 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAAGTGTCTACTGATCATCTA 300

QY 414 CCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAGAAAATGTTAAACATCCAGTCTC 473

Db 301 CCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAGAAAATGTTAAACATCCAGTCTC 360

QY 474 TCTAAGCCGAGCAAACTTTGTAGGTGTGGTTTTCAAAAGACTCCATGTCCTATGAACTTCGT 533

Db 361 TCTAAGCCGAGCAAACTTTGTAGGTGTGGTTTTCAAAAGACTCCATGTCCTATGAACTTCGT 420

QY 534 TTTTTTCTTGATATGATTCAGTATCTTCTATTTTATATGGAATTCAGAGCTGSGTGTTC 593

Db 421 TTTTTTCTTGATATGATTCAGTATCTTCTATTTTATATGGAATTCAGAGCTGSGTGTTC 480

QY 594 AAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTTCACAGTTTTCAGAGCATCCATA 653

Db 481 AAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTTCACAGTTTTCAGAGCATCCATA 540

QY 654 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 713

Db 541 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 600

QY 714 AAAGCTGTTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 773

Db 601 AAAGCTGTTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 660

QY 774 ATTTTAAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACCTTTTGGCAATTCATATC 833

Db 661 ATTTTAAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACCTTTTGGCAATTCATATC 720

QY 834 GTAGCAGAAAAGAAAAAATAFAAAGAAATTTTAAAGATAAATGGGACTTCATGATACT 893

Db 721 GTAGCAGAAAAGAAAAAATAFAAAGAAATTTTAAAGATAAATGGGACTTCATGATACT 780

QY 894 GCCTTTTGGCTTTCCTGGGTTCTCTATATACAAGTTTAAATTTTCTTATGTCCTTCTT 953

Db 781 GCCTTTTGGCTTTCCTGGGTTCTCTATATACAAGTTTAAATTTTCTTATGTCCTTCTT 840

QY 954 ATGGCAGTCATTCGACAGCTTCTTGTATTTCCTCAAAAGTAGCAGCATTCGTGATATT 1013

Db 841 ATGGCAGTCATTCGACAGCTTCTTGTATTTCCTCAAAAGTAGCAGCATTCGTGATATT 900

QY 1014 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTCCTTTTAAATGCTGACACCTCTT 1073

Db 901 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTCCTTTTAAATGCTGACACCTCTT 960

QY 1074 TTTTAAAAAATCAAAACATGTGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATT 1133

Db 961 TTTTAAAAAATCAAAACATGTGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATT 1020

QY 1134 ATTGGCTTATGATAATCCTCATAGAAAAGTTTTCCTCAAAATCGTTAGTGTGGCTTTTCAGT 1193

Db 1021 ATTGGCTTATGATAATCCTCATAGAAAAGTTTTCCTCAAAATCGTTAGTGTGGCTTTTCAGT 1080

QY 1194 CCTTTCTGTCACTGTACTTTTGTGATTGGTATTGCAAGGTCATGCATTTTGAAGATTTT 1253

Db 1081 CCTTTCTGTCACTGTACTTTTGTGATTGGTATTGCAAGGTCATGCATTTTGAAGATTTT 1140

QY 1254 AATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATATTACAAT 1313

Db 1141 AATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATATTACAAT 1200

QY 1314 ATCATGCTCACACTTAATAGTATATTCTATGTCTCTTGGCTGTCTATCTTGATCAAGTC 1373

Db 1201 ATCATGCTCACACTTAATAGTATATTCTATGTCTCTTGGCTGTCTATCTTGATCAAGTC 1260

QY 1374 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTTCTGAAGCCTTCATATTGG 1433

Db 1261 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1320

QY 1434 TCAAAGAGCAAAAAGAAATTTATGAGAGTTATCAGAGGGCAATGTTAATGGAATATTAGT 1493

Db 1321 TCAAAGAGCAAAAAGAAATTTATGAGAGTTATCAGAGGGCAATGTTAATGGAATATTAGT 1380

QY 1494 TTTAGTGAAATTTATTGAGCCAGTTTCTTCAGAAATTTGTAGAAAAGAACCATAGAAT 1553

Db 1381 TTTAGTGAAATTTATTGAGCCAGTTTCTTCAGAAATTTGTAGAAAAGAACCATAGAAT 1440

QY 1554 AGTGGTATTTCAGAAACATACAGAAAAGGGTGAAATTTGAGAGGCTTTGAGAAATTTG 1613

Db 1441 AGTGGTATTTCAGAAACATACAGAAAAGGGTGAAATTTGAGAGGCTTTGAGAAATTTG 1500

QY 1614 TCATTTGACATATATGAGGGTCAGATTACTGCCCTTACTTTGGCCACAGTGGAACAGGAAAG 1673

Db 1501 TCATTTGACATATATGAGGGTCAGATTACTGCCCTTACTTTGGCCACAGTGGAACAGGAAAG 1560

QY 1674 AGTACATTGATGAATATTCTTTGTGGACTCTGCCACCCTCTGATGGGTTTGCACTATA 1733

Db 1561 AGTACATTGATGAATATTCTTTGTGGACTCTGCCACCCTCTGATGGGTTTGCACTATA 1620

QY 1734 TATGGACACAGAGTCTCAGAAATPAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCAAT 1793

Db 1621 TATGGACACAGAGTCTCAGAAATPAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCAAT 1680

QY 1794 TGTCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAGAAAAATTTATCAATTTG 1853

Db 1681 TGTCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAGAAAAATTTATCAATTTG 1740

QY 1854 GCTTCAATCAAAGGGATACCAGCCAAACAATATATATACAAAGTGCAGAAAGTTTACTA 1913

Db 1741 GCTTCAATCAAAGGGATACCAGCCAAACAATATATATACAAAGTGCAGAAAGTTTACTA 1800

QY 1914 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTTAAAAAATTAAGTGGTGCACAAA 1973

Db 1801 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTTAAAAAATTAAGTGGTGCACAAA 1860

QY 1974 AGAAAGCTGTCATTAGGAATGCTGTTCTTGGGAACCCCAAGATACTGCTGCTAGATGA 2033

Db 1861 AGAAAGCTGTCATTAGGAATGCTGTTCTTGGGAACCCCAAGATACTGCTGCTAGATGA 1920

QY 2034 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA 2093

Db 1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA 1980

QY 2094 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTCITGCA 2153

Db 1981 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTCITGCA 2040

QY 2154 GATAGAAAAGCTGTGATATCAAGGAATGCTGAAATGCTGTTGGTCTTCAATGTTCTCTC 2213

Db 2041 GATAGAAAAGCTGTGATATCAAGGAATGCTGAAATGCTGTTGGTCTTCAATGTTCTCTC 2100

QY 2214 AAAAGTAAATGGGGATCGGTACCGCCTGAGCATATACATAGACAAATATTGTGCCACA 2273

Db 2101 AAAAGTAAATGGGGATCGGTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 2160

QY 2274 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTAACAAGAAAT 2333

Db 2161 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTAACAAGAAAT 2220

QY 2334 GACCAACAACCTTGTTGATAGCTTGCCTTTCAAGGACATGACAAAATTTTCAGGTTTGT 2393
Db |||||||
2221 GACCAACAACCTTGTTGATAGCTTGCCTTTCAAGGACATGACAAAATTTTCAGGTTTGT 2280
QY 2394 TCCTGCCCTAGACAGTCATTCAAAATTTGGGTGTCATTTCTTATGTTGTTTCCATGACGACT 2453
Db |||||||
2281 TCCTGCCCTAGACAGTCATTCAAAATTTGGGTGTCATTTCTTATGTTGTTTCCATGACGACT 2340
QY 2454 TTGGAAGACGTTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTTGACCAAGCAGATTATAGT 2513
Db |||||||
2341 TTGGAAGACGTTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTTGACCAAGCAGATTATAGT 2400
QY 2514 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCCAAAATCTTTTGTATGAAATGGAA 2573
Db |||||||
2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCCAAAATCTTTTGTATGAAATGGAA 2460
QY 2574 CAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATTGAGCCTTTGG 2633
Db |||||||
2461 CAGAGCTTACTTATTTCTGAAACCAAGGCTGCTCTAGTGAGCACCATTGAGCCTTTGG 2520
QY 2634 AAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGTTGAAGTAAA 2693
Db |||||||
2521 AAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGTTGAAGTAAA 2580
QY 2694 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2753
Db |||||||
2581 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2640
QY 2754 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACCTTATAT 2813
Db |||||||
2641 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACCTTATAT 2700
QY 2814 TTTCTAAAACCTGGAGACAAACCAATATAAATACAAAACAGTCTGCTTCTTCAAAATCT 2873
Db |||||||
2701 TTTCTAAAACCTGGAGACAAACCAATATAAATACAAAACAGTCTGCTTCTTCAAAATCT 2760
QY 2874 GCTG 2877
Db |||||
2761 GCTG 2764

RESULT 10
ADC51606
ID ADC51606 standard; DNA; 2723 BP.
XX
AC ADC51606;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human macroprotein-94.64 coding sequence, SEQ ID 1.
XX
KW Human; macroprotein-94.64; dementia; arrhythmia; asthma; diabetes; gene;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12..2486
FT /*tag= a
FT /product= "Human macroprotein-94.64"
XX
PN CN1382726-A.
XX
PD 04-DEC-2002.
XX
PF 26-APR-2001; 2001CN-00112765.
XX
PR 26-APR-2001; 2001CN-00112765.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX

DR WPI; 2003-269487/27.
DR P-PSDB; ADC51607.
XX
PT New human macroprotein-94.64, encoding polynucleotide, antagonist and
PT recombinant production, useful for treating dementia, arrhythmia, asthma
PT and diabetes.
XX
PS Claim 6; SEQ ID NO 1; 35pp; Chinese.
XX
CC The present invention relates to human macroprotein-94.64 (ADC51607) and
CC its coding sequence (ADC51606). The protein is useful for treating
CC dementia, arrhythmia, asthma and diabetes.
XX
SQ Sequence 2723 BP; 855 A; 460 C; 518 G; 890 T; 0 U; 0 Other;
Query Match 48.1%; Score 2633; DB 9; Length 2723;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2557 CTTTGTGATGAAATGGAACAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGA 2616
Db |||||||
1 CTTTGTGATGAAATGGAACAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGA 60
QY 2617 GCACCATGAGCCTTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCT 2676
Db |||||||
61 GCACCATGAGCCTTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCT 120
QY 2677 TGAACCGTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG 2736
Db |||||||
121 TGAACCGTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG 180
QY 2737 TTCAGATTTTATGTTTGTGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAAC 2796
Db |||||||
181 TTCAGATTTTATGTTTGTGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAAC 240
QY 2797 TTGTTCCAGACTTATATTTTCTAAAAACCTGGAGACAAACCAATATAAATACAAAACAGTC 2856
Db |||||||
241 TTGTTCCAGACTTATATTTTCTAAAAACCTGGAGACAAACCAATATAAATACAAAACAGTC 300
QY 2857 TGCTTCTTCAAAATTTCTGCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAAGCC 2916
Db |||||||
301 TGCTTCTTCAAAATTTCTGCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAAGCC 360
QY 2917 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGATCCGTGGCTCCCATAGTG 2976
Db |||||||
361 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGATCCGTGGCTCCCATAGTG 420
QY 2977 CGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA 3036
Db |||||||
421 CGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA 480
QY 3037 CTATGGTTTATTTCTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCAFT 3096
Db |||||||
481 CTATGGTTTATTTCTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCAFT 540
QY 3097 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATTACTGATA 3156
Db |||||||
541 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATTACTGATA 600
QY 3157 TAGTTTTTAAAAATTTGAGCTGTATTTTCAAGCAGCTTTTGTGGAATCATTTGTACTGCAA 3216
Db |||||||
601 TAGTTTTTAAAAATTTGAGCTGTATTTTCAAGCAGCTTTTGTGGAATCATTTGTACTGCAA 660
QY 3217 TGCCACCTTACTTTGCCATGGAAATGCAGAGAAATCATAGATCAAAAGCTTATACTCAAC 3276
Db |||||||
661 TGCCACCTTACTTTGCCATGGAAATGCAGAGAAATCATAGATCAAAAGCTTATACTCAAC 720
QY 3277 TTAAACCTTTCAGGTCTTTTGGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCC 3336
Db |||||||
721 TTAAACCTTTCAGGTCTTTTGGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCC 780
QY 3337 CCTTATTTTATCATTTCTTATTTTATGCTAGGAAGCTTATTTGTCATTTATGAT 3396
Db |||||||

Db 781 CCTTATTTTATCATCTCTTATTTTGATGCTAGGAAGCTTACTGGCATTTCATTATGGAT 840
Qy 3397 TATATTTTATACTGTAAAGTCTCTGCTGTGGTTTTTTTGCCCTTATTTGGTTATGTTCCAT 3456
Db 841 TATATTTTATACTGTAAAGTCTCTGCTGTGGTTTTTTTGCCCTTATTTGGTTATGTTCCAT 900
Qy 3457 CAGTATTTCTGTTCACTTATATTTGCTTCTTTTCCACCTTTAAGAAAAATTTTAAATACCAAAG 3516
Db 901 CAGTATTTCTGTTCACTTATATTTGCTTCTTTTCCACCTTTAAGAAAAATTTTAAATACCAAAG 960
Qy 3517 AATTTTGGTCATTTATCTATTTCTGTTGGCAGCGTTGGCTTGATTTGCAATCACTGAAATAA 1020
Db 961 AATTTTGGTCATTTATCTATTTCTGTTGGCAGCGTTGGCTTGATTTGCAATCACTGAAATAA 1020
Qy 3577 CTTTCTTTATGGGATACACAAATTGCAACTATTCTTCAATTAATGCTTTTGTATCATCATTC 3636
Db 1021 CTTTCTTTATGGGATACACAAATTGCAACTATTCTTCAATTAATGCTTTTGTATCATCATTC 1080
Qy 3637 CAATCTATCCACTTCTAGTTGGCTGATTTCTTTTCAATAAGATTTCTTTGGAAGAATGTAC 3696
Db 1081 CAATCTATCCACTTCTAGTTGGCTGATTTCTTTTCAATAAGATTTCTTTGGAAGAATGTAC 1140
Qy 3697 GAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTATATCGCCTT 3756
Db 1141 GAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTATATCGCCTT 1200
Qy 3757 ACCTGCAGTGTGTA CTGTGGATTTTCTCTTTACAATACTATGAGAAAAAATATGGAGGCA 3816
Db 1201 ACCTGCAGTGTGTA CTGTGGATTTTCTCTTTACAATACTATGAGAAAAAATATGGAGGCA 1260
Qy 3817 GATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAAGTCTAAAAATAGGAAGC 3876
Db 1261 GATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAAGTCTAAAAATAGGAAGC 1320
Qy 3877 TTCCAGAAACCACGACAAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGG 3936
Db 1321 TTCCAGAAACCACGACAAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGG 1380
Qy 3937 TCAAAAGAGCTGATGGGTTGGCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 3996
Db 1381 TCAAAAGAGCTGATGGGTTGGCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 1440
Qy 3997 TGCATAAAGAATATGATGACAAAGAAAGATTTTCTTCTTTCAAGAAAGTAAAGAAAGTGG 4056
Db 1441 TGCATAAAGAATATGATGACAAAGAAAGATTTTCTTCTTTCAAGAAAGTAAAGAAAGTGG 1500
Qy 4057 CAACTAAATACATCTCTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 4116
Db 1501 CAACTAAATACATCTCTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 1560
Qy 4117 ATGGTGTCTGGCAAAAGCACAAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAG 4176
Db 1561 ATGGTGTCTGGCAAAAGCACAAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAG 1620
Qy 4177 GCCAGGTATTTTTAGGAGATTATTCTTTCAGAGACAAAGTGAAGATGATGATTCACCTGAAGT 4236
Db 1621 GCCAGGTATTTTTAGGAGATTATTCTTTCAGAGACAAAGTGAAGATGATGATTCACCTGAAGT 1680
Qy 4237 GTATGGGTTACTGTCTCAGATAAAACCCCTTTGTGGCCAGATACTACATTGCAGGAACATT 4296
Db 1681 GTATGGGTTACTGTCTCAGATAAAACCCCTTTGTGGCCAGATACTACATTGCAGGAACATT 1740
Qy 4297 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTCGAAGTGACATGAAGAAGTCTATAAGTC 4356
Db 1741 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTCGAAGTGACATGAAGAAGTCTATAAGTC 1800
Qy 4357 GAATAACACATGCATTGATTTTAAAGAAACATCTTTCAGAAGACTGTAAAGAAACTACCTG 4416
Db 1801 GAATAACACATGCATTGATTTTAAAGAAACATCTTTCAGAAGACTGTAAAGAAACTACCTG 1860
Qy 4417 CAGGAATCAAACGAAAGTTGTGTTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTT 4476
Db 1861 CAGGAATCAAACGAAAGTTGTGTTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTT 1920

RESULT 11
ABK35706

ID ABK35706 standard; cDNA; 1548 BP.

XX AC ABK35706;

XX AC ABK35706;

DT 08-MAY-2002 (first entry)

DE cDNA sequence #97 encoding novel human secreted protein.

XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;
XX immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; allergic condition; neurodegenerative disorder;
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.

OS Homo sapiens.

XX WO200177289-A2.

PN

Qy 4477 TGCTAGATGAACCATCTACAGGTATGGATCCCAAGCCCAACAGCACATGTGGCGAGCAA 4536
Db 1921 TGCTAGATGAACCATCTACAGGTATGGATCCCAAGCCCAACAGCACATGTGGCGAGCAA 1980
Qy 4537 TTCGAACCTGCATTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGG 4596
Db 1981 TTCGAACCTGCATTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGG 2040
Qy 4597 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGCAGTTAAGATGTATCG 4656
Db 2041 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGCAGTTAAGATGTATCG 2100
Qy 4657 GAACAGTACAAACATCTAAAGAGTAAATTTGGAAAAAGGCTACTTTTTGGAAAAATTAATTGA 4716
Db 2101 GAACAGTACAAACATCTAAAGAGTAAATTTGGAAAAAGGCTACTTTTTGGAAAAATTAATTGA 2160
Qy 4717 AGGACTGGATAGAAAAACCTAGAAGTAGACCGCCCTTCAAAAGAGAAAATTCAGTATATTTCC 4776
Db 2161 AGGACTGGATAGAAAAACCTAGAAGTAGACCGCCCTTCAAAAGAGAAAATTCAGTATATTTCC 2220
Qy 4777 CAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAG 4836
Db 2221 CAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAG 2280
Qy 4837 ATGTTCAAGTCCCTTTTCACAATCTTTTTTAAAGCTGGAAAGAACTAAACATGCTTTTGCCA 4896
Db 2281 ATGTTCAAGTCCCTTTTCACAATCTTTTTTAAAGCTGGAAAGAACTAAACATGCTTTTGCCA 2340
Qy 4897 TTGAAGAATATAGCTTTTCTCAAGCAACATTGGAAACAGGTTTTTGTAGAACTCACTAAAG 4956
Db 2341 TTGAAGAATATAGCTTTTCTCAAGCAACATTGGAAACAGGTTTTTGTAGAACTCACTAAAG 2400
Qy 4957 AACAAAGAGGAGGAAGATAATAGTTGTGGAACTTTAAACAGCACACCTTTGGTGGAAACGAA 5016
Db 2401 AACAAAGAGGAGGAAGATAATAGTTGTGGAACTTTAAACAGCACACCTTTGGTGGAAACGAA 2460
Qy 5017 CACAAGAAGATAGAGTAGTATTTTGAATTTGTATGTTTGGTCTGCTTACTGGGACTTCT 5076
Db 2461 CACAAGAAGATAGAGTAGTATTTTGAATTTGTATGTTTGGTCTGCTTACTGGGACTTCT 2520
Qy 5077 TTCTTTTTCACCTTAATTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGGTAACTGGA 5136
Db 2521 TTCTTTTTCACCTTAATTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGGTAACTGGA 2580
Qy 5137 GAACCAAGAACGCACTTGAAATTTTTCTAAGCTCCTTAATTGAAATGCTGTGTTGTGTG 5196
Db 2581 GAACCAAGAACGCACTTGAAATTTTTCTAAGCTCCTTAATTGAAATGCTGTGTTGTGTG 2640
Qy 5197 TTTTGTCTTTTCTTTAAATAAAAACGATGTATATAATTAAGTGAAGC 5240
Db 2641 TTTTGTCTTTTCTTTAAATAAAAACGATGTATATAATTAAGTGAAGC 2684

XX 18-OCT-2001.
PD
XX
PF 29-MAR-2001; 2001WO-US010232.
XX
PR 06-APR-2000; 2000US-0195605P.
XX
PA (GEMY) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
PI Clark HF, Fecthel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
XX
XX WPI; 2002-179322/23.
DR
XX
PT Six hundred and twenty three polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for treating
PT immune deficiencies and disorders such as autoimmune disorders.
XX
PS Claim 1; Page 126; 393pp; English.
XX
CC The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides a
CC method for producing proteins from these polynucleotide sequences. The
CC proteins are useful for identifying compounds that modulate their
CC activity and production. The sequences of the invention are useful for
CC treating diseases such as hyperproliferative disorders (e.g. cancer),
CC immune deficiency disorders (e.g. severe combined immunodeficiency
CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders
CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis),
CC infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma),
CC neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis,
CC coagulation disorders (e.g. haemophilia), and tumours. The polynucleotide
CC sequences of the invention are also useful in gene therapy. ABK35610-
CC ABK36232 represent the cDNA sequences of the invention that encode for
CC novel human secreted proteins
XX
SQ Sequence 1548 BP; 466 A; 273 C; 268 G; 541 T; 0 U; 0 Other;
Query Match 27.3%; Score 1497; DB 6; Length 1548;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2489 AGAAATTGACCAAGCAGATTATAGTGTATTTACTCAGAGCCACTGGAGGAAGAAATGGA 2548
Db 1 AGAAATTGACCAAGCAGATTATAGTGTATTTACTCAGAGCCACTGGAGGAAGAAATGGA 60
QY 2549 TTCAAATCTTTTGATGAAATGGAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTC 2608
Db 61 TTCAAATCTTTTGATGAAATGGAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTC 120
QY 2609 TCTAGTGAGCACCATGAGCCTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTCATTT 2668
Db 121 TCTAGTGAGCACCATGAGCCTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTCATTT 180
QY 2669 CTTTACCTTGAAACGTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTT 2728
Db 181 CTTTACCTTGAAACGTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTT 240
QY 2729 TTTCACAGTTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCC 2788
Db 241 TTTCACAGTTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCC 300
QY 2789 CATCAAACTTGTTCAGACTTATATTTTCTAAACCTGGAGACAAACCCACATAAAATACAA 2848
Db 301 CATCAAACTTGTTCAGACTTATATTTTCTAAACCTGGAGACAAACCCACATAAAATACAA 360
QY 2849 AACAAAGTCTGCTTCTTCAAAATCTGCTGACTCAGATATCAGTGATCTTATAGCTTTT 2908
Db 361 AACAAAGTCTGCTTCTTCAAAATCTGCTGACTCAGATATCAGTGATCTTATAGCTTTT 420
QY 2909 CACAAGCCAGAACATAATGGTGCGATGATTAATGACAGTGACTATGTATCCGTGGCTCC 2968

Db 421 CACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGIGGCTCC 480
QY 2969 CCATAGTGGCGCTTTAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTT 3028
Db 481 CCATAGTGGCGCTTTAAATGTGGTGCAATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTT 540
QY 3029 CAACAGTACTATGGTTTTTATCTTTTACCTATATTTAGTGAATATCATTAGTAACCTATCT 3088
Db 541 CAACAGTACTATGGTTTTTATCTTTTACCTATATTTAGTGAATATCATTAGTAACCTATCT 600
QY 3089 TTATCATTTTAAATGTGACTGAAACCATCCAGATCTGAGTAGTACCCCATCTCTTCAAGAAAT 3148
Db 601 TTATCATTTTAAATGTGACTGAAACCATCCAGATCTGAGTAGTACCCCATCTCTTCAAGAAAT 660
QY 3149 TACTGATATAGTTTTTAAANTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGT 3208
Db 661 TACTGATATAGTTTTTAAANTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGT 720
QY 3209 TACTGCAATGCCACCTTACTTTGCCATGGAAAAATGCAGAGAATCATAGATCAAAAGCTTA 3268
Db 721 TACTGCAATGCCACCTTACTTTGCCATGGAAAAATGCAGAGAATCATAGATCAAAAGCTTA 780
QY 3269 TACTCAACTTAAACTTTTCAAGTCTTTTGCCATCTGCATATTTGGATTGGACAAGCTGTTGT 3328
Db 781 TACTCAACTTAAACTTTTCAAGTCTTTTGCCATCTGCATATTTGGATTGGACAAGCTGTTGT 840
QY 3329 TGATATCCCTTATTTTATCATCTTATTTTGAAGTAGGAAGCTTATTTGGCAATTTCA 3388
Db 841 TGATATCCCTTATTTTATCATCTTATTTTGAAGTAGGAAGCTTATTTGGCAATTTCA 900
QY 3389 TTATGGATTATATTTTATACTGTAAAGTTCCCTTGCCTGCTGTTTTTGCCTTATTTGGTTA 3448
Db 901 TTATGGATTATATTTTATACTGTAAAGTTCCCTTGCCTGCTGTTTTTGCCTTATTTGGTTA 960
QY 3449 TGTTCATCAGTTATTTCTGTTCACTTATATTTGCTTCTTTCACCTTTAAGAAAAATTTAAA 3508
Db 961 TGTTCATCAGTTATTTCTGTTCACTTATATTTGCTTCTTTCACCTTTAAGAAAAATTTAAA 1020
QY 3509 TACCAAAAGAAATTTTGGTCATTTATCTATTTCTGTGGCAGCGTTGGCTTGTATGCAATCAC 3568
Db 1021 TACCAAAAGAAATTTTGGTCATTTATCTATTTCTGTGGCAGCGTTGGCTTGTATGCAATCAC 1080
QY 3569 TGAATAAATCTTTTATGSGATACACAATTTGCAACTATTTCTTCAATATGCTTTTGTAT 3628
Db 1081 TGAATAAATCTTTTATGSGATACACAATTTGCAACTATTTCTTCAATATGCTTTTGTAT 1140
QY 3629 CATCATTTCCAATCTATCCACTTCTAGGTTGCCTGATTTCTTTCATAAAGATTTCTTTGAA 3688
Db 1141 CATCATTTCCAATCTATCCACTTCTAGGTTGCCTGATTTCTTTCATAAAGATTTCTTTGAA 1200
QY 3689 GAATGTACGAAAAAATGTGGACACCTATAATCCATGSGATAGGCTTTTCAGTAGCTTTAT 3748
Db 1201 GAATGTACGAAAAAATGTGGACACCTATAATCCATGSGATAGGCTTTTCAGTAGCTTTAT 1260
QY 3749 ATCGCTTACCTGCAGTGTACTGTGGATTTTCCCTTTACAATACTATGAGAAAAAATA 3808
Db 1261 ATCGCTTACCTGCAGTGTACTGTGGATTTTCCCTTTACAATACTATGAGAAAAAATA 1320
QY 3809 TGGAGGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAACGAAGTCTAAAAA 3868
Db 1321 TGGAGGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAACGAAGTCTAAAAA 1380
QY 3869 TAGGAAGCTTCCAGAACCCAGACAATGAGGATGAAGATGTCAAAGCTTGAAAG 3928
Db 1381 TAGGAAGCTTCCAGAACCCAGACAATGAGGATGAAGATGTCAAAGCTTGAAAG 1440
QY 3929 ACTAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGTT 3988
Db 1441 ACTAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGTT 1500
QY 3989 CAGCAATTTGCATAAAGAAATATGATGACAAGAAAGATTTTCTTCTTC 4036

Db 1501 CAGCAATTGCATAAAGAATATGATGACAAGAAAGATTTTCTTCTTC 1548

RESULT 12

ABZ35938

ID ABZ35938 standard; cDNA; 2481 BP.

XX AC ABZ35938;

XX DT 10-FEB-2003 (first entry)

XX DE Human secretory polynucleotide SPTM SEQ ID NO 102.

XX KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;

XX KW asthma; Crohn's disease; neurological disorder; epilepsy; cancer;

XX KW Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;

XX KW multiple sclerosis; Parkinson's disease; cell proliferative disorder;

XX KW anti-inflammatory; immunosuppressive; neuroprotective; nootropic;

XX KW neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;

XX KW antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;

XX KW secretory polynucleotide; secretory protein; gene; ss.

OS Homo sapiens.

XX KW Homo sapiens.

PN WO200283876-A2.

PD 24-OCT-2002.

XX PF 27-MAR-2002; 2002WO-US009921.

XX PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.

PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.

PR 20-JUN-2001; 2001US-0299776P.

PR 20-JUN-2001; 2001US-030001P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;

PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;

PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX WPI; 2003-075543/07.

DR P-PSDB; ABP75491.

XX PT New human secretory proteins and polynucleotides, useful for diagnosing,

PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), or

PT neurological disorders (e.g. Alzheimer's), or cell proliferations or

PT cancers.

XX PS Claim 1; SEQ ID NO 102; 458pp + Sequence Listing; English.

XX CC The invention relates to a secretory polynucleotide (designated sptm)

CC comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a

CC naturally occurring polynucleotide sequence at least 90 % identical to

CC the polynucleotide sequence, a polynucleotide complementary to them or an

CC RNA equivalent of them. The polypeptide or polynucleotide are useful for

CC treating, preventing or diagnosing a disease or condition associated with

CC the expression of functional SPTM. These are particularly useful for

CC diagnosing, treating or preventing autoimmune/inflammatory disorders

CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's

CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,

CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,

CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,

CC schizophrenia or amnesia), or cell proliferative disorders (e.g.

CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,

CC leukaemia, lymphoma, melanoma, sarcoma or cancers of the brain,

CC breast, cervix or prostate). Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in electronic

CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 2481 BP; 662 A; 452 C; 477 G; 889 T; 0 U; 1 Other;

Query Match 24.7%; Score 1350; DB 7; Length 2481;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 97 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 156

Db 1081 AGGTTTATTCAGAAAACATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 1140

QY 157 GAACACTTCTACTGAAGAATTACTTAATTAATAATGACAGAACAAAAGAGTAGTGTTCAGG 216

Db 1141 GAACACTTCTACTGAAGAATTACTTAATTAATAATGACAGAACAAAAGAGTAGTGTTCAGG 1200

QY 217 AAATTCCTTTTCCACTATTTTCTTTTATTTTGGTTAATAATTAATAGCATGATGATCAACAA 276

Db 1201 AAATTCCTTTTCCACTATTTTCTTTTATTTTGGTTAATAATTAATAGCATGATGATCAACAA 1260

QY 277 ATAAGAAATATGAAGAAGTGCCTTAATATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 336

Db 1261 ATAAGAAATATGAAGAAGTGCCTTAATATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 1320

QY 337 CTAATCTAATTTCTTGGATATATCTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAG 396

Db 1321 CTAATCTAATTTCTTGGATATATCTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAG 1380

QY 397 TGTCTACTGATCATCTACCTGATGTGTCATAATTACTGAAGAAATATACAAATGAAAAAGAAA 456

Db 1381 TGTCTACTGATCATCTACCTGATGTGTCATAATTACTGAAGAAATATACAAATGAAAAAGAAA 1440

QY 457 TGTTAAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGTGTGGTTTTCAAAGACTCCA 516

Db 1441 TGTTAAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGTGTGGTTTTCAAAGACTCCA 1500

QY 517 TGTCTATGAACCTTCGTTTTTCTCTGATATGATTCAGATATCTTCTATTATATGGAATT 576

Db 1501 TGTCTATGAACCTTCGTTTTTCTCTGATATGATTCAGATATCTTCTATTATATGGAATT 1560

QY 577 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 636

Db 1561 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 1620

QY 637 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA 696

Db 1621 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA 1680

QY 697 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATA 756

Db 1681 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATA 1740

QY 757 CCTTTCCCGGAGGAGTAATTTTAATATACCTAGTTATAGCAATTTTCACCTTTTGGATACT 816

Db 1741 CCTTTCCCGGAGGAGTAATTTTAATATACCTAGTTATAGCAATTTTCACCTTTTGGATACT 1800

QY 817 TTTTGGCAATTCATATCGTAGCAAAAAGAAAAAATAAAGAAATTTTAAAGATAA 876

Db 1801 TTTTGGCAATTCATATCGTAGCAAAAAGAAAAAATAAAGAAATTTTAAAGATAA 1860

QY 877 TGGACTTCATGATACTGCCCTTTGGCTTTCTCTGGGTTCTTCTATATACAAGTTTAATTT 936

Db 1861 TGGACTTCATGATACTGCCCTTTGGCTTTCTCTGGGTTCTTCTATATACAAGTTTAATTT 1920

QY 937 TTCTTATGTCCTTCTTATGGCAGTCATTGCGACAGCTCTTTGTTATTTCCTCAAGATA 996

Db 1921 TTCTTATGTCCTTCTTATGGCAGTCATTGCGACAGCTCTTTGTTATTTCCTCAAGATA 1980

QY 997 GCAGCATTTGTGATATTTCTGCTTTTCTTTTCCCTTTATGATGATATCATCTGATTTTTCCTT 1056

Db 1981 GCAGCATTTGTGATATTTCTGCTTTTCTTTTCCCTTTATGATGATATCATCTGATTTTTCCTT 2040

QY 1057 TAATGCTGACACCTCTTTTAAATAAATCAAAACATGTGGGAATAGTTGAATTTTGTGA 1116
Db 2041 TAATGCTGACACCTCTTTTAAATAAATCAAAACATGTGGGAATAGTTGAATTTTGTGA 2100
QY 1117 CTGTGGCTTTTGGATTTATTTGGCTTATGATAATCCTCATAGAAAGTTTCCAAATCGT 1176
Db 2101 CTGTGGCTTTTGGATTTATTTGGCTTATGATAATCCTCATAGAAAGTTTCCAAATCGT 2160
QY 1177 TAGTGTGGCTTTTCAGTCTCTTCTGTCACTGTACTTTTGTGATTTGGTATTGACAGGTCA 1236
Db 2161 TAGTGTGGCTTTTTCAGTCTCTTCTGTCACTGTACTTTTGTGATTTGGTATTGACAGGTCA 2220
QY 1237 TGCATTTAGAAAGATTTTAATGAAGTGTCTTCATTTTCAAAATTTGACTGCAGGCCATATC 1296
Db 2221 TGCATTTAGAAAGATTTTAATGAAGTGTCTTCATTTTCAAAATTTGACTGCAGGCCATATC 2280
QY 1297 CTCTAATTAATACAATTAATCATGCTCACACTTAATAGTATATATCTATGTCCTCTTGGCTG 1356
Db 2281 CTCTAATTAATACAATTAATCATGCTCACACTTAATAGTATATATCTATGTCCTCTTGGCTG 2340
QY 1357 TCTATCTTGATCAAGTCATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1416
Db 2341 TCTATCTTGATCAAGTCATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 2400
QY 1417 TGAAGCCTTCATATTTGGTCAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG 1476
Db 2401 TGAAGCCTTCATATTTGGTCAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG 2460
QY 1477 TTAATGGAATATATAGTTTGA 1497
Db 2461 TTAATGGAATATATAGTTTGA 2481

RESULT 13

ABK35707
ID ABK35707 standard; cDNA; 3928 BP.

XX AC ABK35707;

XX 08-MAY-2002 (first entry)

XX cDNA sequence #98 encoding novel human secreted protein.

XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;
XX immune deficiency disorder; blood disorder; inflammatory disorder;
XX infectious disorder; allergic condition; neurodegenerative disorder;
XX liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
XX tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
OS Homo sapiens.

XX WO200177289-A2.

XX 18-OCT-2001.

XX 29-MAR-2001; 2001WO-US010232.

XX 06-APR-2000; 2000US-0195605P.

XX (GEMY) GENETICS INST INC.

XX Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;

XX Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;

XX Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;

XX WPI; 2002-179322/23.

XX Six hundred and twenty three polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for treating
PT immune deficiencies and disorders such as autoimmune disorders.

XX Claim 1; Page 127-128; 393pp; English.

XX PS

CC The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides a
CC method for producing proteins from these polynucleotide sequences. The
CC proteins are useful for identifying compounds that modulate their
CC activity and production. The sequences of the invention are useful for
CC treating diseases such as hyperproliferative disorders (e.g. cancer),
CC immune deficiency disorders (e.g. severe combined immunodeficiency
CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders
CC (e.g. thrombocytopenia), inflammatory disorders (e.g. arthritis),
CC infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma),
CC neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis,
CC coagulation disorders (e.g. haemophilia), and tumours. The polynucleotide
CC sequences of the invention are also useful in gene therapy. ABK35610-
CC ABK36232 represent the cDNA sequences of the invention that encode for
CC novel human secreted proteins

XX Sequence 3928 BP; 1139 A; 681 C; 799 G; 1309 T; 0 U; 0 Other;

SQ Query Match 24.5%; Score 1343; DB 6; Length 3928;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1044 GTATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTT 1103

Db 1 GTATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTT 60

QY 1104 GAAATTTTGTCTACTGTGGCTTTTGGATTTATTGGCCCTTATGATAATCCTCATAGAAAGT 1163

Db 61 GAAATTTTGTCTACTGTGGCTTTTGGATTTATTGGCCCTTATGATAATCCTCATAGAAAGT 120

QY 1164 TTTCCCAATCGTTAGTGTGGCTTTTTCAGTCCCTTCTGTCACTGTACTTTTGTGATTGGT 1223

Db 121 TTTCCCAATCGTTAGTGTGGCTTTTTCAGTCCCTTCTGTCACTGTACTTTTGTGATTGGT 180

QY 1224 ATTGCACAGGTCATGCATTTAGAGATTTTAATGAAGGTGCTTCATTTTCAAAATTGACT 1283

Db 181 ATTGCACAGGTCATGCATTTAGAGATTTTAATGAAGGTGCTTCATTTTCAAAATTGACT 240

QY 1284 GCAGGCCCATATCCTCTAATTATTACAATTTATCATGCTCACACTTAATAGTATATTTCTAT 1343

Db 241 GCAGGCCCATATCCTCTAATTATTACAATTTATCATGCTCACACTTAATAGTATATTTCTAT 300

QY 1344 GTCCTCTTGGCTGTCTATCTTGATCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGATCA 1403

Db 301 GTCCTCTTGGCTGTCTATCTTGATCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGATCA 360

QY 1404 TCTTTATATTTCTGAAGCCTTCATATTGGTCAAGAGCAAAAGAAATTTATGAGGAGTTA 1463

Db 361 TCTTTATATTTCTGAAGCCTTCATATTGGTCAAGAGCAAAAGAAATTTATGAGGAGTTA 420

QY 1464 TCAGAGGGCAATGTTAATGGAAATATTAGTTTTAGTGAAATTTATGAGCCAGTTTCTTCA 1523

Db 421 TCAGAGGGCAATGTTAATGGAAATATTAGTTTTAGTGAAATTTATGAGCCAGTTTCTTCA 480

QY 1524 GAAATTTGTAGAAAAGAAAGCCATAAGAAATTAGTGGTATTTCAGAAACATACAGAAAGAAG 1583

Db 481 GAAATTTGTAGAAAAGAAAGCCATAAGAAATTAGTGGTATTTCAGAAACATACAGAAAGAAG 540

QY 1584 GGTGAAAATGTGAGGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATTACT 1643

Db 541 GGTGAAAATGTGAGGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATTACT 600

QY 1644 GCCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACATTGATGAATATCTTTGTGGACTC 1703

Db 601 GCCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACATTGATGAATATCTTTGTGGACTC 660

QY 1704 TGCCCACTTCTGATGGGTTTGCATCTATATATATGACACAGAGTCTCAGAAATAGATGAA 1763

Db 661 TGCCCACTTCTGATGGGTTTGCATCTATATATATGACACAGAGTCTCAGAAATAGATGAA 720

QY 1764 ATGTTTGAAGCAAGAAAAAATGATTGGCAATTTGTCCACAGTTAGATATACATTTGATGTT 1823

Db 721 ATGTTTGAAGCAAGAAAAATGATTGGCAATTTGTCCACAGTTAGATATACACTTTGTATGTT 780
QY 1824 TTGACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAATCAAGGGATACCAGCCAAAT 1883
Db 781 TTGACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAATCAAGGGATACCAGCCAAAT 840
QY 1884 ATAATACAAGAGTGCAGAAGGTTTACTAGATTAGACATGACACTATCAAGATAAC 1943
Db 841 ATAATACAAGAGTGCAGAAGGTTTACTAGATTAGACATGACACTATCAAGATAAC 900
QY 1944 CAAGCTAAAAAATTAAGTGGTCAAAAAAGAAAGCTGTCTATTAGGAATTTGCTTCTT 2003
Db 901 CAAGCTAAAAAATTAAGTGGTCAAAAAAGAAAGCTGTCTATTAGGAATTTGCTTCTT 960
QY 2004 GGGAAACCCAAAGATACTGCTGTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGA 2063
Db 961 GGGAAACCCAAAGATACTGCTGTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGA 1020
QY 2064 CATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAAATCGGTTGACAGTGTTCAGTACT 2123
Db 1021 CATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAAATCGGTTGACAGTGTTCAGTACT 1080
QY 2124 CATTTATGATGAAGCTGACATTTCTGCAGATAGGAAAGCTGTATATCAACAAGGAATG 2183
Db 1081 CATTTATGATGAAGCTGACATTTCTGCAGATAGGAAAGCTGTATATCAACAAGGAATG 1140
QY 2184 CTGAAATGTTGGTTCTTCAATGTTCTCTCAAAAGTAAATGGGGATCGGCTACCGCTG 2243
Db 1141 CTGAAATGTTGGTTCTTCAATGTTCTCTCAAAAGTAAATGGGGATCGGCTACCGCTG 1200
QY 2244 AGCATGTACATAGACAAATATTGTGCGCACAGAATCTCTTCTTCACTGGTTAAACAACAT 2303
Db 1201 AGCATGTACATAGACAAATATTGTGCGCACAGAATCTCTTCTTCACTGGTTAAACAACAT 1260
QY 2304 ATACCTGGAGCTACTTTATTACAACAGAAATGACCAACAACTTGTATAGCTTGCTTTC 2363
Db 1261 ATACCTGGAGCTACTTTATTACAACAGAAATGACCAACAACTTGTATAGCTTGCTTTC 1320
QY 2364 AAGGACATGGACAAAATTTTCAGG 2386
Db 1321 AAGGACATGGACAAAATTTTCAGG 1343

RESULT 14
ABZ35926
ID ABZ35926 standard; cDNA; 1632 BP.

XX AC ABZ35926;

XX DT 10-FEB-2003 (first entry)

XX DE Human secretory polynucleotide SPTM SEQ ID NO 90.

XX KW Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
multiple sclerosis; Parkinson's disease; cell proliferative disorder;
anti-inflammatory; immunosuppressive; neuroprotective; nootropic;
neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
secretory polynucleotide; secretory protein; gene; ss.

XX OS Homo sapiens.

XX PN WO200283876-A2.

XX PD 24-OCT-2002.

XX PF 27-MAR-2002; 2002WO-US009921.

XX PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX (INCY-) INCYTE GENOMICS INC.
PA Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX WPI; 2003-075543/07.
DR P-PSDB; ABP75479.
XX New human secretory proteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),
PT neurological disorders (e.g. Alzheimer's), or cell proliferations or
PT cancers.
XX Claim 1; SEQ ID NO 90; 458pp + Sequence Listing; English.
PS The invention relates to a secretory polynucleotide (designated sptm)
XX comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a
CC naturally occurring polynucleotide sequence at least 90 % identical to
CC the polynucleotide sequence, a polynucleotide complementary to them or an
CC RNA equivalent of them. The polypeptide or polynucleotide are useful for
CC treating, preventing or diagnosing a disease or condition associated with
CC the expression of functional SPTM. These are particularly useful for
CC diagnosing, treating or preventing autoimmune/inflammatory disorders
CC (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's
CC disease), neurological disorders (e.g. epilepsy, Huntington's disease,
CC dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
CC multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety,
CC schizophrenia or amnesia), or cell proliferative disorders (e.g.
CC psoriasis, polycythemia vera, or cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain,
CC breast, cervix or prostate). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1632 BP; 527 A; 205 C; 301 G; 599 T; 0 U; 0 Other;
Query Match 15.1%; Score 829; DB 7; Length 1632;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 829; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4647 AGATGTATCGGAACAGTACACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAA 4706
Db 218 AGATGTATCGGAACAGTACACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAA 277
QY 4707 ATTAATTTGAAGGACTGGATAGAAAACCTAGAGTAGACCGCTTCAAAGAGAAATTCAG 4766
Db 278 ATTAATTTGAAGGACTGGATAGAAAACCTAGAGTAGACCGCTTCAAAGAGAAATTCAG 337
QY 4767 TATATTTTCCCAATGCAAGCCGTCAGGAAAGTTTTCCTATTTTGGCTTATAAAAT 4826
Db 338 TATATTTTCCCAATGCAAGCCGTCAGGAAAGTTTTCCTATTTTGGCTTATAAAAT 397
QY 4827 CCTAAGGAAGATGTTTCAGTCCCTTTTCAATCTTTTTTAAAGCTGGAAGAACTAAACAT 4886
Db 398 CCTAAGGAAGATGTTTCAGTCCCTTTTCAATCTTTTTTAAAGCTGGAAGAACTAAACAT 457
QY 4887 GCTTTTGGCATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTGTAGAA 4946
Db 458 GCTTTTGGCATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTGTAGAA 517
QY 4947 CTCACATAAGAACCAAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTGG 5006
Db 518 CTCACATAAGAACCAAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTGG 577

Db	1145	AGTGCCTTCTGAATTTGTGATTTAAAGGAATTGTAATAGATAAGTTTATTTTAAAGTTAT	1204
QY	5368	CTTTAAGTTTATGCCATCTTCTTAAATAAGTACGTAATGTTCCTCAATCTAAATAAAAAAACT	5427
Db	1205	CTTTAAGTTTATGCCATCTTCTTAAATAAGTACGTAATGTTCCTCAATCTAAATAAAAAAACT	1264
QY	5428	AAT	5430
Db	1265	AAT	1267

Search completed: April 12, 2004, 11:49:10
Job time : 1309 secs

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OM nucleic - nucleic search, using sw model

Run on: April 11, 2004, 21:18:29 ; Search time 13649 Seconds
(without alignments)
17386.117 Million cell updates/sec

Title: US-10-090-458-4
Perfect score: 5475
Sequence: 1 gcgtccgcgcctcgcacag.....cataaagcaatgtgaaagtt 5475

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
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- 26: em_ro:*
- 27: em_sts:*
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- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	5474	100.0	5475	6	AX537473	AX537473 Sequence
2	5373.2	98.1	6525	6	AX473847	AX473847 Sequence
3	5373.2	98.1	6525	9	AY028897	AY028897 Homo sapi
4	5356.6	97.8	5463	6	AX537470	AX537470 Sequence
5	5135.6	93.8	6369	6	AX329331	AX329331 Sequence
6	5083.2	92.8	5096	9	HSA275973	AJ275973 Homo sapi
7	5014.6	91.6	5262	6	AX417828	AX417828 Sequence
8	4922.6	89.9	4929	6	AX417824	AX417824 Sequence
9	4811.6	87.9	4917	6	AX537472	AX537472 Sequence
10	4759	86.9	4785	6	AX417826	AX417826 Sequence
11	3891	71.1	5347	10	AF491842	AF491842 Mus muscu
12	3879.8	70.9	5170	10	RNO426052	AJ426052 Rattus no
13	3873	70.7	4929	10	AB097675	AB097675 Mus muscu
14	3820.4	69.8	4945	10	RNO550165	AJ550165 Rattus no
15	3812.6	69.6	4078	9	HSM806823	BX640746 Homo sapi
16	3256	59.5	3347	6	AX833036	AX833036 Sequence
17	3256	59.5	3347	9	AK094416	AK094416 Homo sapi
18	3175.8	58.0	3268	6	AX714300	AX714300 Sequence
19	3175.8	58.0	3268	9	AK056533	AK056533 Homo sapi
20	2815.2	51.4	2845	9	HSA512612	AJ512612 Homo sapi
21	2646.4	48.3	3112	9	AB067475	AB067475 Homo sapi
22	2436.2	44.5	5243	9	HSM807592	BX647447 Homo sapi
23	1807.6	33.0	1964	9	AK122803	AK122803 Homo sapi
24	1668.4	30.5	2325	6	AX780218	AX780218 Sequence
25	1560	28.5	1560	9	AK058170	AK058170 Homo sapi
26	1484.4	27.1	4921	10	AK129463	AK129463 Mus muscu
27	1182	21.6	1346	6	AX331591	AX331591 Sequence
28	1182	21.6	1346	6	AX332287	AX332287 Sequence
29	1182	21.6	1346	6	AX410760	AX410760 Sequence
30	1149.8	21.0	6181	6	AX473850	AX473850 Sequence
31	1149.8	21.0	6181	9	AY028900	AY028900 Homo sapi
32	1149.2	21.0	5722	6	AX657703	AX657703 Sequence
33	1149.2	21.0	6333	9	AY247065	AY247065 Homo sapi
34	1126.2	20.6	4875	9	AF423307	AF423307 Homo sapi
35	1121.4	20.5	5981	6	AX473849	AX473849 Sequence
36	1121.4	20.5	5981	9	AY028899	AY028899 Homo sapi
37	1119.8	20.5	4875	6	AX535879	AX535879 Sequence
38	1119.8	20.5	5018	6	AX535877	AX535877 Sequence
39	1090.6	19.9	5296	6	AX473848	AX473848 Sequence
40	1090.6	19.9	5296	9	AY028898	AY028898 Homo sapi
41	1089	19.9	4984	9	AF373290	AF373290 Homo sapi
42	1089	19.9	5211	6	AX575480	AX575480 Sequence
43	1085.8	19.8	4854	6	AX538009	AX538009 Sequence
44	1085.8	19.8	5332	6	AX538007	AX538007 Sequence
45	1084	19.8	5680	6	AX657701	AX657701 Sequence

ALIGNMENTS

RESULT 1
AX537473
LOCUS AX537473 5475 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 4 from Patent WO02070690.
ACCESSION AX537473
VERSION AX537473.1 GI:25269282
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen,H., Kilinski,L. and le Bihan,S.
TITLE Abca5 transporter and uses thereof
JOURNAL Patent: WO 02070690-A 4 12-SEP-2002;

Db	1981	TGTCATTAGGAATTGCTGTTCTTTGGGAACCCAAAGATACTGCTGTCTAGATGAACCAACAG	2040
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Qy	2101	ATCGGGTGACAGTGTTCAGVACTCATTTCATGGATGAAGCTGACATTTCTTGACAGATAGGA	2160
Db	2101	ATCGGGTGACAGTGTTCAGTACTCATTTCATGGATGAAGCTGACATTTCTTGACAGATAGGA	2160
Qy	2161	AAGCTGTGATATCACAAAGGAATGCTGAAATGTTGGTCTTCAATGTTCCCTCAAAAAGTA	2220
Db	2161	AAGCTGTGATATCACAAAGGAATGCTGAAATGTTGGTCTTCAATGTTCCCTCAAAAAGTA	2220
Qy	2221	AATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCCACAGAAATCTC	2280
Db	2221	AATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCCACAGAAATCTC	2280
Qy	2281	TTTCTTCACCTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAATGACCAAC	2340
Db	2281	TTTCTTCACCTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAATGACCAAC	2340
Qy	2341	AACCTGTGTATAGCTTGCCCTTCAAGGACATGGACAAAATTTTCAGGTTTGTCTGCCC	2400
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Qy	2461	ACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATGACCAAGCAGATTAATAGTGTATTTA	2520
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Qy	2521	CTCAGCAGCCACTGGAGGAAGAAATGGATTCAAATCTTTTGATGAAATGGAACAGAGCT	2580
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Qy	2581	TACTTATCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGGAAACAAC	2640
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Qy	2761	ATCACTCTTTTAAAAATGCTGTGGTCCCATCAAACTGTCTGCTCTTCAAAATCTGTCTAA	2820
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Qy	3121	TCCTGAGTACCCCATTTCTTTCAAGAAATTACTGATATAGTTTTTAAAAATTGAGCTGTATT	3180
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Qy	3301	CTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCCCTTATTTTTTATCATTTCTTATT	3360
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Qy	3361	TGATGCTAGGAAGCTTTATTGGCATTTTCATTATGGATTATATTTTTTATCTGTAAGTTCC	3420
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Qy	3481	CTTCTTTTCACTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCATTTATCTATTCTG	3540
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Qy	4141	TTAATATTCTGGTTGGTGATATTCAACCAACTTCAGGCCAGGTATTTTTTAGGAGATTATT	4200
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QY 577 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTCACAG 636
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QY	5137	GAACCAAGACGCACCTTGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGTTGTGTG	5196
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QY	5197	TTTTGCTTTTCTTTAAATAAAACGATGTATATAATTAAAGTGAAGCTGCATGTTTGATTGA	5256
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QY	5257	AGTATATTGAACTATATAGTTTGTATGTCATCTTTTTCACCATTCAGAAACAGTCTTCT	5316
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QY	5317	GAATTTGTGATTTAAAGGAATTGTAATAGAATAGTTTTTAAAGTTATCTTTAAGTT	5376
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RESULT 3	AY028897	6525.bp	mRNA	linear	PRI 01-DEC-2001
LOCUS	Homo sapiens ATP-binding cassette A5 mRNA, complete cds.				
DEFINITION	AY028897				
ACCESSION	AY028897.1				
VERSION	GI:17223619				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 6525)				
AUTHORS	Schröml,L.M., Arnould,I., Prades,C., Lachtermacher-Rocha,M., Schneider,T., Maintoux,C., Lemoine,C., Debono,D., Devaud,C., Naudin,L., Bauche,S., Annat,M., Alikmets,R., Deneffe,P., Rosier,M. and Dean,M.				
TITLE	Identification and characterization of a cluster of five new ATP-binding cassette transporter genes on human chromosome 17q24: a novel sub-group within the ABCA sub-family				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 6525)				
AUTHORS	Schröml,L.M., Arnould,I., Prades,C., Lachtermacher-Rocha,M., Schneider,T., Maintoux,C., Lemoine,C., Debono,D., Devaud,C., Naudin,L., Bauche,S., Annat,M., Alikmets,R., Deneffe,P., Rosier,M. and Dean,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-MAR-2001) Evry Genomics Center, Aventis Pharma, 2 Rue Gaston Cremieux, Evry 91057, France				
FEATURES	Location/Qualifiers				
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ORIGIN

Query Match		98.1%	Score 5373.2;	DB 9;	Length 6525;
Best Local Similarity		99.9%;	Pred. No. 0;		
Matches 5375;		Conservative	0;	Mismatches	4;
		Indels		0;	Gaps
		0;			
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QY	157	GAACACTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAAAGAGTAGTGTTCAGG	216		
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SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	1		
AUTHORS	Chen,H., Kilinski,L. and le Bihan,S.		
TITLE	Abca5 transporter and uses thereof		
JOURNAL	Patent: WO 02070690-A 1 12-SEP-2002;		
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Best Local Similarity 99.0%; Pred.No. 0;			
Matches 5440; Conservative 0; Mismatches 4; Indels 50; Gaps 3;			
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Db	1	GCGTCCGCGCCCTCGCACAGATCCNAGCTGGTCACCCGCACTGAGTCAACAGACTCGAGC	60
QY	61	GCGTCCAGGCCTGACAGCTCTGCGGCTCGGGCCCTGAGGTTTATTTCAGAAAACATGTCCA	120

Db	61	GCGTCCAGGCCTGACAGCTCTGCGGCTCGGGCCCTGAGGTTTATTTCAGAAAACATGTCCA	120
QY	121	CTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTTACTGAAGAATTACT	180
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QY	361	CAGTGACTAATATTAACAAGCAGCATCATGCGAGAAAAGTGTCTACTGATCATCTACCTGATG	420
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
-AUTHORS Yue,H., Thornton,M., Ramkumar,J., Tang,Y.T., Azimzai,Y.,
Baughn,M.R., Yang,J., Yao,M.G., Lal,P., Wallia,N.K., Gandhi,A.R.,
Hafalia,A.J., Nguyen,D.B., Patterson,C., Elliott,V.S.,
Tribouley,C.M., Lu,D.A., Xu,Y., Reddy,R., Hernandez,R.,
Borowsky,M.L., Lo,T.P., Lu,Y., Policky,J.L., Greene,B.D.,
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Ding,L., Das,D., Kallilick,D.A., Khan,F.A. and Seilhamer,J.J.
JOURNAL Patent: WO 0212340-A 33 14-FEB-2002;
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RESULT 6
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DEFINITION Homo sapiens mRNA for ATP-binding cassette protein of the ABCA subfamily).
ACCESSION AJ275973
VERSION AJ275973.3 GI:22080663
KEYWORDS ABCA subfamily; ATP-binding cassette protein.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petry, F., Kotthaus, A. and Hirsch-Ernst, K.I.
TITLE Molecular cloning and tissue distribution of a novel ATP-binding cassette (ABC) transporter belonging to the subfamily ABCA unpublished
JOURNAL
REFERENCE 2
AUTHORS Hirsch-Ernst, K.I.
TITLE Direct Submission
JOURNAL Submitted (02-MAR-2000) Hirsch-Ernst K.I., Department of Toxicology, University of Goettingen, Robert-Koch-Strasse 40, Lowery Saxony, D-37075, GERMANY revised by [3]
REFERENCE 3 (bases 1 to 5096)
AUTHORS Hirsch-Ernst, K.I.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2001) Hirsch-Ernst K.I., Department of Toxicology, University of Goettingen, Robert-Koch-Strasse 40, Lowery Saxony, D-37075, GERMANY
COMMENT On Aug 1, 2002 this sequence version replaced gi:17046099.
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ORIGIN

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LOCUS AX417828 5262 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 5 from Patent WO231147.
ACCESSION AX417828

VERSION AX417828.1 GI:21522944
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hu, Y. and Nepomnichy, B.
TITLE Human transporter proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0231147-A 5 18-APR-2002;
LEXICON GENETICS INC (US)
FEATURES Location/Qualifiers
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 5014; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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Db 298 GAACACTTCTACTGAAGAATTACTTAATTAATGAGAAACCAAAAGAGTAGTGTTCAGG 357
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Db	1078	TTCTTATGTCCCTTCTTATGGCAGTCAATTGGCAGACAGCTTCTTTTGGTTATTTCCCTCAAAGTA	1137
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Db	1498	TCTATCTTGATCAAGTCAATCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC	1557
QY	1417	TGAAGCCTTTCATATTGGTCAAAGAGCAAAGAAATATAGGAGGTATCAGAGGGCAATG	1476
Db	1558	TGAAGCCTTTCATATTGGTCAAAGAGCAAAGAAATATAGGAGGTATCAGAGGGCAATG	1617
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QY	1537	AAGAAGCCATAAGAAATAGTGGTATTTCAGAAGACATACAGAAGAAGGGTGAAATGTGG	1596
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Db	1858	ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAA	1917
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Db	1978	AAAAATTTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCAAATATAATACAAAG	2037
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Db	2038	TGCAGAAGGTTTTACTAGATTTTAGACATGCAGACTATCAAGAGATAACCAAGCTAAAAAAT	2097

QY	1957	TAAGTGGTGGTCAAAAAAGAAAGCTGTCTATTAGGAATTGCTGTTCTTGGGAACCCAAAAGA	2016
Db	2098	TAAGTGGTGGTCAAAAAAGAAAGCTGTCTATTAGGAATTGCTGTTCTTGGGAACCCAAAAGA	2157
QY	2017	TACTGCTGTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA	2076
Db	2158	TACTGCTGTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA	2217
QY	2077	ATCTTTTAAAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG	2136
Db	2218	ATCTTTTAAAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG	2277
QY	2137	AAGCTGACATTTCTTGACATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTG	2196
Db	2278	AAGCTGACATTTCTTGACATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTTG	2337
QY	2197	GTTCTTCAATGTTTCTCAAAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAG	2256
Db	2338	GTTCTTCAATGTTTCTCAAAAAGTAAATGGGGGATCGGCTACCGCCTGAGCATGTACATAG	2397
QY	2257	ACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTA	2316
Db	2398	ACAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTA	2457
QY	2317	CTTTATTACAACAGAAATGACCAACAACCTTGTGTATAGCTTGCCCTTCAAGGACATGGACA	2376
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QY	2437	GTGTTTCCATGACGACTTTTGGGAAGACGTAATTTTAAAGCTAGAAGTTGAAAGCAGAAATTG	2496
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QY	2557	CTTTTGATGAAATGGAAACAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGA	2616
Db	2698	CTTTTGATGAAATGGAAACAGAGCTTACTTATTTCTGAAACCAAGGCTKCTCTAGTGA	2757
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Db	2758	GCACCATGAGCCTTTGGAAAAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCT	2817
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Db	4198	CAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA	4257
QY	4117	ATGGTGTCTGGCAAAAGCACAAATTATTATATTTCTGGTTGGTGATATTGAACCAACTTCAG	4176

Db	4258	ATGGTGTCTGGCAAAAGCACAATATATTAAATTTCTGGTTGGTGATATTGAAACCAACTTCAG	4311
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QY	4537	TTCGAACTGCAATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATATGGAGG	4596
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RESULT 8				
AX417824				
LOCUS	AX417824	4929 bp	DNA	linear
DEFINITION	Sequence 1	from Patent WO0231147.		
ACCESSION	AX417824			
VERSION	AX417824.1	GI:21522942		

KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1	
AUTHORS	Hu, Y. and Nepomnichy, B.	
TITLE	Human transporter proteins and polynucleotides encoding the same	
JOURNAL	Patent: WO 0231147-A 1 18-APR-2002;	
FEATURES	LEXICON GENETICS INC (US)	
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Best Local Similarity	99.9%;	Pred. No. 0;
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Db	61	AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCCTTTCCACTA 120
QY	234	TTTTTTTATTTGGTTAATAATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 293
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VERSION AX537472.1 GI:25269279
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Chen, H., Kilinski, L. and le Bihan, S.
TITLE Abca5 transporter and uses thereof
JOURNAL Patent: WO 02070690-A 3 12-SEP-2002;
FEATURES Active Pass Pharmaceuticals, Inc. (CA)
source Location/Qualifiers
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ORIGIN

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RESULT 10
AX417826
LOCUS AX417826 4785 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 3 from Patent WO0231147.
ACCESSION AX417826
VERSION AX417826.1 GI:21522943
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Hu, Y. and Nepomnichy, B.
TITLE Human transporter proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0231147-A 3 18-APR-2002;
LEXICON GENETICS INC (US)

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	/mol_type="unassigned DNA"				
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ORIGIN					
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Best Local Similarity	99.8%;	Pred. No. 0;			
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Db	1	ATGTCACCTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACAC	TTCTTCTACTGAAG	60	
QY	174	AATTACTTTAATTAAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAAATTC	TTTTTCCACTA	233	
Db	61	AATTACTTTAATTAAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAAATTC	TTTTTCCACTA	120	
QY	234	TTTTTTTTTATTTTGGTTAATTAATTAATAGCATGATGTCATCCAAATAAGAAATATGAAGAA	293		
Db	121	TTTTTTTTTATTTTGGTTAATTAATTAATAGCATGATGTCATCCAAATAAGAAATATGAAGAA	180		
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Db	181	GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTGGGA	240		
QY	354	TATACTCCAGTGACTAATATTACAAGCAGCATCATCGAGAAAAGTGTCTACTGATCATCTA	413		
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Db	301	CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC	360		
QY	474	TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTC	CAAAGACTCCATGTCCTATGAACTTCGT	533	
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QY	1314	ATCATGCTCACAC	TTAATAGTATATTCTATGT	CTCCTCTTGGCTGTCTATCTTTGATCAAGTC 1373
Db	1201	ATCATGCTCACAC	TTAATAGTATATTCTATGT	CTCCTCTTGGCTGTCTATCTTTGATCAAGTC 1260
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QY	1434	TCAAAGAGCAAAA	AGAAATTTATGAGGAGTTAT	TCAGAGGGCAATGTTAATGGAAATATTAGT 1493
Db	1321	TCAAAGAGCAAAA	AGAAATTTATGAGGAGTTAT	TCAGAGGGCAATGTTAATGGAAATATTAGT 1380
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QY	1914	GATTTAGACAT	GCAGACTATCAAAGATAAC	CAAGCTAAAAATTAAGTGGTGGTCAAAAA 1973
Db	1801	GATTTAGACAT	GCAGACTATCAAAGATAAC	CAAGCTAAAAATTAAGTGGTGGTCAAAAA 1860
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QY	2094	AAAGCCAAAT	CGGGTGACAGTGTTCAGT	ACTCATTTTCATGGATGAAGCTGACATTTCTTGCA 2153
Db	1981	AAAGCCAAAT	CGGGTGACAGTGTTCAGT	ACTCATTTTCATGGATGAAGCTGACATTTCTTGCA 2040

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QY	2274	GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTAACAAGAAT	2333
Db	2161	GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTAACAAGAAT	2220
QY	2334	GACCAACAACCTTGCTGATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAAGTTTGT	2393
Db	2221	GACCAACAACCTTGCTGATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAAGTTTGT	2280
QY	2394	TCTGCCCTAGACAGTCATTCAAATTTGGGTGTCATTTCTTATGGTGTTCATGACGACT	2453
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QY	2754	TTGGTTTCATCCTCTTTTAAATATGCTGTGGTTCCTCCATCAAACTGTTCCAGACTTATAT	2813
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QY	3054	CCTATATTAGTGAATATCATTAAGTAACTACTATCTTTTATCATTTAAATGTGACTGAAACC	3113
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QY	3114	ATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTAAGTAAATGTTTAAATTTAG	3173
Db	3001	ATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTAAGTAAATGTTTAAATTTAG	3060
QY	3174	CTGTATTTTCAAGCAGCTTTGCTTGGATCATGTTTACTGCAATGCCACCTTACTTTGCC	3233
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QY	3654	GGTTGCCCTGATTTCTTTCATAAAGATTTCTTGGAAAGAAATGTACGAAAATAATGTGGACACC	3713
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QY	3714	TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTTATATCGCCTTACCTGCAGTGTGTA	3773
Db	3601	TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTTATATCGCCTTACCTGCAGTGTGTA	3660
QY	3774	TGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGAT	3833
Db	3661	TGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGAT	3720
QY	3834	CCCTTTTTCAGAAAACCTTTCAACGAAAGTCTPAAAAATAGGAAGCTTCCAGAACCCAGAC	3893
Db	3721	CCCTTTTTCAGAAAACCTTTCAACGAAAGTCTPAAAAATAGGAAGCTTCCAGAACCCAGAC	3780
QY	3894	AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGT	3953
Db	3781	AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGT	3840
QY	3954	TGCCAGTGTGTGAGGAGAAACCATCCATTTATGTTGTCAGCAATTTGCATAAAGAAATATGAT	4013
Db	3841	TGCCAGTGTGTGAGGAGAAACCATCCATTTATGTTGTCAGCAATTTGCATAAAGAAATATGAT	3900
QY	4014	GACAAGAAAAGATTTTCTTTTCAAGAAAAGTAAAGAAAAGTGGCACTAAATACATCTCT	4073
Db	3901	GACAAGAAAAGATTTTCTTTTCAAGAAAAGTAAAGAAAAGTGGCACTAAATACATCTCT	3960
QY	4074	TTCTGTGTGAAAAAGGAGAGATCTTTAGGACTATTGGGTCCAAATGCTGGCAAAAGC	4133
Db	3961	TTCTGTGTGAAAAAGGAGAGATCTTTAGGACTATTGGGTCCAAATGCTGGCAAAAGC	4020
QY	4134	ACAATTATTAATTTCTGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTATAGGA	4193
Db	4021	ACAATTATTAATTTCTGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTATAGGA	4080
QY	4194	GATTATTTCTTCAGAGACAAGTGAAGATGATTCACCTGAAGTGTATGGGTACTGTCTCT	4253
Db	4081	GATTATTTCTTCAGAGACAAGTGAAGATGATTCACCTGAAGTGTATGGGTACTGTCTCT	4140
QY	4254	CAGATAAACCCCTTTGTGGCCAGATACATTCAGGAGAACATTTTGAATTTATGGAGCT	4313
Db	4141	CAGATAAACCCCTTTGTGGCCAGATACATTCAGGAGAACATTTTGAATTTATGGAGCT	4200
QY	4314	GTCAAAGGAATGAGTGCAAGTGACATGAAAGAAAGTCAATAAGTCAATAACACATGCACCTT	4373

Db	4201	GTCAAAGGAATGAGTGAAGTACATGAAAGAGTCAATAAGTCGAATAACACATGCAC	4260
Qy	4374	GATTTAAAGAAACATCTTCAGAAGACTGTAAAGAACTACCTGCAGGAATCAAACGAAAG	4433
Db	4261	GATTTAAAGAAACATCTTCAGAAGACTGTAAAGAACTACCTGCAGGAATCAAACGAAAG	4320
Qy	4434	TTGTGTTTTTGTCTAAAGTATGCTAGGGAATCCTCAGATTACTTTTGTAGATGAACCATCT	4493
Db	4321	TTGTGTTTTTGTCTAAAGTATGCTAGGGAATCCTCAGATTACTTTTGTAGATGAACCATCT	4380
Qy	4494	ACAGGTATGGATCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAAA	4553
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Qy	4554	AACAGAAAGCGGGTGTCTATTCTGACCACTCACTATATGGAGGAGGCAGGCTGTCTGT	4613
Db	4441	AACAGAAAGCGGGTGTCTATTCTGACCACTCACTATATGGAGGAGGCAGGCTGTCTGT	4500
Qy	4614	GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA	4673
Db	4501	GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA	4560
Qy	4674	AAGAGTAAATTTGGAAAAAGGCTACTTTTGGAAATTAATTAAGGACTGGATAGAAAAAC	4733
Db	4561	AAGAGTAAATTTGGAAAAAGGCTACTTTTGGAAATTAATTAAGGACTGGATAGAAAAAC	4620
Qy	4734	CTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCA	4793
Db	4621	CTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCA	4680
Qy	4794	GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA	4853
Db	4681	GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA	4740
Qy	4854	CAATCTTTTTTTAAAGCTGGAAGAAGCT	4880
Db	4741	CAATCTTTTTTTAAAGCTGGAAGAAGGT	4767

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RESULT 11
AF491842
LOCUS      5347 bp      mRNA      linear      ROD 25-FEB-2003
DEFINITION Mus musculus ATP-binding cassette transporter sub-family A member 5
            (Abca5) mRNA, complete cds.
ACCESSION  AF491842
VERSION     AF491842.1  GI:22087247
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 5347)
            Annillo, T., Chen, Z.Q., Shulenin, S. and Dean, M.
            Evolutionary analysis of a cluster of ATP-binding cassette (ABC)
            genes
            Mamm. Genome 14 (1), 7-20 (2003)
            22419899
            PUBMED 12532264
REFERENCE   2 (bases 1 to 5347)
            Annillo, T., Chen, Z.-Q., Shulenin, S. and Dean, M.
            Direct Submission
            Submitted (12-MAR-2002) Laboratory of Genomic Diversity, National
            Cancer Institute, Frederick, MD 21702, USA
FEATURES             Location/Qualifiers
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         /strain="BALB/c"
         /db_xref="taxon:10090"
     1..5347
         /gene="Abca5"
     210..5138
         CDS

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ORIGIN

	Query Match	71.1%;	Score 3891;	DB 10;	Length 5347;
	Best Local Similarity	85.1%;	Pred. No. 0;		
	Matches 4379;	Conservative	0;	Mismatches 740;	Indels 24; Gaps 2;
QY	107	AGAAACATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACAGACCAGAACACATTCT	166		
DB	203	AGAAACATGGCTACTGCAATTAGGGATGTGGAGTTTGGAGACAGACAGACCAGAACACATTCT	262		
QY	167	ACTGAAGAATTACTTAATTAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAATTCCTTT	226		
DB	263	ACTGAAAAATTACCTAATTAATGCAGGACTAAAAAAAAGTAGTGTTCAGGAATTCCTTT	322		
QY	227	TCCACTATTTTTTTTATTTTGGTTAATATTAATTAGCATGATGCATCCAAATAAAGAAATA	286		
DB	323	TCCTCTATTTTCTTATTTTGGCTGATATTAGTTAGCATGATGCATCCAAATAAAGAAATA	382		
QY	287	TGAAGAGTGCCTAAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAATCTAAT	346		
DB	383	TGAAGAGGTATCTGATATAGAGCTCAGCCCTATGGACAAATTTCAGCCTTTTCCAACGTTAT	442		
QY	347	TCCTTGGATATACTCCAGTGACTAATATTAACAAGCAGCATCATGCAGAAAAGTGCTACTGA	406		
DB	443	TCCTTGGATACACTCCCGTGACTAACATTACAAGCAGCATTATGCAGAGGGTTTCTACCGA	502		
QY	407	TCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATC	466		
DB	503	TCATCTTCCCAAGGTTATAGTTACTGAAGAATACGCAAAATGAGAAAGAACTGGTAGCCGC	562		
QY	467	CAGTCTCTAAAGCCGAGCAACTTTGTAGGTGTGGTTTTTCAAAGACTCCATGTCTCTATGA	526		
DB	563	AAGTCTTTCTAAGTCCAGCAACTTCGTAGGTGTGGTTTTTCAAAGACACACCATGTCTCTATGA	622		
QY	527	ACTTCGTTTTTTTTTCTGATATGATTCAGTATCTTCTATTTTATATGGATTCAGAGCTGG	586		
DB	623	ACTTCGTTTTTTTTTCTGAAATGATTCAGTGTCTTCTATTTTATATGAATTCAGAGAAAGG	682		

QY 587 CTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTTACAAGC 646
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QY 647 ATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTTGGGAAGGAGCTGGA 706
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Db 1103 GATCTTTCTACTGGTCTTCTTATATGGATTGTCTATCTGTGTTTTTGTACCGTGGTGT 1162
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Db 4463 AGCCCTTGATTTGAAAGAAACATCTTCAGAAAGACTGTAAAAGAAAGCTACCTGCAGGGATCAA 4522

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Db 5003 CAGCTTTTCTCAAGCAACCCCTGGAAACAGGTTTTTTGTAGAACTTACTAAAGAGCAAGAGGA 5062

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LOCUS RNO426052 5170 bp mRNA linear ROD 08-JAN-2003
DEFINITION Rattus norvegicus mRNA for Abca5 protein.
ACCESSION AJ426052
VERSION AJ426052.2 GI:27368658
KEYWORDS abca5 gene; ATP-binding cassette protein.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Petry,F., Kotthaus,A. and Hirsch-Ernst,K.I.
TITLE Cloning of human and rat ABCA5/Abca5 and detection of a human
splice variant
JOURNAL Biochem. Biophys. Res. Commun. 300 (2), 343-350 (2003)
MEDLINE 22392638
PUBMED 12504089
REFERENCE 2 (bases 1 to 5170)
AUTHORS Petry,F.
TITLE Direct Submission
JOURNAL Submitted (19-DEC-2001) Petry F., Department of Toxicology,
Georg-August-University Goettingen, Robert-Koch-Strasse 40, Lower
Saxony, D-37075 Goettingen, GERMANY
REMARK revised by author [27-AUG-2002]
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ORIGIN

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RESULT 13

AB097675

LOCUS

DEFINITION

Mus musculus abca5 mRNA for ABC transporter subfamily A mABCA5, complete cds.

AB097675

AB097675.1 GI:29420876

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Kubo,Y., Satsuma,Y., Sekiya,S., Nada,S. and Yamaguchi,A.

Molecular cloning of mABCA5, the mouse homologue of ABCA5

Unpublished

2 (bases 1 to 4929)

Kubo,Y., Satsuma,Y., Sekiya,S., Nada,S. and Yamaguchi,A.

Direct Submission

Submitted (06-DEC-2002) Yoshiyuki Kubo, I.S.I.R., Osaka Univ.; Mihogaoxa 8-1, Ibaraki City, Osaka 567-0047, Japan

(E-mail:kubo37@sanken.osaka-u.ac.jp, Tel:81-06-6879-8546, Fax:81-06-6879-8549)

FEATURES

source

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gene

CDS

ORIGIN

Query Match 70.7%; Score 3873; DB 10; Length 4929;

Best Local Similarity 86.6%; Pred. No. 0;

Matches 4269; Conservative 0; Mismatches 660; Indels 0; Gaps 0;

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Db 1 ATGGCTACTGCAATTAGGGATGTGGGAGTTTGGAGACAGACCAGAACACATTCTACTGAAA 60

QY 174 AATTACTTAATAAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCACTA 233

Db 61 AATTACCTAATAAATGCAGGACTAAAAAAGTAGTGTTCAGGAAATTCCTTTTCTCTA 120

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RESULT 14
RNO550165
LOCUS
DEFINITION RNO550165 4945 bp mRNA linear ROD 24-MAR-2003
Rattus norvegicus mRNA for ATP-binding cassette protein 5 (Abca5 gene), splice variant V+16.
ACCESSION AJ550165
VERSION AJ550165.1 GI:29170395
KEYWORDS Abca5 gene; alternative splicing; ATP-binding cassette protein 5.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Petry, F. and Hirsch-Ernst, K.I.
TITLE Identification of novel highly conserved splice variants of rat Abca5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4945)
AUTHORS Petry, F.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-2003) Petry F., Toxicology, University of Goettingen, Robert-Koch-Strasse 40, Goettingen, Lower Saxony,

D-37075, GERMANY	
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ORIGIN	
Query Match 69.8%; Score 3820.4; DB 10; Length 4945;	
Best Local Similarity 86.0%; Pred. No. 0;	
Matches 4252; Conservative 0; Mismatches 676; Indels 16; Gaps 1;	
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Db	2 AGAAAACATGGCTACTGCAATTAGGGATGTGGCGGTTTGGAGACAGACCAGAACACTTCT 61
Qy	167 ACTGAAGAATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAATTCCTTT 226
Db	62 TCTGAAGAATTACCTCGTCAAATGCAGGACTAAAAGAGTAGTGTTCAGGAATTCCTTT 121
Qy	227 TCCACTATTTTTTTATTTTGGTTAATTAATTAGCATGATGCATCCAAATAAGAAATA 286
Db	122 TCCTCTATTTTCTTATTTTGGCTGATATTAATTAGCATGATGCATCCAAATAAGAAATA 181
Qy	287 TGAAGAAGTGCCTAAATATAGAACTCAATCCTATGGACAAGTTTACTCTTCTTAATCTAAT 346
Db	182 TGAAGAAGTATCTGATATAGAACTCAGCCCTATGGACAATCCATCCTTCCAACTTAT 241
Qy	347 TCTTGGATATACCTCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGCTACTGA 406
Db	242 CCTGGGTACACTCCAGTGACTAATACTACAAGCAGCGTCATGCAGAGAGTTTCTACCGA 301
Qy	407 TCATCTACCTGATGTCATAATTACTGAAGATATACAAATGAAAAGAAATGTTAACATC 466
Db	302 TCATCTCCCGACGTTCTAGTTACTGAAGATACGCCAGTGAAGAGGAGCTGTGGCATC 361
Qy	467 CAGTCTCTTAAGCCGAGCAACTTTGTAGGTGGTGTGTTTCAAAGACTCCATGTCCCTATGA 526
Db	362 CAGTTTGTCTAAGCCCGAGCAACTTCGTGGGTGGTGTGTTTCAAAGACGTCATGTCCCTATGA 421
Qy	527 ACTTCGTTTTTTTTCCTGATATGATTCAGTATCTTCTATTTATATGGATTCAGAGCTGG 586
Db	422 ACTGCGGTTTTTTTTCCTGATATGGTTCAGTGTCTTCTGTTTATATGGATTCAGAGCAGG 481

Qy	587	CTGTTCAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAGTTTACAGTTCACAAGC 646
Db	482	CTGTTCAAAGTCATGTGATGCTGCTCAGTACTGGTCTTCAGGGTTTACAGCTTTACAGGC 541
Qy	647	ATCCATAGATGCTGCCATTATATACAGTTGAAGACCAATGTTTCTCTTTTGGAGGAGCTGGA 706
Db	542	CTCAATAGATGCTGCCATTATATACAGTTGAAGACCAATGTTTCTCTGTGGAGGAGCTGGA 601
Qy	707	GTCAACTAAAGCTGTTATTATGGGAGAAAACACTGCTGTTGTAGAAATAGATACCTTTCCCG 766
Db	602	GTCAACCAAGCTGTCATCATGGGGAAGCTGCGGTGCTGAGATTGACACCTTCCCACG 661
Qy	767	AGGAGTAATTTTAATATACCTAGTTATAGCATTTTCACTTTTGGATACCTTTTGGCAAT 826
Db	662	AGGGTCACTCCTCATCTACCTGTCATAGCCTTCTCGCCCTCGGGTACTTTCTGGCAAT 721
Qy	827	TCATATCGTAGCAGAAAAGAAAATAAAAGAAATTTTAAAGATAATGGGACTTCA 886
Db	722	TCACATTGTAGCAGAAAAGAAAAGAGGTTAAAGGAGTTTAAAGATAATGGGACTTCA 781
Qy	887	TGATACCTGCTTTTGGCTTCTCTGGGTTCTTCTATATACAAGTTTAAATTTTCTTATGTC 946
Db	782	CGACACTGCTTTTGGCTGCTCTGGGTTCTTCTGTACACGAGTTTGATCTTCTTATGTC 841
Qy	947	CCTTCTTATGGCAGTCATTGGCAGACTTCTTGTGTTATTTCTCTCAAAGTAGCAGCATGT 1006
Db	842	CCTTCTTATGGCCGTCATTGCAACAGCGTCTCGTTATTTCCCTCAGAGTAGCAGCATCGT 901
Qy	1007	GATATTTCTGCTTTTTTCTTTATGGATTATCATCTGATTTTTTGTCTTAAATGCTGAC 1066
Db	902	GATTTTCTGCTCTTCTTCTGTFACGGATTGTCACTGTGTTTTTGTCTTAAATGTTGAC 961
Qy	1067	ACCTCTTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTGTACTGTGGCTTT 1126
Db	962	GCCTCTTTTAAAAAATCAAAAGCAGTGGGAGTCGTTGAGTTTTTGTACCCGTGGTGT 1021
Qy	1127	TGGATTTATTTGGCCTTATGATAATCCTCATAGAAAGTTTTCCCAAATCGTTAGTGGCT 1186
Db	1022	TGGCTTTGTGGCCTGTTGATAGTCCTCGTAGAAAGTTTCCCCAGGTGCTAGTGGCT 1081
Qy	1187	TTTCAGTCTCTTCTGTCACTGACCTTTTGTGATTTGTTATGACACAGGTGATGCAATTTAGA 1246
Db	1082	CTTCAGTCTCTTGTGTGAGTGGCCTTTCTGATTTGGGATTTGACAGGTGATGCAATTTAGA 1141
Qy	1247	AGATTTTAATGAAGGTGCTTCAATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATAT 1306
Db	1142	AGATTTCAATGAAGGAGCCTTATTTTCTAGTTTGAAGGCCCCCTACCCGCTAATAT 1201
Qy	1307	TACATTTATCATGCTCACACTTAATAGTATATTTCTATGCTCTTGGCTGTCTATCTTGA 1366
Db	1202	CACCTTACCATGCTCGTCTGACAGTGTGTTCTATGCTCTGCTGCTGTGTACCTTGA 1261
Qy	1367	TCAAGTCATTTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTC 1426
Db	1262	TCAGGTCAATCCAGGGGAATTTGGCTTGAAGGAGTTCATCTTTGACTTCTTAAAGCATC 1321
Qy	1427	ATATTGTCAAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGA 1486
Db	1322	ATATTGTCAAAAAACAAAAGAACTATAAGGAGCTATCAGAGGGCAACATCAATGGA 1381
Qy	1487	TATTAGTTTGTAGTGAAATTTATGAGCCAGTTTCTTTCAGAAATTTGTAGGAAAAGAGCCAT 1546
Db	1382	TATTAGTCTCAATGAAATTTGTGAGCCCGTTTTCTTCAGAAATTTATAGGAAAAGAGCTAT 1441
Qy	1547	AAGAAATTAGTGGTATTCAGAAAGACATACAGAAAGAGGTGAAATGTGGAGGCTTTGAG 1606
Db	1442	AAGAAATAAGTGGTATTCAGAAAGCCCTATAGGAAGAAAGATGAGACCGTGGAGGCTTTGAG 1501
Qy	1607	AAATTTGTCATTTGACATATATGAGGTCAGATTACTGCTTACTTGGCCACAGTGGAAAC 1666
Db	1502	AAATTTGTCGTTTGACATCTATGAAGGCCAGATTACTGCTCTGTGGGCCACAGTGGAAAC 1561
Qy	1667	AGGAAAGAGTACATTGATGAATATTTCTTTGTGGACTCTGCCACCTTCTGTATGGGTTTGC 1726

Db 1562 AGGAAAAGCACACTAATGAATATCTGTGGACTGTGCCACCTTCTGATGGGTTGC 1621
Qy 1727 ATCTATATATGGACACAGAGTCTCAGAAAATAGATGAAATGTTTGAAGCAAGAAAATGAT 1785
Db 1622 TTCTATATATGGACACAGAGTCTCTGAAATAGATGAAATGTTTGAAGCGGAAATGAT 1681
Qy 1787 TGSCATTTGTCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAGAAAATTTATC 1845
Db 1682 TGGCATATGTCCACAGTCAGATATGAACCTTTGATGTTCTGACAGTAGAAGAAAATTTATC 1741
Qy 1847 AATTTTGGCTTCAATCAAAAGGGATACCAGCCAAACAATATAATACAAGAGTGCAGAAGGT 1906
Db 1742 AATTTTGGCTTCAGTCAAAAGGAATACCAGCCAAACAACATAAATTCAGGAAGTACAGAAAAT 1801
Qy 1907 TTACTAGATTTAGACATGACAGACTATCAAGAGATAACCAAGCTAAAAAATAAGTGGTGG 1956
Db 1802 TTTACTGGATTTGGACATGCAAGCCATCAAAGATAATCAAGCGAAAATAAAGTGGTGG 1861
Qy 1967 TCAAAAAAGAAAGCTGTCTATTAGGAATTGCTGTTCTTGGGAACCCAAAGACTACTGCTGCT 2026
Db 1862 CCAAAAGAGAAAGCTGCTTTAGGAATTGCAGTTCTTGGGAATCCAAAGATCCTCCTGCT 1921
Qy 2027 AGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTTGATGGAATCTTTTAAA 2086
Db 1922 AGATGAGCCGACAGCAGGAATGGACCCCTGCTCTCGCCACATGTTTGGAAATCTTCTCAA 1981
Qy 2087 ATACAGAAAAGCCAAATCGGCTGACAGTGTTCAGTACTCATTTCAATGGATGAAGCTGACAT 2146
Db 1982 GTACAGGAAGGCTAACCCGAGTGACAGTCTTCAGCACTCACTTCATGGATGAGGCCGACAT 2041
Qy 2147 TCTTGCAGATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTGGTCTTTCAAT 2206
Db 2042 TCTTGCAGACAGGAAAGCTGTCTATATCACAAGGAATGCTGAAATGTGTGGTCTTTCAAT 2101
Qy 2207 GTTCTCTCAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTG 2266
Db 2102 TTTCTCTGAAAAGTAAATGGGGAATCGGCTACCGCTGAGCATGTATATAGACAGGTACTG 2161
Qy 2267 TGCCACAGAAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACA 2326
Db 2162 TGCCACAGAGTCGCTCTCGTCGCTGGTTAGACAGACATCCCTGCGGCCGCTCTGCTGCA 2221
Qy 2327 ACAGAAATGACCAACAACTGTGTATAGCTTGCCCTTCAAGGACATGGACAAAATTTTCAGG 2386
Db 2222 GCAGAAATGACCAGCAGATGTCTATAGCTTGCCCTTCAAAGACATGGACAAAATTTTCAGG 2281
Qy 2387 TTTGTTTCTGCCCCTAGACAGTCAATTCAAATTTGGGTGTCAATTTCTTATGGTGTTCAT 2446
Db 2282 CTTGTTTCTGCTCTAGACATTCATTCAAACCTGGGTGTAATTTCTTATGGTGTTCAT 2341
Qy 2447 GACGACTTTGGAAGACGTATTTTAAAGCTAGAAAGTGAAGCAGAAAATGACCAAGCAGA 2506
Db 2342 GACGACATTTGGAAGACGTGTTTAAAGCTAGAAAGTGAAGCAGAAAATGACCAAGCAGA 2401
Qy 2507 TTATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAAATGGATTCAAAATCTTTTGATGA 2566
Db 2402 TTATAGTGTATTTACCCAGCAGCCACGGAGGAAGAAAACAGATTCAAAAGTCTTTTGATGA 2461
Qy 2567 AATGGAACAGAGCTTACTTATCTTTCTGAAAACCAAGGCTTCTCTAGTGAGCACCATGAG 2626
Db 2462 AATGGAACAGAGTTTACTTATCTCTCTGAAAACCAAGCTTCTCTAGTGAGCACCATGAG 2521
Qy 2627 CCTTTGGAAAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGTGA 2686
Db 2522 TCTCTGGAAGCAGCAAGTATCTACAATAGCAAAAGTTTCATTTCTCTCACTGAAGCGAGA 2581
Qy 2687 AAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTT 2746
Db 2582 AAGCAAAATCAGTGCCTCTGTGTGCTTCTGCTTTTAAATTTTTCAGTTCAGATTTT 2641
Qy 2747 TATGTTTTTGGTTCATCCTTTTAAAAATGCTGTGGTTCCTCATCAAACCTTGTTCACAGA 2806

Db 2642 TATGTTTTTGGTCCATCATCTTTTAAAAAATGCTGTGGTTCCTATCAAGCTCGTTCCAGA 2701
Qy 2807 CTTATATTTTCTAAAACTGGAGACAAAACCCACATAAAATACAAAACAAAGTCTGCTTCTTCA 2866
Db 2702 CTTGATATTTTCTAAAACTGGAGATAAAACCTCATAAAATACAAAACAAAGCCTGCTGCTTCA 2761
Qy 2867 AAATCTGCT-----GACTCAGATATCAGTGATCTTATTAGCTTTTTCATCA 2910
Db 2762 AAATCTACTGGTGAGAGCGGTGTGAAGATTCAGATATCAATGATCTTATTGACTTTTTCAT 2821
Qy 2911 CAAGCCAGAAACATAAATGAGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCC 2970
Db 2822 CACAGCAGAAACATAAATGTGGCCATGTTTAAATGACAGTGACTATGTGTCTGCTGCTCCTC 2881
Qy 2971 ATAGTGGGCTTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGGCAGCTGTTTTTCA 3030
Db 2882 ATAGTGGGCTCTCAATGTGGTGCAAGTCAGTCAAGAAAAGGACTATGTTTTTACTGCTGTTTTCA 2941
Qy 3031 ACAGTACTATGGTTTTTATCTTTTACCTATATATTAGTGAATATCATTAGTAACCTACTATCTTT 3090
Db 2942 ACAGTACTATGGTTTTTATCTTTTGGCCAGTAATGATGAACATCATTAGTAACCTACTATCTCT 3001
Qy 3091 ATCATTTAAATGTGACTGAAACCATCCAGATCTGAGTACCCCATTTCTTTCAAGAAATTA 3150
Db 3002 ATCATTTAAATGTGACTGACACTATCCAGATCTGAGTACCCCGTTCAATTCAGGAAATTA 3061
Qy 3151 CTGATATAGTTTTTAAATGTGAGTGTATTTTTCAAGCAGCTTTTGCTTGGAAATCATTTGTTA 3210
Db 3062 CTGACATGTTTTTAAAGTTGAGCTATATTTTCAAGCAGCTTTTGCTTGGAAATCATTTGTTA 3121
Qy 3211 CTGCAATGCCACCTTACTTTTGGCCATGGAAAATGCAGAGAATCATAGATCAAAAGCTTATA 3270
Db 3122 CTGCAATGCCACCTTACTTTTGGCCATGGAAAATGCAGAGAATCATAGATCAAAAGCTTACA 3181
Qy 3271 CTCAACTTAAACCTTTCAGGTCTTTTGGCCATCTGCATATTTGGATTGGACAGCTGTTGTTG 3330
Db 3182 CTCAGCTTAAACCTTTCAGGTCTTTTGGCCATCCGCTACTGGATTGGACAGGCTGTTGTTG 3241
Qy 3331 ATATCCCTTATTTTTTATCATCTTATTTTTGATGCTAGGAAGCTTATTGGCATTTTCATT 3390
Db 3242 ACATTTCCCTGTTTTTGTGTTCTGACCTTTGATGCTGGGAAGTTTATTATGCTTTTCATC 3301
Qy 3391 ATGGATTATATTTTTTACTGTAAAGTTCCCTTGTGTGGTTTTTTTGGCTTATTGTTTATG 3450
Db 3302 ACGGACTGTATTTTTTATCTGTAAAGTTTCTTGTGTGGTTTTTTTGGCTTCAATGCTTATG 3361
Qy 3451 TTCCATCAGTTATCTGTTCACCTTATATTGCTTCTTTTCAACCTTTAAGAAAATTTTAAATA 3510
Db 3362 TGCCCTCGGTTATCTGTTCACCTTATATAGCTTCGTTACCTTTAAGAAAATTTTAAATA 3421
Qy 3511 CCAAAGAAATTTTGGTCATTTTCTATTCTGTGGCAGCGTTGGCTTGATTTGCAATCACCTG 3570
Db 3422 CCAAGGAATTTTGGTCATTTTCTATTCTGTGACAGCATTTGGCTTGTGTGCGAGTCACGG 3481
Qy 3571 AAATAACTTTCTTTATGGGATACACAATTTGCAACTATTCTTCATTTATGCTTTTGTATCA 3630
Db 3482 AAATAACTTTCTTTCTGGGGTATGGAGTTACGGCTGTTTTTTCATTTACACCTTCTGCTAG 3541
Qy 3631 TCATTTCCAAATCTATCCACTTCTAGGTTGCCGTGATTTCTTTCATAAAGATTTCTTTGGAAGA 3690
Db 3542 CCATCCCAATCTACCCGCTCCTGGGTTGTCTGATTTCTTTTCATAAAGGGTCTTTGGAAGA 3601
Qy 3691 ATGTACGAAAAAATGTGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATAT 3750
Db 3602 ATATACCAAAAACTGAGAAATGCCCTACAATCCCTGGGACAGACTTTTAGTTGCTGTAAATCA 3661
Qy 3751 GCGCTTACCTGCAGTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAAATATG 3810
Db 3662 TGCCCTACCTGCAGTGTACTGTGGATTTTCTCTTACAACACTATGAGAAAAAACAATG 3721
Qy 3811 GAGGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACCTTTCAACGAGTCTAAAAATA 3870
Db 3722 GAGGCAGATCAATAAGAAAAAGATCCGCTTTTTCAGGGCCCTCTCACAAAAAGCCAAACATA 3781

Query Match 69.6%; Score 3812.6; DB 9; Length 4078; Best Local Similarity 95.9%; Pred. No. 0; Matches 4014; Conservative 0; Mismatches 4; Indels 169; Gaps 3;									
QY	1101	GTTGAATTTTGTACTGTGGCTTTTGGATTTATTGGCCTTATGATAAATCCTCATAGAA	1160						
Db	1	GTTGAATTTTGTACTGTGGCTTTTGGATTTATTGGCCTTATGATAAATCCTCATAGAA	60						
QY	1161	AGTTTCCCAAAATCGTTAGTGTGGCTTTTCAGTCCCTTCTGTCACTGTACTTTTGTGATT	1220						
Db	61	AGTTTCCCAAAATCGTTAGTGTGGCTTTTCAGTCCCTTCTGTCACTGTACTTTTGTGATT	120						
QY	1221	GGTATTGCACAGTCATGCAATTTAGAGATTTTAATGAAGTGCTTCATTTTCAAATTTG	1280						
Db	121	GGTATTGCACAGTCATGCAATTTAGAGATTTTAATGAAGTGCTTCATTTTCAAATTTG	180						
QY	1281	ACTGCAGGCCCATATCCTCTAATTTATACAATATCATGCTCACACTTAATAGTATATTC	1340						
Db	181	ACTGCAGGCCCATATCCTCTAATTTATACAATATCATGCTCACACTTAATAGTATATTC	240						
QY	1341	TATGTCCTCTGGCTGTCTATCTTGATCAAGTCATTCAGGGGAATTTGGCTTACGGAGA	1400						
Db	241	TATGTCCTCTGGCTGTCTATCTTGATCAAGTCATTCAGGGGAATTTGGCTTACGGAGA	300						
QY	1401	TCATCTTTATATTTCTGAAGCCTTCATATTTGGTCAAAGAGCAAAAGAAATTAATGAGGAG	1460						
Db	301	TCATCTTTATATTTCTGAAGCCTTCATATTTGGTCAAAGAGCAAAAGAAATTAATGAGGAG	360						
QY	1461	TTATCAGAGGSCAATGTTAATGGAAATATTAGTTTGTAGTGAATATTGAGCCAGTTTCT	1520						
Db	361	TTATCAGAGGSCAATGTTAATGGAAATATTAGTTTGTAGTGAATATTGAGCCAGTTTCT	420						
QY	1521	TCAGAAATTTGTAGGAAAAGAGCCATAGAATTTAGTGGTATTTCAGAAAGACATACAGAAAG	1580						
Db	421	TCAGAAATTTGTAGGAAAAGAGCCATAGAATTTAGTGGTATTTCAGAAAGACATACAGAAAG	480						
QY	1581	AAGGTTGAAATGTGGAGGCTTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATT	1640						
Db	481	AAGGTTGAAATGTGGAGGCTTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATT	540						
QY	1641	ACTGCCCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACATTGATGAATATTTCTTTTGGA	1700						
Db	541	ACTGCCCTTACTTGGCCACAGTGGAAACAGGAAAGAGTACATTGATGAATATTTCTTTTGGA	600						
QY	1701	CTCTGCCACCTCTGATGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGAT	1760						
Db	601	CTCTGCCACCTCTGATGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGAT	660						
QY	1761	GAAATGTTTGACCAAGAAAATGATTGGCAATTTGTCCAAGTTAGATATACACTTTGAT	1820						
Db	661	GAAATGTTTGACCAAGAAAATGATTGGCAATTTGTCCAAGTTAGATATACACTTTGAT	720						
QY	1821	GTTTGTGACAGTAGAAGAAAATTTATCAATTTTGGCTTCAATCAAAAGGGATACCAGCCAAC	1880						
Db	721	GTTTGTGACAGTAGAAGAAAATTTATCAATTTTGGCTTCAATCAAAAGGGATACCAGCCAAC	780						
QY	1881	AATATAATACAGAAAGTGCAGAAAGTTTACTAGATTTTAGACATGCAGACTATCAAAGAT	1940						
Db	781	AATATAATACAGAAAGTGCAGAAAGTTTACTAGATTTTAGACATGCAGACTATCAAAGAT	840						
QY	1941	AACCAAGCTAAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGTCATTAGGAATTTGCTGTT	2000						
Db	841	AACCAAGCTAAAAAATTAAGTGGTGGTCAAAAAAGAAAGCTGTCATTAGGAATTTGCTGTT	900						
QY	2001	CTTGGGAACCCAAAGATACCTGCTGCTAGATGAACCAACAGCTGGAAATGGACCCCTGTTCT	2060						
Db	901	CTTGGGAACCCAAAGATACCTGCTGCTAGATGAACCAACAGCTGGAAATGGACCCCTGTTCT	960						
QY	2061	CGACATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGT	2120						
Db	961	CGACATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGT	1020						
QY	2121	ACTCATTTTCATGGATGAAGCTGACATTTCTTGACAGATAGGAAAGCTGTGATATCACAGGA	2180						
QY	1021	ACTCATTTTCATGGATGAAGCTGACATTTCTTCAGATAGGAAAGCTGTGATATCACAGGA	1080						
QY	2181	ATGCTGAAATGTGTTGGTCTTCAATGTTCCTCAAAAGTAATGGGGATCGGCTACCGC	2240						
Db	1081	ATGCTGAAATGTGTTGGTCTTCAATGTTCCTCAAAAGTAATGGGGATCGGCTACCGC	1140						
QY	2241	CTGAGCATGTACATAGACAAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAA	2300						
Db	1141	CTGAGCATGTACATAGACAAAATATTGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAA	1200						
QY	2301	CATATACCTGGAGCTACTTTTATTACAACAGAAATGACCAACAACTTGTGTATAGCTTGCCT	2360						
Db	1201	CATATACCTGGAGCTACTTTTATTACAACAGAAATGACCAACAACTTGTGTATAGCTTGCCT	1260						
QY	2361	TTCAAGGACATGGACAAAATTTTTCAG-----GT 2387							
Db	1261	TTCAAGGACATGGACAAAATTTTTCAGGAATTCCTTGATAGACAAAAGGATGTTATTGATGT	1320						
QY	2388	TTGTTTTCTGCCCTAGACAGTCATTCAAAATTTGGGTGTCAATTTCTTATGGTGTTCCTATG	2447						
Db	1321	TTGTTTTCTGCCCTAGACAGTCATTCAAAATTTGGGTGTCAATTTCTTATGGTGTTCCTATG	1380						
QY	2448	ACGACTTTTGGAAAGACGTATTTTTTAAAGCTAGAAAGTTGAAGCAGAAATTGACCAAGCAGAT	2507						
Db	1381	ACGACTTTTGGAAAGACGTATTTTTTAAAGCTAGAAAGTTGAAGCAGAAATTGACCAAGCAGAT	1440						
QY	2508	TATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTATGAA	2567						
Db	1441	TATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTATGAA	1500						
QY	2568	ATGGAACAGAGCTTACTTATTTCTTTTCTGAAACCAAGGCTTCTTAGTGAGCACCATGAGC	2627						
Db	1501	ATGGAACAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTTAGTGAGCACCATGAGC	1560						
QY	2628	CTTTGGAAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGTGAA	2687						
Db	1561	CTTTGGAAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGTGAA	1620						
QY	2688	AGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTTTCACAGTTCAGATTTTTT	2747						
Db	1621	AGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTTTCACAGTTCAGATTTTTT	1680						
QY	2748	ATGTTTTTGTGTTTCATCTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGAC	2807						
Db	1681	ATGTTTTTGTGTTTCATCTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGAC	1740						
QY	2808	TTATATTTTCTAAAAACCTGGAGACAAACCAATATAAATACAAAACAGTCTGCTTCTTCAA	2867						
Db	1741	TTATATTTTCTAAAAACCTGGAGACAAACCAATATAAATACAAAACAGTCTGCTTCTTCAA	1800						
QY	2868	AATTCTGCT-----GACTCAGATATCAGTGTATCTTATTAGCTTTTTTTCAC 2911							
Db	1801	AATTCTGCTGCTGAGAGTGTGTGAAGACTCAGATATCAGTGTATCTTATTAGCTTTTTTCAC	1860						
QY	2912	AAGCCAGAACATAAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCA	2971						
Db	1861	AAGCCAGAACATAAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCA	1920						
QY	2972	TAGTCCGGCTTTAAATGTGATGTCATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTTCAA	3031						
Db	1921	TAGTCCGGCTTTAAATGTGATGTCATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTTCAA	1980						
QY	3032	CAGTACTATGGTTTATCTTTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTA	3091						
Db	1981	CAGTACTATGGTTTATCTTTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTA	2040						
QY	3092	TCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCAATCTTTCAAGAAATTAC	3151						
Db	2041	TCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCAATCTTTCAAGAAATTAC	2100						
QY	3152	TGATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTTGCTTGAATCATTTGTTAC	3211						

Db 2101 TGATATAGTTTTTAAATTTGAGCTGTAATTTCAAGCAGCTTTGCTTGAATCATTTGTAC 2160

Qy 3212 TGCAATGCCACCTTACTTTGCCATGGAAAAATGCAGAGAAATCATAAAGATCAAAGCTTATAC 3271

Db 2161 TGCAATGCCACCTTACTTTGCCATGGAAAAATGCAGAGAAATCATAAAGATCAAAGCTTATAC 2220

Qy 3272 TCAACTTAAACTTTTCCAGGCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGA 3331

Db 2221 TCAACTTAAACTTTTCCAGGCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGA 2280

Qy 3332 TATCCCTTATTTTATCAATCTTATTTTGATGCTAGGAAGCTTATTGGCATTTTCAATTA 3391

Db 2281 TATCCCTTATTTTATCAATCTTATTTTGATGCTAGGAAGCTTACTGGCATTTTCAATTA 2340

Qy 3392 TGGATTATATTTTATACTGTAAAGTTCTTGTCTGTGGTTTTTTTGCCTTATTGGTTATGT 3451

Db 2341 TGGATTATATTTTATACTGTAAAGTTCTTGTCTGTGGTTTTTTTGCCTTATTGGTTATGT 2400

Qy 3452 TCCATCAGTTATCTGTTTCACTTATATTTGCTTCTTTCACCTTTAAGAAAAATTTTAAATAC 3511

Db 2401 TCCATCAGTTATCTGTTTCACTTATATTTGCTTCTTTCACCTTTAAGAAAAATTTTAAATAC 2460

Qy 3512 CAAAGAAATTTGGTCAATTTATCTATTTCTGTTGGCAGCGTTGGCTTGTATTGCAATCACTGA 3571

Db 2461 CAAAGAAATTTGGTCAATTTATCTATTTCTGTTGGCAGCGTTGGCTTGTATTGCAATCACTGA 2520

Qy 3572 AATAACTTTCTTTATGGGATACACAATTTGCAACTATTCTTCATTATGCTTTTGTATCAT 3631

Db 2521 AATAACTTTCTTTATGGGATACACAATTTGCAACTATTCTTCATTATGCTTTTGTATCAT 2580

Qy 3632 CATTCCAATCTATCCACTTCTTAGGTTGCCTGATTTCTTTCATATAAGATTTTCTTGAAGAA 3691

Db 2581 CATTCCAATCTATCCACTTCTTAGGTTGCCTGATTTCTTTCATATAAGATTTTCTTGAAGAA 2640

Qy 3692 TGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATC 3751

Db 2641 TGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATC 2700

Qy 3752 GCCTTACCTGCAGTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAAATATGG 3811

Db 2701 GCCTTACCTGCAGTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAAATATGG 2760

Qy 3812 AGGAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACCTTTCAACGAAGCTTAAAAATAG 3871

Db 2761 AGGAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACCTTTCAACGAAGCTTAAAAATAG 2820

Qy 3872 GAAGCTTCCAGAACCCACGACAAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACT 3931

Db 2821 GAAGCTTCCAGAACCCACGACAAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACT 2880

Qy 3932 AAAGSTCAAAGAGCTGATGGSTGCCAGTGTGTGAGGAGAAAACCATCCATTATGTTGTCAG 3991

Db 2881 AAAGSTCAAAGAGCTGATGGSTGCCAGTGTGTGAGGAGAAAACCATCCATTATGTTGTCAG 2940

Qy 3992 CAATTGTCATAAAGAAATATGATGACAAGAAAGATTTTCTTTCAGAAAAAGTAAAGAA 4051

Db 2941 CAATTGTCATAAAGAAATATGATGACAAGAAAGATTTTCTTTCAGAAAAAGTAAAGAA 3000

Qy 4052 AGTGCCAACTAAATACATCTCTTCTGTGTGAAAAAAGAGAGATCTTAGGACTATTGGG 4111

Db 3001 AGTGCCAACTAAATACATCTCTTCTGTGTGAAAAAAGAGAGATCTTAGGACTATTGGG 3060

Qy 4112 TCCAAATGGTGTGCGCAAAAGCACAAATTATTAATATCTGGTTGGTGATATTGAACCAAC 4171

Db 3061 TCCAAATGGTGTGCGCAAAAGCACAAATTATTAATATCTGGTTGGTGATATTGAACCAAC 3120

Qy 4172 TTCAGGCCAGGTATTTTTTAGGAGATTATTTCTTCAGACACAAGTGAAGATGATTCAC 4231

Db 3121 TTCAGGCCAGGTATTTTTTAGGAGATTATTTCTTCAGACACAAGTGAAGATGATTCAC 3180

Qy 4232 GAAGTGTATGGGTTACTGTCTCCTCAGATAAAACCCCTTTGTGGCCAGATACATTCAGGA 4291

Db 3181 GAAGTGTATGGGTTACTGTCTCCTCAGATAAAACCCCTTTGTGGCCAGATACATTCAGGA 3240

Qy 4292 ACATTTTGAATTTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAAGAGTCAT 4351

Db 3241 ACATTTTGAATTTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAAGAGTCAT 3300

Qy 4352 AAGTCGAATAACACATGCACCTTGATTTAAAAAGAACATCTTTCAGAAGACTGTAAAGAACT 4411

Db 3301 AAGTCGAATAACACATGCACCTTGATTTAAAAAGAACATCTTTCAGAAGACTGTAAAGAACT 3360

Qy 4412 ACCTGCAGGAATCAAACGAAAAGTTGTGTTTTGCTCTTAAGTATGCTAGGGAATCCTCAGAT 4471

Db 3361 ACCTGCAGGAATCAAACGAAAAGTTGTGTTTTGCTCTTAAGTATGCTAGGGAATCCTCAGAT 3420

Qy 4472 TACTTTGCTPAGATGAACCATCTACAGGTATGGATCCCAAAGSCAAAACAGCACATGTGGCG 4531

Db 3421 TACTTTGCTPAGATGAACCATCTACAGGTATGGATCCCAAAGSCAAAACAGCACATGT---- 3476

Qy 4532 AGCAATTCGAACTGCATTTTAAAAACAGAAAAGCGGCTGCTATTCTGACCACCTCACATAT 4591

Db 3477 ----- 3476

Qy 4592 GGAGGAGGCAGAGGCTGCTGTGATCGAGTAGCTATCATGCTGTCTGGCAGTTAAGAIG 4651

Db 3477 -----GATG 3480

Qy 4652 TATCGGAACAGTACAACATCTAAAAGAGTAAATTTTGAAAAAGGCTACTTTTGGAAATTA 4711

Db 3481 TATCGGAACAGTACAACATCTAAAAGAGTAAATTTTGAAAAAGGCTACTTTTGGAAATTA 3540

Qy 4712 ATTGAAGGACTGGATAGAAAACCTAGAAAGTAGACCGCTTCAAAGAGAAATTCAGTATAT 4771

Db 3541 ATTGAAGGACTGGATAGAAAACCTAGAAAGTAGACCGCTTCAAAGAGAAATTCAGTATAT 3600

Qy 4772 TTTCCCAAATGCAAGCCGTCAGAAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAA 4831

Db 3601 TTTCCCAAATGCAAGCCGTCAGAAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAA 3660

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Db 3661 GGAAGATGTTTCAGTCCCTTTCACAATCTTTTTTTAAGCTGGAAGAAGCTAAACATGCTTT 3720

Qy 4892 TGCCATTGAAGAAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCAC 4951

Db 3721 TGCCATTGAAGAAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCAC 3780

Qy 4952 TAAAGAACAAAGAGGAGGAGAGATAATAGTTGTGGAACTTTTAAACAGCACACTTTGGTGGGA 5011

Db 3781 TAAAGAACAAAGAGGAGGAGAGATAATAGTTGTGGAACTTTTAAACAGCACACTTTGGTGGGA 3840

Qy 5012 ACGAACACAAGAAAGATAGAGTAGTATTTTGAATTTTGTATTGTTCCGTTCTGCTTACTGGGA 5071

Db 3841 ACGAACACAAGAAAGATAGAGTAGTATTTTGAATTTTGTATTGTTCCGTTCTGCTTACTGGGA 3900

Qy 5072 CTTCTTTCTTTTTCATTAATTTTAACTTTTGGTTTTTAAAGTTTTTTTATTGGAATGGTAA 5131

Db 3901 CTTCTTTCTTTTTCATTAATTTTAACTTTTGGTTTTTAAAGTTTTTTTATTGGAATGGTAA 3960

Qy 5132 CTGAGAACCAAGAACCGACTTGAATTTTCTAAGCTCCTTAATTTGAAATGCTGCTGTT 5191

Db 3961 CTGAGAACCAAGAACCGACTTGAATTTTCTAAGCTCCTTAATTTGAAATGCTGCTGTT 4020

Qy 5192 GTGTGTTTTGCTTTTCTTTAAATAAAACGATATGTATAATTAAGTGAA 5238

Db 4021 GTGTGTTTTGCTTTTCTTTAAATAAAACGATATGTATAATTAAGTGAA 4067

CC polynucleotide encoding it (II) are useful as targets for developing
CC modulating agents to regulate a variety of cellular processes,
CC particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC (BBB), as targets for developing modulating agents of multi-drug
CC resistance, as diagnostic and therapeutic tools, or to treat disorders
CC associated with aberrant or unwanted ABCA5 transporter expression or
CC activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC screening assays, detection assays (e.g., chromosomal mapping, tissue
CC typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC (III) are useful as reagents or targets in assays applicable to treatment
CC and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC -hybrid or three-hybrid assay; and to identify other proteins which bind
CC to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC activity; to locate gene regions associated with genetic disease or to
CC associate ABCA5 with the disease, to identify an individual from a minute
CC biological sample (tissue typing), and to aid in forensic identification
CC of the biological sample. This sequence encodes a novel human ATP binding
CC cassette (ABC) A5 transporter
XX
SQ Sequence 5475 BP; 1705 A; 917 C; 1048 G; 1804 T; 0 U; 1 Other;

Query Match 100.0%; Score 5474; DB 7; Length 5475;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGTCCGGCCCTCGCACAGATCCNAGCTGGTCAACCGCACTGAGTCAACAGACTCGAGC 60
DB 1 GCGTCCGGCCCTCGCACAGATCCNAGCTGGTCAACCGCACTGAGTCAACAGACTCGAGC 60
QY 61 GCGTCCAGGCTGACAGCTCTGCGGCTCGGCGCTGGGCTGAGTTATTTCAGAAAACATGTCCA 120
DB 61 GCGTCCAGGCTGACAGCTCTGCGGCTCGGCGCTGGGCTGAGTTATTTCAGAAAACATGTCCA 120
QY 121 CTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAATTACT 180
DB 121 CTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAGAATTACT 180
QY 181 TAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAATCTTTTCCACTATTTTTT 240
DB 181 TAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAATCTTTTCCACTATTTTTT 240
QY 241 TATTTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAGTGCCTA 300
DB 241 TATTTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAGTGCCTA 300
QY 301 ATATAGACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTGGATATACTC 360
DB 301 ATATAGACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTGGATATACTC 360
QY 361 CAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTACCTGATG 420
DB 361 CAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTACCTGATG 420
QY 421 TCATAATTACTGAAGAAATATACAAATGAAAAGAAATGTTAAACATCCAGTCTCTTAAGC 480
DB 421 TCATAATTACTGAAGAAATATACAAATGAAAAGAAATGTTAAACATCCAGTCTCTTAAGC 480
QY 481 CGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGTCCTATGAACCTCGTTTTTTC 540
DB 481 CGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGTCCTATGAACCTCGTTTTTTC 540
QY 541 CTGATATGATCCAGTATCTTCTATTATATGGAATCAAGAGCTGGCTGTTCAAAATCAT 600
DB 541 CTGATATGATCCAGTATCTTCTATTATATGGAATCAAGAGCTGGCTGTTCAAAATCAT 600
QY 601 GTGAGGCTGCTCAGTACTGGTCTCAGGTTTTCAGGTTTACAAGCATCCATAGATGCTG 660

DB 601 GTGAGGCTGCTCAGTACTGGTCTCCTCAGGTTTTCACAGTTTTCACAGCATCCATAGATGCTG 660
QY 661 CCATTATACAGTTGAAGACCAATGTTTCTCTTTTGGAAAGGAGTGGAGTCAACTAAAGCTG 720
DB 661 CCATTATACAGTTGAAGACCAATGTTTCTCTTTTGGAAAGGAGTGGAGTCAACTAAAGCTG 720
QY 721 TTATTATGGGAGAAAACCTGCTGTTGTAGAAAATAGATACCTTTCCCGGAGGAGTAATTTAA 780
DB 721 TTATTATGGGAGAAAACCTGCTGTTGTAGAAAATAGATACCTTTCCCGGAGGAGTAATTTAA 780
QY 781 TATACCTAGTTATAGCATTTTTCACCTTTTGGATACCTTTTGGCAATTCATATCGTAGCAG 840
DB 781 TATACCTAGTTATAGCATTTTTCACCTTTTGGATACCTTTTGGCAATTCATATCGTAGCAG 840
QY 841 AAAAAGAAAAAAATAAAAGAAATTTTAAAGATAATGGGACTTCATGATACTGCCTTTT 900
DB 841 AAAAAGAAAAAAATAAAAGAAATTTTAAAGATAATGGGACTTCATGATACTGCCTTTT 900
QY 901 GGCTTTCTGGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTTATGGCAG 960
DB 901 GGCTTTCTGGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTTATGGCAG 960
QY 961 TCATTGCGACAGCTTCTTTTGTATTCTCTCAAGTAGGAGCATTTGTGATATTTCTGCTTT 1020
DB 961 TCATTGCGACAGCTTCTTTTGTATTCTCTCAAGTAGGAGCATTTGTGATATTTCTGCTTT 1020
QY 1021 TTTTCTCTTATGGATTATCATCTGTATTTTGTGCTTTTAAATCTGACACCTCTTTTAAAA 1080
DB 1021 TTTTCTCTTATGGATTATCATCTGTATTTTGTGCTTTTAAATCTGACACCTCTTTTAAAA 1080
QY 1081 AATCAAAACATGTGGGAATAGTTGAATTTTGTGCTGCTTTTGGATTTATGGCC 1140
DB 1081 AATCAAAACATGTGGGAATAGTTGAATTTTGTGCTGCTTTTGGATTTATGGCC 1140
QY 1141 TTATGAPAAATCCTCATAGAAAGTTTCCAAATCGTTAGTGTGGCTTTTCAGTCCCTTCT 1200
DB 1141 TTATGAPAAATCCTCATAGAAAGTTTCCAAATCGTTAGTGTGGCTTTTCAGTCCCTTCT 1200
QY 1201 GTCACGTACTTTTGTGATTGGTATTGCACAGGTCAATGCAATTTAGAAAGATTTAATGAAG 1260
DB 1201 GTCACGTACTTTTGTGATTGGTATTGCACAGGTCAATGCAATTTAGAAAGATTTAATGAAG 1260
QY 1261 GTGCTTCATTTTCAAAATTTGACTGCAGGCCCATATCTCTAATATTACAATTAATCATGC 1320
DB 1261 GTGCTTCATTTTCAAAATTTGACTGCAGGCCCATATCTCTAATATTACAATTAATCATGC 1320
QY 1321 TCACACTTAATAGTATATTCTATGTCCTCTTGGCTGCTATCTTGTCAAGTCAATCCAG 1380
DB 1321 TCACACTTAATAGTATATTCTATGTCCTCTTGGCTGCTATCTTGTCAAGTCAATCCAG 1380
QY 1381 GGGAAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTTCATATTTGGTCAAAGA 1440
DB 1381 GGGAAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTTCATATTTGGTCAAAGA 1440
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DB 1441 GCAAAAGAAATTAATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGTTTAGTG 1500
QY 1501 AAATTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAAATTTAGTGTA 1560
DB 1501 AAATTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAAATTTAGTGTA 1560
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DB 1561 TTCAGAAGACATACAGAAAGGGTGAAAATGTGGAGGCTTTTGAGAAATTTGTCATTTG 1620
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DB 1621 ACATATATGAGGGTCAGATTACTGCTTACTTTGSCCAGTGGAAACAGGAAAGATACAT 1680
QY 1681 TGATGAATATTCTTTGTGGACTCTGCCCCACCTTCTGATGGGTTTGCATCTATATATGGAC 1740
DB 1681 TGATGAATATTCTTTGTGGACTCTGCCCCACCTTCTGATGGGTTTGCATCTATATATGGAC 1740

QY 1741 ACAGAGTCTCAGAAAATAGATGAATGTTTGAAGCAAGAAAAATGATTGGCATTTTGTCCAC 1800
Db |||||
1741 ACAGAGTCTCAGAAAATAGATGAATGTTTGAAGCAAGAAAAATGATTGGCATTTTGTCCAC 1800
QY 1801 AGTTAGATATACACTTTTGATGTTTTCACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAA 1860
Db |||||
1801 AGTTAGATATACACTTTTGATGTTTTCACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAA 1860
QY 1861 TCAAAGGGATACCAGCCCAACAATATAATACAAGAACTGCAGAAAGTTTTACTAGATTTAG 1920
Db |||||
1861 TCAAAGGGATACCAGCCCAACAATATAATACAAGAACTGCAGAAAGTTTTACTAGATTTAG 1920
QY 1921 ACATGCAGACTATCAAAGATAACCAAGCTAAAAATTTAAGTGGTGGTCAAAAAAGAAAGC 1980
Db |||||
1921 ACATGCAGACTATCAAAGATAACCAAGCTAAAAATTTAAGTGGTGGTCAAAAAAGAAAGC 1980
QY 1981 TGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACGCTGCTAGATGAACCAACAG 2040
Db |||||
1981 TGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACGCTGCTAGATGAACCAACAG 2040
QY 2041 CTGGAATGGAACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATAACAGAAAAGCCA 2100
Db |||||
2041 CTGGAATGGAACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATAACAGAAAAGCCA 2100
QY 2101 ATCGGTTGACAGTGTTCAGTACTCATTTTCATGGATGAAGTGCATCTTTGCAGATAGGA 2160
Db |||||
2101 ATCGGTTGACAGTGTTCAGTACTCATTTTCATGGATGAAGTGCATCTTTGCAGATAGGA 2160
QY 2161 AAGCTGTGATATACAAGGAATGCTGAAATGTGTGGTCTTCAATGTTCCCTCAAAAGTA 2220
Db |||||
2161 AAGCTGTGATATACAAGGAATGCTGAAATGTGTGGTCTTCAATGTTCCCTCAAAAGTA 2220
QY 2221 AATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTTGTGCCACAGAACTC 2280
Db |||||
2221 AATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTTGTGCCACAGAACTC 2280
QY 2281 TTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACACAGAAATGACCAAC 2340
Db |||||
2281 TTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACACAGAAATGACCAAC 2340
QY 2341 AACTTGTGTATAGCTTGCCCTTTCAGGACATGGACAAATTTTCAGGTTTGTGTTTCTGCC 2400
Db |||||
2341 AACTTGTGTATAGCTTGCCCTTTCAGGACATGGACAAATTTTCAGGTTTGTGTTTCTGCC 2400
QY 2401 TAGACAGTCAATTCAAATTTTGGGTGTCAATTTCTTATGGTGTTCATGACGACITTTGGAAG 2460
Db |||||
2401 TAGACAGTCAATTCAAATTTTGGGTGTCAATTTCTTATGGTGTTCATGACGACITTTGGAAG 2460
QY 2461 ACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTATAGTGTATTTA 2520
Db |||||
2461 ACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATTATAGTGTATTTA 2520
QY 2521 CTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAAACAGAGCT 2580
Db |||||
2521 CTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAAACAGAGCT 2580
QY 2581 TACTTATCTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTTGGAAACAAAC 2640
Db |||||
2581 TACTTATCTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTTGGAAACAAAC 2640
QY 2641 AGATGTATACAAATAGCAAAAGTTTCAATTTCTTTTACCTTGAAACGTGAAAGTAATCAGTGA 2700
Db |||||
2641 AGATGTATACAAATAGCAAAAGTTTCAATTTCTTTTACCTTGAAACGTGAAAGTAATCAGTGA 2700
QY 2701 GATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTTTGGTTTC 2760
Db |||||
2701 GATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTTTGGTTTC 2760
QY 2761 ATCACTCTTTTAAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATTTCTAA 2820
Db |||||
2761 ATCACTCTTTTAAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATTTCTAA 2820

QY 2821 AACCTGGAGACAAAACACATAAATACAAAAACAAGTCTGCTTCTTCAAAAATTTCTGCTGACT 2880
Db |||||
2821 AACCTGGAGACAAAACACATAAATACAAAAACAAGTCTGCTTCTTCAAAAATTTCTGCTGACT 2880
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Db |||||
2881 CAGATATCAGTGTATCTTATTAGCTTTTTCACAAGCCAGAACATAAATGGTGACGATGATTA 2940
QY 2941 ATGACAGTGAATGTATCCGTGGCTCCCATAGTGCAGCTTTTAAATGTGATGCAATTCAG 3000
Db |||||
2941 ATGACAGTGAATGTATCCGTGGCTCCCATAGTGCAGCTTTTAAATGTGATGCAATTCAG 3000
QY 3001 AAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTTATTCTTTACCTATAT 3060
Db |||||
3001 AAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTTATTCTTTACCTATAT 3060
QY 3061 TAGTGAATATCATTAGTAACACTACTATCTTTTATCATTTTAAATGTGACTGAAACCATCCAGA 3120
Db |||||
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QY 3181 TTCAAGCAGCTTTGCTTGGAAATCATTTTACTGCAATGCCACTTACTTTGCCATGGAAA 3240
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Db |||||
3241 ATGCAGAGAAATCATAAGATCAAAAGCTTATACTCAACTTAAACTTTTCAGGTCTTTTGCCAT 3300
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Db |||||
3301 CTGCATATTTGGATTGGACAAGCTGTGTGATATCCCTTATTTTTTATCATTTCTTTATT 3360
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Db |||||
3361 TGATGCTAGGAAGCTTATTGGCAATTTTCATTATGGATTATATTTTTTATCTGTAAGTTCC 3420
QY 3421 TTGCTGTGGTTTTTTGCTTATTTGCTTATTTGCTTATGTTCCATCAGTTATTTCTGTTCACTTATATG 3480
Db |||||
3421 TTGCTGTGGTTTTTTGCTTATTTGCTTATTTGCTTATGTTCCATCAGTTATTTCTGTTCACTTATATG 3480
QY 3481 CTTCTTTACCTTTAAGAAAAATTTTAAATACCAAAGAAATTTGGTCAATTTATCTATTCTG 3540
Db |||||
3481 CTTCTTTACCTTTAAGAAAAATTTTAAATACCAAAGAAATTTGGTCAATTTATCTATTCTG 3540
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Db |||||
3541 TGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATACACAATTG 3600
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Db |||||
3601 CAACTATTCTTCATTATGCCTTTTTGTATCATCTCCATCTATCCACTTCTAGGTTGCC 3660
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Db |||||
3721 CATGGATAGGCTTTTCAGTAGCTGTATATCGCCTTACCTGCACTGTGTACTGTGGATT 3780
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Db |||||
3781 TCCTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGATCCCTTTT 3840
QY 3841 TCAGAAACCTTTCAACGAAAGTCTAAAAAATAGGAAGCTTCCAGAACCCAGACAATGAGG 3900
Db |||||
3841 TCAGAAACCTTTCAACGAAAGTCTAAAAAATAGGAAGCTTCCAGAACCCAGACAATGAGG 3900
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Db 4501 TGGATCCCAAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGCATTTAAAAACAGAA 4560
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Db 4561 AGCGGGTCTATTCTGACCACTCACTATATGGAGGAGGAGGCTGTCTGTGATCGAG 4620
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QY 4741 TAGACCGCTTCAAAGAGAAAATTCAGTATATTTTCCCAATGCAAGCCGTCAGGAAAAGTT 4800
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Db 5041 GAATTTGTATTGTTGGTCTGCTTACTGCGACTTCTTTCTTTTTCACCTAAATTTTAACTT 5100
QY 5101 TGGTTTAAAAAGTTTTTTTATTGGAATGGTAAGTGGAGAACCAAGAACGCACTTGAAATTT 5160
Db 5101 TGGTTTAAAAAGTTTTTTTATTGGAATGGTAAGTGGAGAACCAAGAACGCACTTGAAATTT 5160
QY 5161 TTCTAAGCTCCCTTAATTAATGAAATGCTGTGGTTGTGTTTGTCTTTTCTTTAAATAAAACG 5220
Db 5161 TTCTAAGCTCCCTTAATTAATGAAATGCTGTGGTTGTGTTTGTCTTTTCTTTAAATAAAACG 5220
QY 5221 TATGTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTGAACCTATATAGTTTGT 5280
Db 5221 TATGTATAATTAAGTGAAGCTGCATGTTTGTATTGAAGTATATTGAACCTATATAGTTTGT 5280
QY 5281 ATGTCATCTTTTTCACCATTCAGAAACAGTCTTCTGAATTTGTGATTTAAAGGAATTTGT 5340
Db 5281 ATGTCATCTTTTTCACCATTCAGAAACAGTCTTCTGAATTTGTGATTTAAAGGAATTTGT 5340
QY 5341 AATAGAAATAGTTTTTATTTTAAAGTTATCTTTTAAAGTTTATGCCATCTTCTTTAAATAAGTAC 5400
Db 5341 AATAGAAATAGTTTTTATTTTAAAGTTATCTTTTAAAGTTTATGCCATCTTCTTTAAATAAGTAC 5400
QY 5401 GTAATGTTCCCAATCTAAATAAAAAAATAATTCATACTAATGCATAGAAAAGATACATAA 5460
Db 5401 GTAATGTTCCCAATCTAAATAAAAAAATAATTCATACTAATGCATAGAAAAGATACATAA 5460
QY 5461 AGCAATGTGAAAGTT 5475
Db 5461 AGCAATGTGAAAGTT 5475

RESULT 2
ABN89594
ID ABN89594 standard; cDNA; 6525 BP.
XX
AC ABN89594;
XX
DT 18-SEP-2002 (first entry)
XX
DE Human ATP-binding cassette transporter ABCA5 cDNA SEQ ID NO:1.
XX
KW Human; ABCA5; ABCA6; ABCA9; ABCA10; ATP-binding cassette transporter;
KW chromosome 17; chromosome 17q; chromosome 17q24; antiarteriosclerotic;
KW gene therapy; cholesterol; lipophilic molecule; inflammation;
KW prostaglandin; prostacyclin; arteriosclerosis; transport; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200246458-A2.
XX
PD 13-JUN-2002.
XX
PF 07-DEC-2001; 2001WO-EP015401.
XX
PR 07-DEC-2000; 2000EP-00403440.
PR 23-JAN-2001; 2001US-0263231P.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Deneffe P, Rosier-Montus M, Prades C, Arnould-Reguigne I;
PI Duverger N, Allikmets R, Dean M;
XX
DR WPI; 2002-557584/59.
DR P-PSDB; ABB81574.
XX
PT A novel nucleic acid corresponding to ATP-binding cassette transporter
PT genes and the encoded polypeptide, useful for preventing or treating a
PT dysfunction in reverse transport of cholesterol.

XX	Claim 1; Page 151-153; 216pp; English.	
PS	The present invention describes human ATP-binding cassette transporters	
XX	(ABC). Specifically described are the human ABCA5, ABCA6, ABCA9 and	
CC	ABCA10 genes (see ABN89594 to ABN89597) which encode the proteins given	
CC	in AB81574 to AB81577). ABN89598 to ABN89715 represent ABCA5, ABCA6,	
CC	ABCA9 and ABCA10 nucleotide fragments; and ABN89716 to ABN89806 represent	
CC	primers for ABCA5, ABCA6, ABCA9 and ABCA10 genes which are used in the	
CC	exemplification of the present invention. The ABC sequences have	
CC	antiartherosclerotic activities and can be used in gene therapy. ABC	
CC	sequences can be used in the manufacture of a medicament intended for the	
CC	prevention and/or treatment of a subject affected by a dysfunction in the	
CC	reverse transport of cholesterol. The ABC proteins are involved in the	
CC	reverse transport of cholesterol, in membrane transport of lipophilic	
CC	molecules, in particular inflammation mediating substance such as	
CC	prostaglandins and prostacyclins, or in any pathology whose candidate	
CC	chromosomal region is situated on chromosome 17. They are also useful for	
CC	the manufacture of a medicament intended for prevention of	
CC	arteriosclerosis in various forms. The ABCA5, ABCA6, ABCA9 and ABCA10	
CC	genes are located to chromosome 17, more specifically to the 17q24 locus	
XX		
SQ	Sequence 6525 BP; 1973 A; 1108 C; 1258 G; 2185 T; 0 U; 1 Other;	
	Query Match 98.1%; Score 5373.2; DB 6; Length 6525;	
	Best Local Similarity 99.9%; Pred. No. 0;	
	Matches 5375; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
QY	97 AGGTTTATTGAGAAACATGTCACCTGCAATTAGGGAGGTAGAGTTTGGAGACAGACCA 156	
DB		
QY	994 AGGTTTATTGAGAAACATGTCACCTGCAATTAGGGAGGTAGAGTTTGGAGACAGACCA 1053	
DB		
QY	157 GAACACTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGG 216	
DB		
QY	1054 GAACACTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGG 1113	
DB		
QY	217 AAATTCCTTTTCCACTATTTTCTTTTATTTTGGTTAAATATTATAGCATGATGCATCAA 276	
DB		
QY	1114 AAATTCCTTTTCCACTATTTTCTTTTATTTTGGTTAAATATTATAGCATGATGCATCAA 1173	
DB		
QY	277 ATAAGAAATATGAAGAAGTGCCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 336	
DB		
QY	1174 ATAAGAAATATGAAGAAGTGCCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 1233	
DB		
QY	337 CTAATCTAATTTCTGGATATACTCCAGTGACTAATATTACAGCAGCATCATGCAGAAAG 396	
DB		
QY	1234 CTAATCTAATTTCTGGATATACTCCAGTGACTAATATTACAGCAGCATCATGCAGAAAG 1293	
DB		
QY	397 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAA 456	
DB		
QY	1294 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAA 1353	
DB		
QY	457 TGTTAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGGTTTTTCAAGACTCCA 516	
DB		
QY	1354 TGTTAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGGTTTTTCAAGACTCCA 1413	
DB		
QY	517 TGTCTATGAACCTTCGTTTTTTTCTGATATGATTCAGTATCTTCTATTTATATGGATT 576	
DB		
QY	1414 TGTCTATGAACCTTCGTTTTTTTCTGATATGATTCAGTATCTTCTATTTATATGGATT 1473	
DB		
QY	577 CAAGAGCTGGTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 636	
DB		
QY	1474 CAAGAGCTGGTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 1533	
DB		
QY	637 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGCAATGTTTCTCTTTGGA 696	
DB		
QY	1534 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGCAATGTTTCTCTTTGGA 1593	
DB		
QY	697 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAACTGCTGTTGTAGAAATAGATA 756	
DB		
QY	1594 AGGAGCTGGAGTCAACTAAAGCTGTTATTATGGGAGAACTGCTGTTGTAGAAATAGATA 1653	
DB		
QY	757 CCTTTCCCGAGGAGTAATTTTAAATATACCTAGTTATAGCAATTTTACCTTTTGGATACT 816	
DB		

DB	1654 CCTTTCCCGAGGAGTAATTTTAAATATACCTAGTTATAGCAATTTTACCTTTTGGATACT 1713	
QY	817 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAA 876	
DB	1714 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAA 1773	
QY	877 TGGGACTTCATGATACTGCCCTTTTGGCTTTTCCCTGGGTTCTTCTATATACAAGTTTAAATTT 936	
DB	1774 TGGGACTTCATGATACTGCCCTTTTGGCTTTTCCCTGGGTTCTTCTATATACAAGTTTAAATTT 1833	
QY	937 TTCTTATGTCCTTCTTATGGCAGTCATTCGACAGCTTCTTTGTTATTTCTCCTCAAGTA 996	
DB	1834 TTCTTATGTCCTTCTTATGGCAGTCATTCGACAGCTTCTTTGTTATTTCTCCTCAAGTA 1893	
QY	997 GCAGCAATTTGATATTTTCTGCTTTTCTTCTTTTATGGATTATCATCTGTTTGTCTT 1056	
DB	1894 GCAGCAATTTGATATTTTCTGCTTTTCTTCTTTTATGGATTATCATCTGTTTGTCTT 1953	
QY	1057 TAATGCTGACACCTCTTTTAAATAAATCAAAACATGTGGGAATAGTTGAATTTTGTGTTA 1116	
DB	1954 TAATGCTGACACCTCTTTTAAATAAATCAAAACATGTGGGAATAGTTGAATTTTGTGTTA 2013	
QY	1117 CTGTGGCTTTTGGATTTTATTTGGCTTTATGATAATCCTCATAGAAAGTTTCCCAATCGT 1176	
DB	2014 CTGTGGCTTTTGGATTTTATTTGGCTTTATGATAATCCTCATAGAAAGTTTCCCAATCGT 2073	
QY	1177 TAGTGTGGCTTTTTCAGTCCCTTTCTGTCACCTGTACTTTTGTGATTGGTATTGCACAGGTCA 1236	
DB	2074 TAGTGTGGCTTTTTCAGTCCCTTTCTGTCACCTGTACTTTTGTGATTGGTATTGCACAGGTCA 2133	
QY	1237 TGCATTTTAGAAGATTTTAAATGAAGTGTCTTCATTTTCAAAATTTGACTGCAGGCCCCATATC 1296	
DB	2134 TGCATTTTAGAAGATTTTAAATGAAGTGTCTTCATTTTCAAAATTTGACTGCAGGCCCCATATC 2193	
QY	1297 CTCTAATTATTACAATTATCATGCTGCACACTTAATAGTATATTCTATGCTCTTGGCTG 1356	
DB	2194 CTCTAATTATTACAATTATCATGCTGCACACTTAATAGTATATTCTATGCTCTTGGCTG 2253	
QY	1357 TCTATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1416	
DB	2254 TCTATCTTGATCAAGTCATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 2313	
QY	1417 TGAAGCCTTCATATTTGGTCAAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG 1476	
DB	2314 TGAAGCCTTCATATTTGGTCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG 2373	
QY	1477 TTAATGGAAATATTAGTTTTAGTGAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA 1536	
DB	2374 TTAATGGAAATATTAGTTTTAGTGAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAA 2433	
QY	1537 AAGAAGCCATAAAGAAATTAGTGGTATTTCAGAAAGACATACAGAAAGAGGGTGAAATGTGG 1596	
DB	2434 AAGAAGCCATAAAGAAATTAGTGGTATTTCAGAAAGACATACAGAAAGAGGGTGAAATGTGG 2493	
QY	1597 AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCC 1656	
DB	2494 AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCC 2553	
QY	1657 ACAGTGGACAGGAAAGAGTACATTGATGAATATTCTTTGTGGAATCTGCCCCACCTTCTG 1716	
DB	2554 ACAGTGGACAGGAAAGAGTACATTGATGAATATTCTTTGTGGAATCTGCCCCACCTTCTG 2613	
QY	1717 ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA 1776	
DB	2614 ATGGGTTTGCATCTATATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAA 2673	
QY	1777 GAAAAATGATTGGCATTTTGTCCACAGTTAGATATACACTTTTGATGTTTGTACAGTAGAAG 1836	
DB	2674 GAAAAATGATTGGCATTTTGTCCACAGTTAGATATACACTTTTGATGTTTGTACAGTAGAAG 2733	
QY	1837 AAAATTTATCAATTTTGGCTTCAATCAAGGGGATACCAGGCCAACAAATATATACAAAGAG 1896	
DB		

Db 2734 AAAATTTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCCAACAATATAATACAAGAG 2793

QY 1897 TGCAGAAGGTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAT 1956

Db 2794 TGCAGAAGGTTTACTAGATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAT 2853

QY 1957 TAAGTGGTGGTCAAAAAAGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGA 2016

Db 2854 TAAGTGGTGGTCAAAAAAGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGA 2913

QY 2017 TACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA 2076

Db 2914 TACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGA 2973

QY 2077 ATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG 2136

Db 2974 ATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG 3033

QY 2137 AAGCTGACATTTCTGCAGATAGGAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTG 2196

Db 3034 AAGCTGACATTTCTGCAGATAGGAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTG 3093

QY 2197 GTTCTTCAATGTTCTCAAAAGTAAATGGGGGATCGGCTACCGCTGAGCATGTACATAG 2256

Db 3094 GTTCTTCAATGTTCTCAAAAGTAAATGGGGGATCGGCTACCGCTGAGCATGTACATAG 3153

QY 2257 ACAATATTTGGCCACAGAAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAGCTA 2316

Db 3154 ACAATATTTGGCCACAGAAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAGCTA 3213

QY 2317 CTTTATTACAACAGAAATGACCAACAACTTGTGTATAGCTTGCCCTTCAAGGACATGGACA 2376

Db 3214 CTTTATTACAACAGAAATGACCAACAACTTGTGTATAGCTTGCCCTTCAAGGACATGGACA 3273

QY 2377 AATTTTCAGGTTTGTCTGCCCCTAGACAGTCATTCAAATTTGGGTGTCAATTTCTTATG 2436

Db 3274 AATTTTCAGGTTTGTCTGCCCCTAGACAGTCATTCAAATTTGGGTGTCAATTTCTTATG 3333

QY 2437 GTGTTTCCATGACGACTTTTGAAGACGTAATTTTAAAGCTAGAACTTGAAGCAGAAATG 2496

Db 3334 GTGTTTCCATGACGACTTTTGAAGACGTAATTTTAAAGCTAGAACTTGAAGCAGAAATG 3393

QY 2497 ACCAAGCAGATTATAGTGATTTTACTCAGCAGCCACTGGAGGAGAAATGGATTCAAAT 2556

Db 3394 ACCAAGCAGATTATAGTGATTTTACTCAGCAGCCACTGGAGGAGAAATGGATTCAAAT 3453

QY 2557 CTTTTGATGAATGGAAACAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGA 2616

Db 3454 CTTTTGATGAATGGAAACAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGA 3513

QY 2617 GCACCATGAGCCTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCT 2676

Db 3514 GCACCATGAGCCTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCT 3573

QY 2677 TGAAACGTGAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG 2736

Db 3574 TGAAACGTGAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG 3633

QY 2737 TTCAGATTTTATGTTTTTGGTTCATCACTCTTTTAAATAATGCTGGTTCCTCATCAAC 2796

Db 3634 TTCAGATTTTATGTTTTTGGTTCATCACTCTTTTAAATAATGCTGGTTCCTCATCAAC 3693

QY 2797 TTGTTCCAGACTTATATTTTCTAAAA CCTGGAGACAAACCAATAAATACAAACAAAGTC 2856

Db 3694 TTGTTCCAGACTTATATTTTCTAAAA CCTGGAGACAAACCAATAAATACAAACAAAGTC 3753

QY 2857 TGCTTCTTCAAAATCTGCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCC 2916

Db 3754 TGCTTCTTCAAAATCTGCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAGCC 3813

QY 2917 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTG 2976

Db 3814 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTG 3873

QY 2977 CGGCTTTAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA 3036

Db 3874 CGGCTTTAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA 3933

QY 3037 CTATGGTTTATCTTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCAT 3096

Db 3934 CTATGGTTTATCTTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCAT 3993

QY 3097 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAAAATTAATGATA 3156

Db 3994 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAAAATTAATGATA 4053

QY 3157 TAGTTTTAAATTTAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAA 3216

Db 4054 TAGTTTTAAATTTAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAA 4113

QY 3217 TGCCACCTTACTTTGCCATGGAAAAATGACAGAGAATCATAGATCAAAAGCTTATACTCAAC 3276

Db 4114 TGCCACCTTACTTTGCCATGGAAAAATGACAGAGAATCATAGATCAAAAGCTTATACTCAAC 4173

QY 3277 TTAAACCTTTCAAGTCTTTTGGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCC 3336

Db 4174 TTAAACCTTTCAAGTCTTTTGGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCC 4233

QY 3337 CCTTATTTTATCATTTCTTATTTTGTAGCTAGGAAGCTTATTTGSCATTTCAATATGGAT 3396

Db 4234 CCTTATTTTATCATTTCTTATTTTGTAGCTAGGAAGCTTACTGSCATTTCAATATGGAT 4293

QY 3397 TATATTTTATACTGTAAAGTTCCCTGCTGTGGTTTTTTTGGCTTATTTGTTGTTCCAT 3456

Db 4294 TATATTTTATACTGTAAAGTTCCCTGCTGTGGTTTTTTTGGCTTATTTGTTGTTCCAT 4353

QY 3457 CAGTTATTTCTGTTCACTTATATTGCTTCTTTTCCCTTTTAAAGAAAAATTTAAATACCAAAG 3516

Db 4354 CAGTTATTTCTGTTCACTTATATTGCTTCTTTTCCCTTTTAAAGAAAAATTTAAATACCAAAG 4413

QY 3517 AATTTTGGTCAATTTATCTATTCTGTGGCAGCGTTGGCTTGATTTGCAATCACTGAAATAA 3576

Db 4414 AATTTTGGTCAATTTATCTATTCTGTGGCAGCGTTGNCCTTGATTTGCAATCACTGAAATAA 4473

QY 3577 CTTTCTTTATGGGATACACAAATTTGCAACTATTCTTCATTTATGCCITTTGTTATCATCTC 3636

Db 4474 CTTTCTTTATGGGATACACAAATTTGCAACTATTCTTCATTTATGCCITTTGTTATCATCTC 4533

QY 3637 CAATCTATCCACTTCTAGTTTGCCTGATTTCTTTTCAATAAGATTTTCTTGAAGAAATGTAC 3696

Db 4534 CAATCTATCCACTTCTAGTTTGCCTGATTTCTTTTCAATAAGATTTCTTGAAGAAATGTAC 4593

QY 3697 GAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTT 3756

Db 4594 GAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTT 4653

QY 3757 ACCTGCAGTGTACTGTGGATTTTCTCTTTCAAAACCTTTTCAACGAGTCTAAAAATAGGAAGC 3816

Db 4654 ACCTGCAGTGTACTGTGGATTTTCTCTTTCAAAACCTTTTCAACGAGTCTAAAAATAGGAAGC 4713

QY 3817 GATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAGTCTAAAAATAGGAAGC 3876

Db 4714 GATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAGTCTAAAAATAGGAAGC 4773

QY 3877 TTCCAGAACCCACAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGG 3936

Db 4774 TTCCAGAACCCACAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGG 4833

QY 3937 TCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTTATGGTCAGCAATT 3996

Db 4834 TCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTTATGGTCAGCAATT 4893

QY 3997 TGCATAAAGAAATATGATGACAAAGAAAGATTTTCTTCTTCAAGAAAAAGTAAAGAAAGTGG 4056

Db 4894 TGCATAAAGAAATATGATGACAAAGAAAGATTTTCTTCTTCAAGAAAAAGTAAAGAAAGTGG 4953

QY 4057 CAACATAATACATCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 4116
Db 4954 CAACATAATACATCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 5013
QY 4117 ATGGTGTGGCAAAAGCACAAATTAATAATTTCTGGTTGGTGATATTGAACCAACTTCAG 4176
Db 5014 ATGGTGTGGCAAAAGCACAAATTAATAATTTCTGGTTGGTGATATTGAACCAACTTCAG 5073
QY 4177 GCCAGGTATTTTAGGAGATTATTTCTCAGAGACAAGTGAAGATGATGATTCACCTGAAGT 4236
Db 5074 GCCAGGTATTTTAGGAGATTATTTCTCAGAGACAAGTGAAGATGATGATTCACCTGAAGT 5133
QY 4237 GTATGGGTACTGTCTCCTCAGATAAACCCCTTTGTGGCCAGATACATATTCAGGAACATT 4296
Db 5134 GTATGGGTACTGTCTCCTCAGATAAACCCCTTTGTGGCCAGATACATATTCAGGAACATT 5193
QY 4297 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAGTGCATGAAAGAGTCAATAAGTC 4356
Db 5194 TTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAGTGCATGAAAGAGTCAATAAGTC 5253
QY 4357 GAATAACACATGCACCTTGATTTAAAGAAACATCTTCAGAGACTGTAAAGAAACTACCTG 4416
Db 5254 GAATAACACATGCACCTTGATTTAAAGAAACATCTTCAGAGACTGTAAAGAAACTACCTG 5313
QY 4417 CAGGAATCAACGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTT 4476
Db 5314 CAGGAATCAACGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTT 5373
QY 4477 TGCTAGATGAACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAA 4536
Db 5374 TGCTAGATGAACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAA 5433
QY 4537 TTCGAACTGCATTTAAAAACAGAAAGCGGCTGCTATTCTGACCACCTCACTATATGGAGG 4596
Db 5434 TTCGAACTGCATTTAAAAACAGAAAGCGGCTGCTATTCTGACCACCTCACTATATGGAGG 5493
QY 4597 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGCTGTCTGGCAGTTAAGATGTATCG 4656
Db 5494 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGCTGTCTGGCAGTTAAGATGTATCG 5553
QY 4657 GAACAGTACACATCTAAAGAGTAAATTTGGAAGAGGCTACTTTTGGAAATTTAAATTGA 4716
Db 5554 GAACAGTACACATCTAAAGAGTAAATTTGGAAGAGGCTACTTTTGGAAATTTAAATTGA 5613
QY 4717 AGGACTGGATAGAAAAACCTAGAGTAGACCGCCTTCAAAGAGAAAAATTCAGTATATTTCC 4776
Db 5614 AGGACTGGATAGAAAAACCTAGAGTAGACCGCCTTCAAAGAGAAAAATTCAGTATATTTCC 5673
QY 4777 CAAATGCAAGCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAG 4836
Db 5674 CAAATGCAAGCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAG 5733
QY 4837 ATGTTCAAGTCCTTTTCAAACTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCA 4896
Db 5734 ATGTTCAAGTCCTTTTCAAACTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCA 5793
QY 4897 TTGAAGATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAAG 4956
Db 5794 TTGAAGATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAAG 5853
QY 4957 AACAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGACACACTTTGGTGGGAACGAA 5016
Db 5854 AACAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGACACACTTTGGTGGGAACGAA 5913
QY 5017 CACAAGAGATAGAGTAGTATTTTGAATTTGTATTTGTCGGTCTGCTTACTGGGACTTCT 5076
Db 5914 CACAAGAGATAGAGTAGTATTTTGAATTTGTATTTGTCGGTCTGCTTACTGGGACTTCT 5973
QY 5077 TTCTTTTTCACTTAATTTTAACTTTTGGTTTAAAGTTTTTATTTGGAATGGTAAGTGA 5136
Db 5974 TTCTTTTTCACTTAATTTTAACTTTTGGTTTAAAGTTTTTATTTGGAATGGTAAGTGA 6033
QY 5137 GAACCAAGACGCACTTGAAATTTTCTAAGCTCCTTAATTGAATGCTGTGTTGTTG 5196

Db 6034 GAACCAAGACGCACTTGAAATTTTCTAAGCTCCTTAATTGAATGCTGTGTTGTG 6093
QY 5197 TTTTGTCTTTCTTTAAATAAAACGATGTATATAATTAAGTGAAGTGCATGTTTGTATTGA 5256
Db 6094 TTTTGTCTTTCTTTAAATAAAACGATGTATATAATTAAGTGAAGTGCATGTTTGTATTGA 6153
QY 5257 AGTATATTGAACATATATAGTTTGTATGTATCATCTTTTCCACCAATTCAGAAAACAGTCTTCT 5316
Db 6154 AGTATATTGAACATATATAGTTTGTATGTATCATCTTTTCCACCAATTCAGAAAACAGTCTTCT 6213
QY 5317 GAATTTGTGATTTAAAGGAATTTGAATAGATAGTTTATTTTAAAGTTATCTTTAAAGTT 5376
Db 6214 GAATTTGTGATTTAAAGGAATTTGAATAGATAGTTTATTTTAAAGTTATCTTTAAAGTT 6273
QY 5377 TATGCCATCTTCTTAAATAAGTACGTAATGTTCCAATCTAAATAAAAACTAATTCATAA 5436
Db 6274 TATGCCATCTTCTTAAATAAGTACGTAATGTTCCAATCTAAATAAAAACTAATTCATAA 6333
QY 5437 CTAATGCATAGAAAAGATACATATAAGCAATGTGAAAAGTT 5475
Db 6334 CTAATGCATAGAAAAGATACATATAAGCAATGTGAAAAGTT 6372

RESULT 3
ABS57749
ID ABS57749 standard; cDNA; 5463 BP.
XX
AC ABS57749;
XX
DT 04-FEB-2003 (first entry)
XX
DE cDNA encoding novel human ATP binding cassette ABCA5 transporter #1.
XX
KW Human; ATP binding cassette; ABC; ABCA5; transporter;
KW neurotoxin transport; beta-amyloid peptide; chromosome mapping;
KW blood brain barrier transport; tissue typing; predictive medicine;
KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 114..5030
FT /*tag= a
FT /product= "ABCA5"
FT /note= "ATP binding cassette (ABC) A5 transporter"
FT /transl_except= (pos:3273..3275, aa:Ser)
XX
PN US2002123107-A1.
XX
PD 05-SEP-2002.
XX
PF 01-MAR-2002; 2002US-00090458.
XX
PR 02-MAR-2001; 2001US-0272885P.
XX
PA (ACTI-) ACTIVE PASS PHARM INC.
XX
PI Chen H, Kilinski L, Le Bihan S;
XX
DR WPI; 2003-066798/06.
DR P-PSDB; ABG72423.
XX
PT Novel isolated ATP binding cassette transporter family polypeptide,
PT ABCA5, useful for treating disorders associated with aberrant or unwanted
PT ABCA5 transporter expression or activity.
XX
PS Claim 2; Fig 1; 52pp; English.
XX
CC The invention describes an isolated ATP binding cassette (ABC)
CC transporter family polypeptide (I), designated ABCA5. (I) or the
CC polynucleotide encoding it (II) are useful as targets for developing
CC modulating agents to regulate a variety of cellular processes,

Db 1741 ACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAAATGATTGGCATTTGTCCAC 1800
QY 1801 AGTTAGATATACACTTTTGATGTTTTGACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAA 1850
Db 1801 AGTTAGATATACACTTTTGATGTTTTGACAGTAGAAGAAAAATTTATCAATTTTGGCTTCAA 1850
QY 1861 TCAAAAGGGATACCAAGCCCAACATATATAACAAGAAGTCAGAAAGGTTTTTACTAGATTTAG 1920
Db 1861 TCAAAAGGGATACCAAGCCCAACATATATAACAAGAAGTCAGAAAGGTTTTTACTAGATTTAG 1920
QY 1921 ACATGCAGACTATCAAAAGATAACCAAGCTAAAAAATTAAGTGGTCAAAAAAGAAAGC 1980
Db 1921 ACATGCAGACTATCAAAAGATAACCAAGCTAAAAAATTAAGTGGTCAAAAAAGAAAGC 1980
QY 1981 TGTCATTAGGAATTGCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAAAGCCA 2040
Db 1981 TGTCATTAGGAATTGCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAAAGCCA 2040
QY 2041 CTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAAAGCCA 2100
Db 2041 CTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGAAAAAGCCA 2100
QY 2101 ATCGGTFGACAGTGTTCAGTACTCATTTTCANGGATGAAGCTGACATTTCTTGCGAGATAGGA 2160
Db 2101 ATCGGTFGACAGTGTTCAGTACTCATTTTCANGGATGAAGCTGACATTTCTTGCGAGATAGGA 2160
QY 2161 AAGCTGFGATATCACAAAGGAATGCTGAAATGTGTGGTCTTCAATGTTCTCCTCAAAAAGTA 2220
Db 2161 AAGCTGFGATATCACAAAGGAATGCTGAAATGTGTGGTCTTCAATGTTCTCCTCAAAAAGTA 2220
QY 2221 AATGGGGATCGGCTACCGCCCTGAGCATGTACATAGACAAAAATATTGTGCCACAGAAATCTC 2280
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Db 2401 TAGACAGTCAATTCAAATTTTGGGTGTCAATTTCTTATGGTGTTCATGACGACTTTGGAAG 2460
QY 2461 ACGTATTTTAAAGCTAGAAGTTGAAGCAGAAAAATTGACCAAGCAGATTATATAGTATTTA 2520
Db 2461 ACGTATTTTAAAGCTAGAAGTTGAAGCAGAAAAATTGACCAAGCAGATTATATAGTATTTA 2520
QY 2521 CTCAGCGCCACTGGAGGAAGAAATGGATTCAAATCTTTTGATGAAATGGAACAGAGCT 2580
Db 2521 CTCAGCGCCACTGGAGGAAGAAATGGATTCAAATCTTTTGATGAAATGGAACAGAGCT 2580
QY 2581 TACTTATTTCTTGAAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTTGGAAACAAC 2640
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QY 2641 AGATGATACAAATAGCAAAAGTTTCAATTTCTTTACCTTGAACGCTGAAAGTAAATCAGTGA 2700
Db 2641 AGATGATACAAATAGCAAAAGTTTCAATTTCTTTACCTTGAACGCTGAAAGTAAATCAGTGA 2700
QY 2701 GATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTTCAGATTTTATGTTTTGGTTC 2760
Db 2701 GATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTTCAGATTTTATGTTTTGGTTC 2760
QY 2761 ATCAGTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATTTCTAA 2820
Db 2761 ATCAGTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATTTCTAA 2820
QY 2821 AACCTGGAGACAAACCATATAAATACAAAAACAAGTCTGCTTCTTCAAAATTTCTGCT --- 2876

Db 2821 AACCTGGAGACAAACCATATAAATACAAAACAAGTCTGCTTCTTCAAAATTTCTGCTGGTG 2880
QY 2877 -----GACTCAGATATCAGTGATCTTATTAGCTTTTTTACAAAGCCAGAAACA 2922
Db 2881 AGAGTGTNNGTGAAGACTCAGATATCAGTGATCTTATAGCTTTTTTACAAAGCCAGAAACA 2940
QY 2923 TAAATGGTGACGATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGGCGCTT 2982
Db 2941 TAAATGGTGACGATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGGCGCTT 3000
QY 2983 TAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTGGAGCTGTTTTTCAACAGTACTATGG 3042
Db 3001 TAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTGGAGCTGTTTTTCAACAGTACTATGG 3060
QY 3043 TTTATTTCTTTACCTATATTAGTGAATATCATTTAGTAACTACTATCTTTATCATTTAAATG 3102
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Db 3121 TGACTGAAACCATCCAGATCTGGAGTACCCCATTTCTTTCAAGAAATTAATCTGATATAGTTT 3180
QY 3163 TTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGG- AATCATTTGTTACTGCAATGCCA 3221
Db 3181 TTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTAAGTCAATGCCA 3240
QY 3222 CCTTACTTTGCCATGGAAAAATGCAGAGAAATCATAAAGATCAAAAGCTTATATACTCAACTTAAA 3281
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QY 3282 CTTTCAGGCTTTTGGCCATCTGCATATTGGATTTGGACAAAGCTGTTGTTGATATCCCTTA 3341
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QY 3582 TTTATGGGATACACAAATTGCAACTATTCTTTCATTATGCTTTTGTATCATCATTTCCAATC 3641
Db 3570 TTTATGGGATACACAAATTGCAACTATTCTTTCATTATGCCCTTTGTATCATCATTTCCAATC 3629
QY 3642 TATCCACTTCTAGGTTGCCCTGATTTCTTTCATAAAGATTTTCTTGGAAAGAAATGTACGAAAA 3701
Db 3630 TATCCACTTCTAGGTTGCCCTGATTTCTTTCATAAAGATTTTCTTGGAAAGAAATGTACGAAAA 3689
QY 3702 AATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTTTATATCGCCTTACCTG 3761
Db 3690 AATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTTTATATCGCCTTACCTG 3749
QY 3762 CAGTGTACTGTGGATTTTCTTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCA 3821
Db 3750 CAGTGTACTGTGGATTTTCTTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCA 3809
QY 3822 ATAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAACGAAAGTCTAAAAATAGGAAGCTTCCA 3881
Db 3810 ATAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAACGAAAGTCTAAAAATAGGAAGCTTCCA 3869
QY 3882 GAACCAACCAAGCAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAA 3941
Db 3870 GAACCAACCAAGCAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAA 3929

QY 3942 GAGCTGATGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCAAT 4001
Db |||||
QY 3930 GAGCTGATGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCAAT 3989
Db |||||
QY 4002 AAAGAATATGATGACAAAGAAAGATTTCTTTTCAAGAAAGTAAAGAAAGTGGCAACT 4061
Db |||||
QY 3990 AAAGAATATGATGACAAAGAAAGATTTCTTTTCAAGAAAGTAAAGAAAGTGGCAACT 4049
Db |||||
QY 4062 AAATACATCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGT 4121
Db |||||
QY 4050 AAATACATCTCTTTCTGTGTGAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGT 4109
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QY 4122 GCTGGCAAAAGCACAAATTATTAAATATCTGGTTGGTGATATTGAACCAACTTCAGGCCAG 4181
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QY 4170 GTATTTTATGAGAGATTATTCTTCAGAGACAAGTGAAGATGATGATTCACTGAAGTGTATG 4229
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QY 4710 TGGATAGAAAACCTAGAAAGTAGACCGCCCTTCAAAGAGAAATTCAGTATATTTTCCCAAT 4769
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QY 4782 GCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAATTCCTAAGGAAGATGTT 4841
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QY 4770 GCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAATTCCTAAGGAAGATGTT 4829
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QY 4842 CAGTCCCTTTTCACAATCTTTTTTTTAAAGCTGGAAGAAAGTAAACATGCTTTTGCCATTGAA 4901
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QY 4830 CAGTCCCTTTTCACAATCTTTTTTTTAAAGCTGGAAGAAAGTAAACATGCTTTTGCCATTGAA 4889
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QY 4902 GAATATAGCTTTTCTCAAGCAACATTTGGAAAGAGTGTGTAAGTCACTAAAGAACAA 4961
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QY 5022 GAAGATAGAGTAGTATTTTGAATTTTGTATTGTTCCGTTCTGCTTACTGGGACTTCTTCTT 5081
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QY 5082 TTTCACTTAATTTTAACTTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACTGGAGAAC 5141
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QY 5070 TTTCACTTAATTTTAACTTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACTGGAGAAC 5129
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QY 5310 TGTGATTTAAAGGAATTTGTAATFAGAAATAGTTTATTATTTTAAAGTTATCTTTAAGTTTATGC 5369
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QY 5382 CATCTTCTTAAATAAGTACGTAATGTTTCCAATCTAAATAAAAAAATAATTTCATAACTAAT 5441
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Db |||||
QY 5442 GCATAGAAAAGATACATAAAGCAATGTGAAAGTT 5475
Db |||||
QY 5430 GCATAGAAAAGATACATAAAGCAATGTGAAAGTT 5463
Db |||||

RESULT 4
AAD33648
ID AAD33648 standard; cDNA; 6369 BP.
XX
AC AAD33648;
XX
DT 01-JUL-2002 (first entry)
XX Human TRICH-3 cDNA.
DE Human; transporter and ion channel; TRICH-3; transport disorder; angina;
XX amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder;
KW cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;
KW depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;
KW cell proliferated disorder; infertility; arteriosclerosis; gene therapy;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;
KW myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;
KW acquired immune deficiency syndrome; immunological disorder; scleroderma;
KW endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;
KW cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;
KW epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;
KW muscle disorder; stroke; dementia; anxiety; asthma; cirrhosis;
XX gene; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1238..6166
FT /*tag= a
FT /product= "Human TRICH-3 protein"
XX
PN WO200212340-A2.
XX
PD 14-FEB-2002.
XX
PF 01-AUG-2001; 2001WO-US024217.
XX
PR 03-AUG-2000; 2000US-0223269P.
PR 10-AUG-2000; 2000US-0224456P.
PR 18-AUG-2000; 2000US-0226410P.

QY 1357 TCTATCTTGATCAAGTCATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 1416
Db 2481 TCTATCTTGATCAAGTCATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTC 2540
QY 1417 TGAAGCCTTCAATTTGGTCAAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG 1476
Db 2541 TGAAGCCTTCAATTTGGTCAAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATG 2600
QY 1477 TTAATGGAAATATTTAGTTTATGTAATTTAGTGAGCCAGTTTCTTTCAGAAATTTGTAGGAA 1536
Db 2601 TTAATGGAAATATTTAGTTTATGTAATTTAGTGAGCCAGTTTCTTTCAGAAATTTGTAGGAA 2660
QY 1537 AAGAAGCCATAAGAAATTTAGTTTATGTAATTTAGTGAGCCAGTTTCTTTCAGAAATTTGTAGGAA 1596
Db 2661 AAGAAGCCATAAGAAATTTAGTTTATGTAATTTAGTGAGCCAGTTTCTTTCAGAAATTTGTAGGAA 2720
QY 1597 AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATTTACTGCCTTACTTTGGCC 1656
Db 2721 AGGCTTTGAGAAATTTGTCAATTTGACATATATGAGGGTCAGATTTACTGCCTTACTTTGGCC 2780
QY 1657 ACAGTGGAAACAGGAAGAGTACATTTGATGAATATTTCTTTGTGGACTGTGCCACCTTCTG 1716
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QY 1777 GAAAAATGATTGGCAATTTGTCCACAGTTAGATATACACTTTTGATGTTTTCAGAGTAGAG 1836
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QY 1837 AAAAAATTTATCAATTTTGGCTTCAATCAAGGGATACCAGCCAAACAATATAATACAAGAG 1896
Db 2961 AAAAAATTTATCAATTTTGGCTTCAATCAAGGGATACCAGCCAAACAATATAATACAAGAG 3020
QY 1897 TGCAGAAGGTTTTACTAGATTTAGACATGCGAGACTATCAAAGATAACCAAGCTAAAAAT 1956
Db 3021 TGCAGAAGGTTTTACTAGATTTAGACATGCGAGACTATCAAAGATAACCAAGCTAAAAAT 3080
QY 1957 TAAGTGGTGGTCAAAAAAGAAAGCTGTCAATTAGGAATTTGCTGTTTGGGAAACCCAAAGA 2016
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QY 2077 ATCTTTTAAATFACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATG 2136
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Db 3381 ACAAAATATGTGCCACAGAAATCTCTTTCTTCACTGGTTTAAACAACATATACCTGGAGCTA 3440
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Db 3501 AATTTTCAGGTTTTTCTGCCCTTAGACAGTCATTTCAAATTTGGGTGTCATTTCTTTATG 3560

QY 2437 GTGTTTCCATGACGACTTTTGGAAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAAAAATTG 2496
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Db 3681 CTTTTGATGAAATGGAAACAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGA 3740
QY 2617 GCACCATGAGCCTTTTGGAAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTACCT 2676
Db 3741 GCACCATGAGCCTTTTGGAAACAAACAGATGTATACAATAGCAAAAGTTTCATTTCTTACCT 3800
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Db 3801 TGAAACGCTGAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAG 3860
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Db 3861 TTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAAC 3920
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Db 3921 TTGTTCCAGACTTATATTTTCTAAAACTGGAGACAAACCAATATAAATACAAAACAAGTC 3980
QY 2857 TGCTTCTTCAAATTTCTGCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAAGCC 2916
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QY 2917 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTG 2976
Db 4041 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTG 4100
QY 2977 CGGCTTTAAATGTGATGCAATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA 3036
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Db 4161 CTATGGTTTATTTTACCTATATTTAGTGAATATCATTAGTAACCTACTATCTTTATCATT 4220
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Db 4521 TATATTTTATACTGTAAAGTTCCCTGCTGTGGTTTTTTTGGCTTATTTGGTTATGTTCCAT 4580
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RESULT 5
AAD37620
ID AAD37620 standard; cDNA; 5262 BP.
XX AAD37620;
XX AC
XX DT 10-SEP-2002 (first entry)
XX Human transporter protein cDNA #3.
DE Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application;
KW cosmetic application; polymorphism; ss.
XX Homo sapiens.
XX WO200231147-A2.
PN 18-APR-2002.
XX 04-OCT-2001; 2001WO-US031113.
PF 10-OCT-2000; 2000US-0239629P.
PR (LEXI-) LEXICON GENETICS INC.
XX Hu Y, Nepomnichy B;
XX WPI; 2002-454552/48.
DR XX

PT Novel nucleic acid molecule encoding novel human proteins, useful for
PT therapeutic, diagnostic and pharmacogenomic applications.
XX
PS Disclosure; Page 45-46; 46pp; English.
XX
CC The present sequence is a cDNA coding for novel human protein (NHP),
CC human transporter protein. NHPs shares structural similarity with the
CC mammalian ATP-binding cassette (ABC) transporters and multidrug
CC resistance transporters. NHP polynucleotides are useful for the
CC therapeutic, diagnostic and pharmacogenomic applications. They are used
CC for detecting and treating mental disorders and cancers. They are also
CC used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and
CC disorders, and cosmetic or nutraceutical applications
XX
SQ Sequence 5262 BP; 1615 A; 888 C; 1012 G; 1743 T; 0 U; 4 Other;
Query Match 91.6%; Score 5014.6; DB 6; Length 5262;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5014; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 97 AGGTTTATTCAGAAAACATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 156
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QY 238 AGGTTTATTCAGAAAACATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 297
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QY 157 GAACACCTTCTACTGAAGAATTACTTAAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGG 216
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QY 4417 CAGGAATCAAAACGAAAGTTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTACTT 4476
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Dd 4558 CAGGAATCAAAACGAAAGTTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTACTT 4617
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Dd 4618 TGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAA 4677
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Dd 4678 TTCGAACTGCATTTTAAACAGAAAGCGGGCTGCTATTCTGACCACCTCACTATATGGAGG 4737
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QY 4657 GAACAGTACAACATCTAAAGAGTAAATTTGGAAAGCGCTACTTTTGGAAATTAATTTGA 4716
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Dd 4858 AGGACTGGATAGAAAACCTAGAAAGTAGACCGCCCTTCAAAGAGAAATTCAGTATATTTCC 4917
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QY 4777 CAAATGCAAGCCGTCAGGAAAGTTTCTTCTATTTGGCTTATAAAATCCTAAGGAAG 4836
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Dd 4918 CAAATGCAAGCCGTCAGGAAAGTTTCTTCTATTTGGCTTATAAAATCCTAAGGAAG 4977
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QY 4837 ATGTCAGTCCCTTTTCACAAATCTTTTAAAGCTGGAAGAAAGCTAAACATGCTTTTGCCA 4896
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Dd 4978 ATGTCAGTCCCTTTTCACAAATCTTTTAAAGCTGGAAGAAAGCTAAACATGCTTTTGCCA 5037
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Dd 5038 TTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTGTAGAACTCACTAAAG 5097
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QY 4957 AACAGAGGAGGAAGATATAGTTGTGGAACCTTTAAACAGCACACCTTTGTTGGGAACGAA 5016
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QY 5077 TTCTTTTTCACCTTAATTTTAACTTTGGTTTAAAAAGTTTTT 5117
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RESULT 6

AAD37618

ID AAD37618 standard; cDNA; 4929 BP.

XX

AC AAD37618;

XX

DT 10-SEP-2002 (first entry)

```
XX Human transporter protein cDNA #1.
DE
XX Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application; gene;
KW cosmetic application; polymorphism; ss.
XX Homo sapiens.
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    site"
    2878
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PN
XX 18-APR-2002.
PD
XX
XX 04-OCT-2001; 2001WO-US031113.
PF
XX
XX 10-OCT-2000; 2000US-0239629P.
PR
XX (LEXI-) LEXICON GENETICS INC.
PA
XX Hu Y, Nepomnichy B;
PI
XX WPI; 2002-454552/48.
DR P-PSDB; AAE23656.
DR
XX Novel nucleic acid molecule encoding novel human proteins, useful for
    therapeutic, diagnostic and pharmacogenomic applications.
    Claim 1; Page 34-35; 46pp; English.
XX
CC The present sequence is a cDNA coding for novel human protein (NHP),
    human transporter protein. NHPs shares structural similarity with the
    mammalian ATP-binding cassette (ABC) transporters and multidrug
    resistance transporters. NHP polynucleotides are useful for the
    therapeutic, diagnostic and pharmacogenomic applications. They are used
    for detecting and treating mental disorders and cancers. They are also
    used in gene therapy. NHP polypeptides are useful for diagnosis, drug
    screening, clinical trial monitoring, treatment of diseases and
    disorders, and cosmetic or nutraceutical applications
XX
SQ Sequence 4929 BP; 1544 A; 827 C; 950 G; 1604 T; 0 U; 4 Other;
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Query Match 89.9%; Score 4922.6; DB 6; Length 4929;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 4922; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 114 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 173
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Dd 1 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 60

QY 174 AATTACTTAATTAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCACTA 233
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Dd 61 AATTACTTAATTAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCACTA 120

QY	234	TTTTTTTATATTTGGTTAAATATTAATTTAGCATGATGCATCCAAATAAGAAATATGAAGAA	293
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QY	294	GTGCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTTAATCTAATTTCTTTGGA	353
Db	181	GTGCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTTAATCTAATTTCTTTGGA	240
QY	354	TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA	413
Db	241	TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA	300
QY	414	CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC	473
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QY	474	TCTAAGCCGAGCAACTTTGTAGTGTGGTTTTTCAAAGACTCCATGTCTTATGAACCTTCGT	533
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Db	421	TTTTTTTCTGTATGATTCAGTATCTTCTATTATATGGATTCAAGAGCTGGCTGTTC	480
QY	594	AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTTCAGTTTTCAAGTTTTACAAGCATCCATA	653
Db	481	AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTTCAGTTTTCAAGTTTTACAAGCATCCATA	540
QY	654	GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT	713
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QY	714	AAAGCTGTTATTAATGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA	773
Db	601	AAAGCTGTTATTAATGGAGAACTGCTGTTGTAGAAATAGATACCTTTTCCCGAGGAGTA	660
QY	774	ATTTTAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACCTTTTGGCAATTCAATATC	833
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Db	841	ATGGCAGTCATTGCGACAGCTTCTTTGTTATTTTCCCTCAAAGTAGCAGCATTTGTGATAATT	900
QY	1014	CTGCTTTTTTTTCCCTTTATGGATTATCATCTGTATTTTTTTTGCCTTTAATGCTGACACCTCTT	1073
Db	901	CTGCTTTTTTTTCCCTTTATGGATTATCATCTGTATTTTTTTTGCCTTTAATGCTGACACCTCTT	960
QY	1074	TTTTAAAAATCAAAACATGTGGGAATAGTTGAAATTTTTTTTGTACTGTGGCTTTTGGATT	1133
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QY	1134	ATTGGCCTTATGATAATCCCTCATAGAAAGTTTTTCCCAAATCGTTAGTGTGGCTTTTTCAGT	1193
Db	1021	ATTGGCCTTATGATAATCCCTCATAGAAAGTTTTTCCCAAATCGTTAGTGTGGCTTTTTCAGT	1080
QY	1194	CCTTTCTGTCACTGTACTTTTGTGATTGGTATTGACAGGTCATGCATTTAGAAGATTTT	1253
Db	1081	CCTTTCTGTCACTGTACTTTTGTGATTGGTATTGACAGGTCATGCATTTAGAAGATTTT	1140
QY	1254	AATGAAGGTGCTTCAATTTTCAAATTTGACTGCAGGCCCATATACCTCTCTAATATTACAAT	1313
Db	1141	AATGAAGGTGCTTCAATTTTCAAATTTGACTGCAGGCCCATATACCTCTCTAATATTACAAT	1200
QY	1314	ATCATGCTCACACTTAATAGATATTTCTATGTCTCTTTGGCTGTCTATCTTGTATCAAGTC	1373

Db	1201	ATCATGCTCACACTTAATAGTATATCTATATGCTCTCTTGGCTGTCTATCTTGTATCAAGTC	1260
Qy	1374	ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCTATATTGG	1433
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Qy	1494	TTTAGTGAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAACCCATFAAGAATT	1553
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Qy	1554	AGTGGTATTCAGAAAGACATACAGAAAAGAGGTGAAAATGTGGAGGCTTTGAGAAAATTTG	1613
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Qy	1614	TCATTTGACATATATGAGGGTCAGATTACTGCTTACTTTGGCCACAGTGGAAACAGGAAAAG	1673
Db	1501	TCATTTGACATATATGAGGGTCAGATTACTGCTTACTTTGGCCACAGTGGAAACAGGAAAAG	1560
Qy	1674	AGTACATTTGATGAATATTTCTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCACTCTATA	1733
Db	1561	AGTACATTTGATGAATATTTCTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCACTCTATA	1620
Qy	1734	TATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAATGATGGGCATT	1793
Db	1621	TATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAATGATGGGCATT	1680
Qy	1794	TGTCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAGAAAATTTATCAATTTTG	1853
Db	1681	TGTCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAGAAAATTTATCAATTTTG	1740
Qy	1854	GCTTCAATCAAAGGGATACCAGCCAAACAATATAATACAAGPAGTGCAGAACGTTTACTA	1913
Db	1741	GCTTCAATCAAAGGGATACCAGCCAAACAATATAATACAAGPAGTGCAGAACGTTTACTA	1800
Qy	1914	GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA	1973
Db	1801	GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA	1860
Qy	1974	AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA	2033
Db	1861	AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA	1920
Qy	2034	CCACAGCTGGAAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA	2093
Db	1921	CCACAGCTGGAAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA	1980
Qy	2094	AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGTGCATCTCTTGCA	2153
Db	1981	AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGTGCATCTCTTGCA	2040
Qy	2154	GATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTGGTCTTCAATGTTTCTCTC	2213
Db	2041	GATAGGAAAGCTGTGATATCACAAGGAATGCTGAAATGTGTGGTCTTCAATGTTTCTCTC	2100
Qy	2214	AAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAAATATTGTGCCACA	2273
Db	2101	AAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAAATATTGTGCCACA	2160
Qy	2274	GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTAACAACAGAAT	2333
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Qy	2334	GACCAACAACCTTGTGTATAGCTTGCCCTTCAAGGACATGGACAAAATTTTCAAGGTTTGT	2393
Db	2221	GACCAACAACCTTGTGTATAGCTTGCCCTTCAAGGACATGGACAAAATTTTCAAGGTTTGT	2280
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Db 4921 GTATTTTGA 4929
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RESULT 7

ABS57750
ID ABS57750 standard; cDNA; 4917 BP.

XX
AC ABS57750;

XX 04-FEB-2003 (first entry)

XX Coding sequence of human ATP binding cassette ABCA5 transporter #1.

XX Human; ATP binding cassette; ABC; ABCA5; transporter;
KW neurotoxin transport; beta-amyloid peptide; chromosome mapping;
KW blood brain barrier transport; tissue typing; predictive medicine;
KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.
XX Homo sapiens.

XX
FH Key Location/Qualifiers
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FT /note= "ATP binding cassette (ABC) A5 transporter"
FT /transl_except= (pos:3160..3162, aa:Ser)

PN US2002123107-A1.

XX 05-SEP-2002.

PF 01-MAR-2002; 2002US-00090458.

PR 02-MAR-2001; 2001US-0272885P.

XX (ACTI-) ACTIVE PASS PHARM INC.

XX Chen H, Kilinski L, Le Bihan S;

DR WPI; 2003-066798/06.

DR P-PSDB; ABG72423.

XX Novel isolated ATP binding cassette transporter family polypeptide.

PT ABCA5, useful for treating disorders associated with aberrant or unwanted
PT ABCA5 transporter expression or activity.
XX
PS Claim 2; Fig 1; 52pp; English.
XX
CC The invention describes an isolated ATP binding cassette (ABC)
CC transporter family polypeptide (I), designated ABCA5. (I) or the
CC polynucleotide encoding it (II) are useful as targets for developing
CC modulating agents to regulate a variety of cellular processes,
CC particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC (BBB), as targets for developing modulating agents of multi-drug
CC resistance, as diagnostic and therapeutic tools, or to treat disorders
CC associated with aberrant or unwanted ABCA5 transporter expression or
CC activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC screening assays, detection assays (e.g., chromosomal mapping, tissue
CC typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC (III) are useful as reagents or targets in assays applicable to treatment
CC and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC -hybrid or three-hybrid assay; and to identify other proteins which bind
CC to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC activity; to locate gene regions associated with genetic disease or to
CC associate ABCA5 with the disease, to identify an individual from a minute
CC biological sample (tissue typing), and to aid in forensic identification
CC of the biological sample. This sequence encodes a novel human ATP binding
CC cassette (ABC) A5 transporter
XX
SQ Sequence 4917 BP; 1540 A; 821 C; 955 G; 1599 T; 0 U; 2 Other;

Query Match 87.9%; Score 4811.6; DB 7; Length 4917;

Best Local Similarity 98.9%; Pred. No. 0;

Matches 4894; Conservative 0; Mismatches 4; Indels 50; Gaps 3;

QY 114 ATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG 173
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Db 1 ATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG 60
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QY 174 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 233
|||||
Db 61 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 120
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|||||
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|||||
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Db 421 TTTTCTTCTGATATGATTCAGTATCTTCTATTATATATGGAATCAAGAGCTGGCTGTTCA 480
|||||
QY 594 AAATCATGTGAGGTGCTCAGTACTGGTCTCTCAGTTTTCACAGTTTTCACAGCATCCATA 653
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Db 481 AAATCATGTGAGGTGCTCAGTACTGGTCTCTCAGTTTTCACAGTTTTCACAGCATCCATA 540
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QY 654 GATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGAAGGAGCTGGAGTCAACT 713
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QY 714 AAAGCTGTTATTATGGGAGAACTGCTGTGTGTAGAAATAGATACCTTTCCCGAGGAGTA 773
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QY 1014 CTGCTTTTCTTCTTATGGAATATCATCTGTAATTTTCTTAAATGCTGACACCTCTT 1073
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QY 1074 TTTAAAAAATCAAAACATGCGGAATAGTTGAATTTTGTGTTACTGTTGGCTTTTGGATT 1133
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QY 1134 ATTTGGCTTATGATAATCCTCATAGAAAGTTTCCCAAAATCGTTAGTGTGGCTTTTCACT 1193
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QY 2034 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATGTTGGAATCTTTTAAAAATACAGA 2093
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Db 2281 TCTGCCCTAGACAGTCAATCAAAATTTGGGTGTCATTTCTTATGGTGTTCCTCATGACGACT 2340
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Db 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAATGGAA 2460
QY 2574 CAGAGCTTACTTATTTCTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 2633
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QY 2634 AAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTTACCTTGAAACGTGAAAGTAA 2693
Db 2521 AAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTTACCTTGAAACGTGAAAGTAA 2580
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QY 5015 AACACAAGATAGAGTAGTAGTATTTTGA 5042
Db 4890 AACACAAGATAGAGTAGTAGTATTTTGA 4917

RESULT 8
AAD37619
ID AAD37619 standard; cDNA; 4785 BP.
XX
AC AAD37619;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human transporter protein cDNA #2.
XX
KW Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application; gene;
KW cosmetic application; polymorphism; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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PN WO200231147-A2.
XX
PD 18-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031113.
XX
PR 10-OCT-2000; 2000US-0239629P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B;
XX
DR WPI; 2002-454552/48.
DR P-PSDB; AAE23657.
XX
PT Novel nucleic acid molecule encoding novel human proteins, useful for
PT therapeutic, diagnostic and pharmacogenomic applications.
XX
PS Claim 1; Page 39-41; 46pp; English.
XX
CC The present sequence is a cDNA coding for novel human protein (NHP),
CC human transporter protein. NHPs shares structural similarity with the
CC mammalian ATP-binding cassette (ABC) transporters and multidrug
CC resistance transporters. NHP polynucleotides are useful for the
CC therapeutic, diagnostic and pharmacogenomic applications. They are used
CC for detecting and treating mental disorders and cancers. They are also
CC used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and
CC disorders, and cosmetic or nutraceutical applications
XX
SQ Sequence 4785 BP; 1489 A; 807 C; 917 G; 1568 T; 0 U; 4 Other;

Query Match 86.9%; Score 4759; DB 6; Length 4785;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 4759; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
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QY 414 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC 473
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Db 721 GTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT 780
QY 894 GCCTTTTGGCTTCTCTGGTTCTTCTATATATACAAGTTTAAATTTTCTTATGTCCCTTCTT 953
Db 781 GCCTTTTGGCTTCTCTGGTTCTTCTATATAWACAAGTTTAAATTTTCTTATGTCCCTTCTT 840
QY 954 ATGGCAGTCATGCGACAGCTTCTTGTGTTATTTCTCTCAAAGTAGCAGCATTTGTGATATT 1013
Db 841 ATGGCAGTCATGCGACAGCTTCTTGTGTTATTTCTCTCAAAGTAGCAGCATTTGTGATATT 900
QY 1014 CTGCTTTTCTTCTTTATGGATTATCATCTGTATTTTCTTTTAAATGCTGACACCTCTT 1073
Db 901 CTGCTTTTCTTCTTTATGGATTATCATCTGTATTTTCTTTTAAATGCTGACACCTCTT 960
QY 1074 TTTAAAAAATCAAAACATGTGGGATAGTTGAATTTTGTGTTACTGTGGCTTTTGGATT 1133
Db 961 TTTAAAAAATCAAAACATGTGGGATAGTTGAATTTTGTGTTACTGTGGCTTTTGGATT 1020

QY 1134 ATTGGCCTTATGATAATCCTCATAGAAAAGTTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 1193
Db 1021 ATTGGCCTTATGATAATCCTCATAGAAAAGTTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 1080
QY 1194 CCTTCTGTCACTGTACTCTTTTGTGATTGGTATTGCAACAGGTTCATGCATTTAGAAGATTTT 1253
Db 1081 CCTTCTGTCACTGTACTCTTTTGTGATTGGTATTGCAACAGGTTCATGCATTTAGAAGATTTT 1140
QY 1254 AATGAAGGTGCTTCAATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAAATATTACAATT 1313
Db 1141 AATGAAGGTGCTTCAATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAAATATTACAATT 1200
QY 1314 ATCATGTCTCACACTTAATAGTATATTCTATGTCCCTTTGGCTGTCTATCTTGTATCAAGTC 1373
Db 1201 ATCATGTCTCACACTTAATAGTATATTCTATGTCCCTTTGGCTGTCTATCTTGTATCAAGTC 1260
QY 1374 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1433
Db 1261 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1320
QY 1434 TCAAAGAGCAAAAAGAAATTAAGAGGAGTTATCAGAGGGCAANTGTTAAATGGAATATTAGT 1493
Db 1321 TCAAAGAGCAAAAAGAAATTAAGAGGAGTTATCAGAGGGCAANTGTTAAATGGAATATTAGT 1380
QY 1494 TTTAGTGAAATTAATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAAAGCCATAAGAAATT 1553
Db 1381 TTTAGTGAAATTAATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAAAGCCATAAGAAATT 1440
QY 1554 AGTGGTATTTCAGAAGACATACAGAAAAGAGGGTGAAAATGTGGAGGCTTTGAGAAAATTTG 1613
Db 1441 AGTGGTATTTCAGAAGACATACAGAAAAGAGGGTGAAAATGTGGAGGCTTTGAGAAAATTTG 1500
QY 1614 TCATTTGACATATATGAGGGTCAGATTACTGCTTACTTGCCACCTCTGATGGGTTTGCATCTATA 1733
Db 1501 TCATTTGACATATATGAGGGTCAGATTACTGCTTACTTGCCACCTCTGATGGGTTTGCATCTATA 1620
QY 1674 AGTACATTGATGAATATTCTTTGTGGACTCTGCCACCTCTGATGGGTTTGCATCTATA 1733
Db 1561 AGTACATTGATGAATATTCTTTGTGGACTCTGCCACCTCTGATGGGTTTGCATCTATA 1620
QY 1734 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAATGATGGGCATT 1793
Db 1621 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAATGATGGGCATT 1680
QY 1794 TGTCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAGAAAATTTATCAATTTTG 1853
Db 1681 TGTCCACAGTTAGATATACACTTTTGATGTTTGTGACAGTAGAAGAAAATTTATCAATTTTG 1740
QY 1854 GCTTCAATCAAAGGGATACCAGCCAAACAATATAATACAGAAGTGCAGAAGGTTTACTA 1913
Db 1741 GCTTCAATCAAAGGGATACCAGCCAAACAATATAATACAGAAGTGCAGAAGGTTTACTA 1800
QY 1914 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTTAAAAAATTAAGTGGTGGTCAAAAA 1973
Db 1801 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTTAAAAAATTAAGTGGTGGTCAAAAA 1860
QY 1974 AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 2033
Db 1861 AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 1920
QY 2034 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATAACAGA 2093
Db 1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATAACAGA 1980
QY 2094 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTTGCA 2153
Db 1981 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTTGCA 2040
QY 2154 GATAGGAAAGCTGTGATATCACAGAAGGAATGCTGAAAATGTTGGTCTTTCATGTTTCCTC 2213
Db 2041 GATAGGAAAGCTGTGATATCACAGAAGGAATGCTGAAAATGTTGGTCTTTCATGTTTCCTC 2100
QY 2214 AAAAGTAAATGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCCACA 2273

Db 2101 AAAAGTAAATGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCCACA 2160
QY 2274 GAATCTCTTTCTTCACTGGTTAAAAACAACATATACCTGGAGCTACTTTATTACACAGAAAT 2333
Db 2161 GAATCTCTTTCTTCACTGGTTAAAAACAACATATACCTGGAGCTACTTTATTACACAGAAAT 2220
QY 2334 GACCAACAACTTGTGTATAGTTGCCCTTTCAAGGACATGGACAAAATTTTCAGGTTTGTTT 2393
Db 2221 GACCAACAACTTGTGTATAGTTGCCCTTTCAAGGACATGGACAAAATTTTCAGGTTTGTTT 2280
QY 2394 TCTGCCCTAGACAGTCATTCAAAATTTGGGTGTCAITTTTATGGTGTTCATTCATGACGACT 2453
Db 2281 TCTGCCCTAGACAGTCATTCAAAATTTGGGTGGCATTTCTTATGGGTTCATTCATGACGACT 2340
QY 2454 TTGGAAGACGTATTTTAAAGCTAGAAAGTTTGAAGCAGAAAATTTGACCAAGCAGATTATAGT 2513
Db 2341 TTGGAAGACGTATTTTAAAGCTAGAAAGTTTGAAGCAGAAAATTTGACCAAGCAGATTATAGT 2400
QY 2514 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAATCTTTTGTATGAAATGGAA 2573
Db 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAAATCTTTTGTATGAAATGGAA 2460
QY 2574 CAGAGCTTACTTATCTTTCTGAAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 2633
Db 2461 CAGAGCTTACTTATCTTTCTGAAAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTGG 2520
QY 2634 AAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTTACCTTGAAACGTTGAAAAGTAAA 2693
Db 2521 AAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTTACCTTGAAACGTTGAAAAGTAAA 2580
QY 2694 TCAGTGAGATCAGTGTTCCTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTT 2753
Db 2581 TCAGTGAGATCAGTGTTCCTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTT 2640
QY 2754 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCTCATCAAACTTGTTCAGACTTATAT 2813
Db 2641 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCTCATCAAACTTGTTCAGACTTATAT 2700
QY 2814 TTTTCTAAAAACCTGGAGACAACCCACATAAATACAAAAACAAGTCTGCTTCTTCAAAAATCT 2873
Db 2701 TTTTCTAAAAACCTGGAGACAACCCACATAAATACAAAAACAAGTCTGCTTCTTCAAAAATCT 2760
QY 2874 GCTGACTCAGATATCAGTGATCTTTATTAGCTTTTTCACAAGCCAGAACATAATGTTGACG 2933
Db 2761 GCTGACTCAGATATCAGTGATCTTTATTAGCTTTTTCACAAGCCAGAACATAATGTTGACG 2820
QY 2934 ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGGGCTTTTAAATGTTGATG 2993
Db 2821 ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGGGCTTTTAAATGTTGATG 2880
QY 2994 CATTAGAAAAGGACTATGTTTGTGACGCTGTTTTCACACAGTACTATGGTTTATTTCTTTA 3053
Db 2881 CATTAGAAAAGGACTATGTTTGTGACGCTGTTTTCACACAGTACTATGGTTTATTTCTTTA 2940
QY 3054 CCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCATTTTAAATGTGACTGAAACC 3113
Db 2941 CCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCATTTTAAATGTGACTGAAACC 3000
QY 3114 ATCCAGATCTGGAGTACCCCAATCTTTCAAGAAAATTAATGATATAGTTTAAAAATTGAG 3173
Db 3001 ATCCAGATCTGGAGTACCCCAATCTTTCAAGAAAATTAATGATATAGTTTAAAAATTGAG 3060
QY 3174 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAATGCCACCTTACTTTGCC 3233
Db 3061 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAATGCCACCTTACTTTGCC 3120
QY 3234 ATGGAATAATGCAGAGAATCATAGATCAAAAGCTTATACTCAACTTAAACTTTCAGGCTCT 3293
Db 3121 ATGGAATAATGCAGAGAATCATAGATCAAAAGCTTAYACTCAACTTAAACTTTCAGGCTCT 3180
QY 3294 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTT 3353

Db 3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTT 3240
QY 3354 CTTATTTTGTGCTAGGAAGCTTATTCGCAATTCATATATGGAATTATATTTTATACTGTA 3413
Db 3241 CTTATTTTGTGCTAGGAAGCTTATTCGCAATTCATATATGGAATTATATTTTATACTGTA 3300
QY 3414 AAGTTCCCTGCTGCTGTTTTCCTTATGTTTATGTTCCATCAGTTATTTCTGTTCACT 3473
Db 3301 AAGTTCCCTGCTGCTGTTTTCCTTATGTTTATGTTCCATCAGTTATTTCTGTTCACT 3360
QY 3474 TATATTCCTTCTTTTACCTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCATTTATC 3533
Db 3361 TATATTCCTTCTTTTACCTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCATTTATC 3420
QY 3534 TATTTCTGTCGAGCGTTGGCTTGTATGCAATCACTGAAATAACTTTCTTTATGGGATAC 3593
Db 3421 TATTTCTGTCGAGCGTTGGCTTGTATGCAATCACTGAAATAACTTTCTTTATGGGATAC 3480
QY 3594 ACAATTCGAATATTCTTTCATTTATGCTTTTGTATCATCATTCCTCAATCTATCCACTTCTA 3653
Db 3481 ACAATTCGAATATTCTTTCATTTATGCTTTTGTATCATCATTCCTCAATCTATCCACTTCTA 3540
QY 3654 GGTTCCTGATTTCTTTTCATAAAGATTCTTGGAAAGATGACGAAAAAATGTGGACACC 3713
Db 3541 GGTTCCTGATTTCTTTTCATAAAGATTCTTGGAAAGATGACGAAAAAATGTGGACACC 3600
QY 3714 TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCCCTTACCTGCAGTGTACTG 3773
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QY 3774 TGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGAT 3833
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QY 3834 CCCTTTTTCAGAAACCTTTTCAACGAAAGTCTAAAAATAGGAAGCTTCCAGAACCCAGAC 3893
Db 3721 CCCTTTTTCAGAAACCTTTTCAACGAAAGTCTAAAAATAGGAAGCTTCCAGAACCCAGAC 3780
QY 3894 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGTCAAAGAGCTGATGGGT 3953
Db 3781 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGTCAAAGAGCTGATGGGT 3840
QY 3954 TGCCAGTGTGTGAGGAGAAACCATCCATTTATGTCAGCAATTTGCATAAAGAAATATGAT 4013
Db 3841 TGCCAGTGTGTGAGGAGAAACCATCCATTTATGTCAGCAATTTGCATAAAGAAATATGAT 3900
QY 4014 GACAAGAAAGATTTCTTCTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 4073
Db 3901 GACAAGAAAGATTTCTTCTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 3960
QY 4074 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGC 4133
Db 3961 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGC 4020
QY 4134 ACAATTAATAATTTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 4193
Db 4021 ACAATTAATAATTTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 4080
QY 4194 GATTATTTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAAGTATGGGTACTGTCTCT 4253
Db 4081 GATTATTTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAAGTATGGGTACTGTCTCT 4140
QY 4254 CAGATAAACCCCTTTGTGGCCAGATACATTCAGGAACATTTTGAATTTATGGAGCT 4313
Db 4141 CAGATAAACCCCTTTGTGGCCAGATACATTCAGGAACATTTTGAATTTATGGAGCT 4200
QY 4314 GTCAAAGGAATGAGTGCAGATGACATGAAAGAGTCAATAAGTCAATAACACATGCACCT 4373
Db 4201 GTCAAAGGAATGAGTGCAGATGACATGAAAGAGTCAATAAGTCAATAACACATGCACCT 4260
QY 4374 GATTTAAAGAACATCTTCAGAGACTGTAAAGAAACTACCTGCAGGAATCAAAACGAAAG 4433
Db 4261 GATTTAAAGAACATCTTCAGAGACTGTAAAGAAACTACCTGCAGGAATCAAAACGAAAG 4320

QY 4434 TTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4493
Db 4321 TTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4380
QY 4494 ACAGGTATGGATCCCAAGCCAAACAGACACATGTGGCGAGCAATTCGAACTGCATTTAA 4553
Db 4381 ACAGGTATGGATCCCAAGCCAAACAGACACATGTGGCGAGCAATTCGAACTGCATTTAA 4440
QY 4554 AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGGAGAGGCAGAGGCTGTCTGT 4613
Db 4441 AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGGAGAGGCAGAGGCTGTCTGT 4500
QY 4614 GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA 4673
Db 4501 GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA 4560
QY 4674 AAGAGTAAATTTGGAAGAGGCTACTTTTGGAAATTTAAATTTGAAGGACTGGATAGAAAC 4733
Db 4561 AAGAGTAAATTTGGAAGAGGCTACTTTTGGAAATTTAAATTTGAAGGACTGGATAGAAAC 4620
QY 4734 CTAGAAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAG 4793
Db 4621 CTAGAAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAG 4680
QY 4794 GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCCCTTTTCA 4853
Db 4681 GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCCCTTTTCA 4740
QY 4854 CAATCTTTTTTAAAGCTGGAAGAGCT 4880
Db 4741 CAATCTTTTTTAAAGCTGGAAGAGGT 4767

RESULT 9

ADA53416
ID ADA53416 standard; cdna; 3268 BP.

XX
AC ADA53416;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human coding sequence, SEQ ID 984.

XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease; gene; ss.

OS Homo sapiens.

XX EPI293569-A2.

XX 19-MAR-2003.

XX 21-MAR-2002; 2002EP-00006586.

XX 14-SEP-2001; 2001JP-00328381.

PR 24-JAN-2002; 2002US-0350435P.

XX (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX
DR WPI; 2003-395539/38.
DR P-PSDS; ADA55055.

XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.

PS	Claim 1; SEQ ID NO 984; 205pp; English.	
XX	The present invention relates to novel human secretory or membrane proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-ADA54071). The coding sequences are useful in the gene therapy of diseases caused by abnormalities of the proteins, e.g. cancer, inflammatory diseases, osteoporosis or neurological disease.	
XX		
SQ	Sequence 3268 BP; 1022 A; 540 C; 622 G; 1084 T; 0 U; 0 Other;	
	Query Match 58.0%; Score 3175.8; DB 7; Length 3268;	
	Best Local Similarity 98.8%; Pred. No. 0;	
	Matches 3223; Conservative 0; Mismatches 7; Indels 33; Gaps 1;	
QY	2205 ATGTTCCCAAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATAT 2264	3072 ATTAGTAACTACTATCTTTTATCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACC 3131
Db	6 ATGTTCCCAAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATAT 65	906 ATTAGTAACTACTATCTTTTATCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACC 965
QY	2265 TGTGCCACAGAAATCTTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTA 2324	3132 CCATTCITTTCAAGAAATTACTGTATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCT 3191
Db	66 TGTGCCACAGAAATCTTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTA 125	966 CCATTCITTTCAAGAAATTACTGTATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCT 1025
QY	2325 CAACAGAAATGACCAACAACCTTGTGTATAGCTTGCCTTTCAAGGACATGGACAATTTTCA 2384	3192 TTGCTTGGAAATCATTGTTACTGCAATGCCACCTTACTTTGCCATGGAAAAATGCAGAGAA 3251
Db	126 CAACAGAAATGACCAACAACCTTGTGTATAGCTTGCCTTTCAAGGACATGGACAATTTTCA 185	1026 TTGCTTGGAAATCATTGTTACTGCAATGCCACCTTACTTTGCCATGGAAAAATGCAGAGAA 1085
QY	2385 G-----GTTTGGTTTCTGCCCTAGACATCAT 2411	3252 CATAAGATCAAAAGCTTATATCTCAACTTAAACTTTTCAGGTCCTTTTGCCATCTGCATATTGG 3311
Db	186 GGAATTGCTTGATAGACAAAAGGATGTTATTGATGTTTGTGTTTCTGCCCTAGACATCAT 245	1086 CATAAGATCAAAAGCTTATATCTCAACTTAAACTTTTCAGGTCCTTTTGCCATCTGCATATTGG 1145
QY	2412 TCAAAATTTGGGTGTCAATTTCTTTATGGTGTTCCTCATGACGACTTTGGAAGACGTAATTTTA 2471	3312 ATTTGGACAAGCTGTTGTTGATATCCCTTATTTTATCTTATTTTATCTTCTTATTTGATGCTAGGA 3371
Db	246 TCAAAATTTGGGTGTCAATTTCTTTATGGTGTTCCTCATGACGACTTTGGAAGACGTAATTTTA 305	1146 ATTTGGACAAGCTGTTGTTGATATCCCTTATTTTATCTTCTTATTTTATTTGATGCTAGGA 1205
QY	2472 AAGCTAGAAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGATTTTACTCAGCAGCCCA 2531	3372 AGCTTATTGGCAATTCATTATGGATATATTTTATATCTGFAAAGTTTCTTGTCTGTGGTT 3431
Db	306 AAGCTAGAAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGTGATTTTACTCAGCAGCCCA 365	1206 AGCTTACTGGCATTTTCATTATGGATATATTTTATATCTGFAAAGTTTCTTGTCTGTGGTT 1265
QY	2532 CTGGAGGAAGAAATGGATTCAAATCTTTTGTAGTAAATGGAAACAGAGCTTACTTATCTT 2591	3432 TTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACTTATATTGCTTCTTTTCACC 3491
Db	366 CTGGAGGAAGAAATGGATTCAAATCTTTTGTAGTAAATGGAAACAGAGCTTACTTATCTT 425	1266 TTTTGCCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACTTATATTGCTTCTTTTCACC 1325
QY	2592 TCTGAAACCAAGGCTTCTCTAGTGAGCACCATTAGCCCTTTGGAAACAACAGATGTATACA 2651	3492 TTTAAGAAAAATTTTAAATACCAAAGAAATTTTGGTCATTTATCTTCTGTGGCAGCGTTG 3551
Db	426 TCTGAAACCAAGGCTTCTCTAGTGAGCACCATTAGCCCTTTGGAAACAACAGATGTATACA 485	1326 TTTAAGAAAAATTTTAAATACCAAAGAAATTTTGGTCATTTATCTTCTGTGGCAGCGTTG 1385
QY	2652 ATAGCAAAAGTTTCATTTCTTTACCTTGAACCGTGAAGFAAATCAGTGAGATCAGTGTG 2711	3552 GCTTGTATTGCAATCACCTGAAATAAATCTTTTATGGGATACACAATTGCAACTATTCTT 3611
Db	486 ATAGCAAAAGTTTCATTTCTTTACCTTGAACCGTGAAGFAAATCAGTGAGATCAGTGTG 545	1386 GCTTGTATTGCAATCACCTGAAATAAATCTTTTATGGGATACACAATTGCAACTATTCTT 1445
QY	2712 CTTCTGCTTTTAATTTTTCACAGTTTCAGATTTTATGTTTTTGGTTTCATCACTCTTTT 2771	3612 CATTTATGCTTTTGTATCATCATTTCCAATCTATCCACTTCTAGGTTGCCGTGATTTCTTTC 3671
Db	546 CTTCTGCTTTTAATTTTTCACAGTTTCAGATTTTATGTTTTTGGTTTCATCACTCTTTT 605	1446 CATTTATGCTTTTGTATCATCATTTCCAATCTATCCACTTCTAGGTTGCCGTGATTTCTTTC 1505
QY	2772 AAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATTTTCTAAAACTGGAGAC 2831	3672 ATAAAGATTTCTTTGGAAGAATGTACGAAAAAATGTGGACACTATAATCCATGGGATAGG 3731
Db	606 AAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATTTTCTAAAACTGGAGAC 665	1506 ATAAAGATTTCTTTGGAAGAATGTACGAAAAAATGTGGACACTATAATCCATGGGATAGG 1565
QY	2832 AAACCATATAAATACAAAACAAGTCTGCTTCTTCAAAATTCGTGACTCAGATATCAGT 2891	3732 CTTTTCAGTAGCTGTTATATATCGCTTACCTGCAGTGTGTACTGTGGATTTTCTCTTACAA 3791
Db	666 AAACCATATAAATACAAAACAAGTCTGCTTCTTCAAAATTCGTGACTCAGATATCAGT 725	1566 CTTTTCAGTAGCTGTTATATATCGCTTACCTGCAGTGTGTACTGTGGATTTTCTCTTACAA 1625
QY	2892 GATCTTATTAGCTTTTTCACAGCCAGAACATAATGGTGACGATGATTAATGACAGTGAC 2951	3792 TACTATGAGAAAAAATATATGGAGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACTT 3851
Db	726 GATCTTATTAGCTTTTTCACAGCCAGAACATAATGGTGACGATGATTAATGACAGTGAC 785	1626 TACTATGAGAAAAAATATATGGAGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACTT 1685
QY	2952 TATGTATCCGTGGCTCCCCATAGTGGGCTTTTAAATGTGATGCTTTCAGAAAAAGGACTAT 3011	3852 TCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACAGACAATGAGGATGAAGATGAA 3911
Db	786 TATGTATCCGTGGCTCCCCATAGTGGGCTTTTAAATGTGATGCTTTCAGAAAAAGGACTAT 845	1686 TCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACAGACAATGAGGATGAAGATGAA 1745
QY	3012 GTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTTTATCTTTTACCTATATTAGTGAATATC 3071	3912 GATGTCAAAAGCTGAAAGACTTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAG 3971
Db	846 GTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTTTATCTTTTACCTATATTAGTGAATATC 905	1746 GATGTCAAAAGCTGAAAGACTTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAG 1805

Db 61 GCACCATGAGCCTTTGGAAACAAACAGATGTATACAATAGCAAGTTTCATTTCCTTACCT 120

Qy 2677 TGAACCGTGAAGTAATAATCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTTTCACAG 2736

Db 121 TGAACCGTGAAGTAATAATCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTTTCACAG 180

Qy 2737 TTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGTGGTCCCATCAAAC 2796

Db 181 TTCAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGTGGTCCCATCAAAC 240

Qy 2797 TTGTTCCAGACTTATATTTTCTAAAACTGGAGACAAACCAATAAATACAAAACAAGTC 2856

Db 241 TTGTTCCAGACTTATATTTTCTAAAACTGGAGACAAACCAATAAATACAAAACAAGTC 300

Qy 2857 TGCTTCTTCAAAAATTCTGCTGACTCAGATATCAGTGATCTTTATAGCTTTTTCACAGCC 2916

Db 301 TGCTTCTTCAAAAATTCTGCTGACTCAGATATCAGTGATCTTTATAGCTTTTTCACAGCC 360

Qy 2917 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTG 2976

Db 361 AGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTG 420

Qy 2977 CGGCTTTAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA 3036

Db 421 CGGCTTTAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTA 480

Qy 3037 CTATGGTTTATCTTTACCTATATAGTGAATATCATTAGTAACCTACTATCTTTATCATT 3096

Db 481 CTATGGTTTATCTTTACCTATATAGTGAATATCATTAGTAACCTACTATCTTTATCATT 540

Qy 3097 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCAATCTTTCAAGAAATTAAGTATA 3156

Db 541 TAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCAATCTTTCAAGAAATTAAGTATA 600

Qy 3157 TAGTTTTTAAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCA 3216

Db 601 TAGTTTTTAAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCA 660

Qy 3217 TGCCACCTTACTTTGCCATGGAAAAATGCAGAGAATCATAAAGATCAAAGCTTATACTCAAC 3276

Db 661 TGCCACCTTACTTTGCCATGGAAAAATGCAGAGAATCATAAAGATCAAAGCTTATACTCAAC 720

Qy 3277 TTAAACTTTCAGGCTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTGATATCC 3336

Db 721 TTAAACTTTCAGGCTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTGATATCC 780

Qy 3337 CCTTATTTTATCACTTATTTTATGCTAGGAGCTTATGGCATTTTCAATATGGAT 3396

Db 781 CCTTATTTTATCACTTATTTTATGCTAGGAGCTTACTGGCATTTTCAATATGGAT 840

Qy 3397 TATATTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTGCCTTATTTGGTTATGTTCCAT 3456

Db 841 TATATTTTATACTGTAAAGTTCCTTGCTGTGGTTTTTGCCTTATTTGGTTATGTTCCAT 900

Qy 3457 CAGTTATTTCTGTTCACTTATATTGCTTCTTCAACCTTTAAGAAAAATTTTAAATACCAAAG 3516

Db 901 CAGTTATTTCTGTTCACTTATATTGCTTCTTCAACCTTTAAGAAAAATTTTAAATACCAAAG 960

Qy 3517 AATTTTGGTCATTTATCTATTCTGTGGCAGCGTTGGCTTGATTGCAATCACTGAAATAA 3576

Db 961 AATTTTGGTCATTTATCTATTCTGTGGCAGCGTTGGCTTGATTGCAATCACTGAAATAA 1020

Qy 3577 CTTTCTTTATGGGATACAAATTGCAACTATTTCTTCAATATGCTTTTGTATCATCATTC 3636

Db 1021 CTTTCTTTATGGGATACAAATTGCAACTATTTCTTCAATATGCTTTTGTATCATCATTC 1080

Qy 3637 CAATCTATCCACTTCTAGGTTGCCTGATTTCTTTTCAAAAGATTTCTTGGAAAGATGTAC 3696

Db 1081 CAATCTATCCACTTCTAGGTTGCCTGATTTCTTTTCAAAAGATTTCTTGGAAAGATGTAC 1140

Qy 3697 GAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTT 3756

Db 1141 GAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTT 1200

Qy 3757 ACCTGCAGTGTGTACTGTGGATTTTCCCTTACAATACTATGAGAAAAAATATGGAGGCA 3816

Db 1201 ACCTGCAGTGTGTACTGTGGATTTTCCCTTACAATACTATGAGAAAAAATATGGAGGCA 1260

Qy 3817 GATCAATAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAACGAAGTCTAAAAATAGGAAGC 3876

Db 1261 GATCAATAAGAAAAAGATCCCTTTTTCAGAAAACTTTTCAACGAAGTCTAAAAATAGGAAGC 1320

Qy 3877 TTCCAGAACCCACAGACAATGAGGATGAAGATGTCAAAAGCTGAAAGACTAAAGG 3936

Db 1321 TTCCAGAACCCACAGACAATGAGGATGAAGATGTCAAAAGCTGAAAGACTAAAGG 1380

Qy 3937 TCAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 3996

Db 1381 TCAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATT 1440

Qy 3997 TGCATAAAGAATATGATGACAAGAAAGATTTTCTTCTTCAAGAAAAAGTAAAGAAAGTGG 4056

Db 1441 TGCATAAAGAATATGATGACAAGAAAGATTTTCTTCTTCAAGAAAAAGTAAAGAAAGTGG 1500

Qy 4057 CAACATAATACATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 4116

Db 1501 CAACATAATACATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAA 1560

Qy 4117 ATGGTGTGGCAAAAAGCACAAATTATTAATATTCTGTTGGTGATATTGAACCAACTTCAG 4176

Db 1561 ATGGTGTGGCAAAAAGCACAAATTATTAATATTCTGTTGGTGATATTGAACCAACTTCAG 1620

Qy 4177 GCCAGTATTTTTTAGGAGATTAATCTTTCAGAGACAAGTGAAGATGATTCACCTGAAGT 4236

Db 1621 GCCAGTATTTTTTAGGAGATTAATCTTTCAGAGACAAGTGAAGATGATTCACCTGAAGT 1680

Qy 4237 GTATGGGTACTGTCTCAGATAAACCCCTTTGTGGCCAGATACATTCAGGAAACATT 4296

Db 1681 GTATGGGTACTGTCTCAGATAAACCCCTTTGTGGCCAGATACATTCAGGAAACATT 1740

Qy 4297 TTGAAATTTATGGAGCTGTCAAGGAATGAGTGCAGTGAACATGAAAGAAAGTCATAAGTC 4356

Db 1741 TTGAAATTTATGGAGCTGTCAAGGAATGAGTGCAGTGAACATGAAAGAAAGTCATAAGTC 1800

Qy 4357 GAATAACACATGCATCTGATTTAAAAAGAACATCTTCAGAGACTGTAAAGAAACTACCTG 4416

Db 1801 GAATAACACATGCATCTGATTTAAAAAGAACATCTTCAGAGACTGTAAAGAAACTACCTG 1860

Qy 4417 CAGGAATCAAAACGAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTT 4476

Db 1861 CAGGAATCAAAACGAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTT 1920

Qy 4477 TGCTAGATGAACCATCTACAGTATGGATCCCAAGCCAAAACAGCACATGTGGCGAGCAA 4536

Db 1921 TGCTAGATGAACCATCTACAGTATGGATCCCAAGCCAAAACAGCACATGTGGCGAGCAA 1980

Qy 4537 TTCGAACCTGCATTTAAAAACAGAAAAAGCGGGCTGCTATTCTGACCACTCAGTATATGGAGG 4596

Db 1981 TTCGAACCTGCATTTAAAAACAGAAAAAGCGGGCTGCTATTCTGACCACTCAGTATATGGAGG 2040

Qy 4597 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGCTGTCTGGCAGTTAAGATGTATCG 4656

Db 2041 AGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGCTGTCTGGCAGTTAAGATGTATCG 2100

Qy 4657 GAACAGTACAAACATCTAAAGAGTAAATTTTGGAAAAAGGCTACTTTTTTGGAAAAATTAATGA 4716

Db 2101 GAACAGTACAAACATCTAAAGAGTAAATTTTGGAAAAAGGCTACTTTTTTGGAAAAATTAATGA 2160

Qy 4717 AGGACTGGATAGAAAAACCTAGAAAGTAGACCCGCCCTTCAAAAGAGAAATTCAGTATATTTTCC 4776

Db 2161 AGGACTGGATAGAAAAACCTAGAAAGTAGACCCGCCCTTCAAAAGAGAAATTCAGTATATTTTCC 2220

Qy 4777 CAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTTAAGGAAG 4836

Db 2221 CAAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTTAAGGAAG 2280

QY 4837 ATGTTAGTCCCTTTCACAACTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTGCCA 4896
Db |||||||
QY 2281 ATGTTAGTCCCTTTCACAACTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTGCCA 2340
Db |||||||
QY 4897 TTGAAGATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAAG 4956
Db |||||||
QY 2341 TTGAAGATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAAG 2400
Db |||||||
QY 4957 AACAAAGAGGAAGATATAGTTGTGGAACCTTTAAACAGCACACTTTTGGTGGGAACGAA 5016
Db |||||||
QY 2401 AACAAAGAGGAAGATATAGTTGTGGAACCTTTAAACAGCACACTTTTGGTGGGAACGAA 2460
Db |||||||
QY 5017 CACAAGAGATAGATAGTATTTTGAATTTGTATTTGTTCCGTTCTTACTGGGACTTCT 5076
Db |||||||
QY 2461 CACAAGAGATAGATAGTATTTTGAATTTGTATTTGTTCCGTTCTTACTGGGACTTCT 2520
Db |||||||
QY 5077 TTCTTTTCACTTAATTTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGTTAACTGGA 5136
Db |||||||
QY 2521 TTCTTTTCACTTAATTTTAACTTTGGTTTAAAAAGTTTTTATTGGAATGTTAACTGGA 2580
Db |||||||
QY 5137 GAACCAAGACGCACCTTGAAATTTTCTTAAGCTCCTTAATTTGAAATGCTGTGGTTGTG 5196
Db |||||||
QY 2581 GAACCAAGACGCACCTTGAAATTTTCTTAAGCTCCTTAATTTGAAATGCTGTGGTTGTG 2640
Db |||||||
QY 5197 TTTTGCCTTTCTTTAAATAAAACGATGTATATAATTAAGTGAAGCTGCA 5244
Db |||||||
QY 2641 TTTTGCCTTTCTTTAAATAAAACGATGTATATAATTAAGTGAAGCCGAA 2688
Db |||||||

RESULT 11

ABK35707
ID ABK35707 standard; cDNA; 3928 BP.
XX
AC ABK35707;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA sequence #98 encoding novel human secreted protein.
XX

KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; allergic condition; neurodegenerative disorder;
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
XX
OS Homo sapiens.
XX

PN WO200177289-A2.
XX
XX 18-OCT-2001.
PD
XX
PF 29-MAR-2001; 2001WO-US010232.
XX
PR 06-APR-2000; 2000US-0195605P.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, McCooy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
XX
DR WPI; 2002-179322/23.
XX

PT Six hundred and twenty three polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for treating
PT immune deficiencies and disorders such as autoimmune disorders.
XX

PS Claim 1; Page 127-128; 393pp; English.
XX
CC The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides a
CC method for producing proteins from these polynucleotide sequences. The

CC proteins are useful for identifying compounds that modulate their
CC activity and production. The sequences of the invention are useful for
CC treating diseases such as hyperproliferative disorders (e.g. cancer),
CC immune deficiency disorders (e.g. severe combined immunodeficiency
CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders
CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis),
CC infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma),
CC neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis,
CC coagulation disorders (e.g. haemophilia), and tumours. The polynucleotide
CC sequences of the invention are also useful in gene therapy. ABK35610-
CC ABK36232 represent the cDNA sequences of the invention that encode for
CC novel human secreted proteins

XX
SQ Sequence 3928 BP; 1139 A; 681 C; 799 G; 1309 T; 0 U; 0 Other;
Query Match 32.7%; Score 1791; DB 6; Length 3928;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1834; Conservative 0; Mismatches 0; Indels 33; Gaps 1;

QY 1044 GTATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGAAATAGTT 1103
Db |||||||
1 GTATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGAAATAGTT 60
QY 1104 GAATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGAAATAGTT 1163
Db |||||||
61 GAATTTTGTCTTAAATGCTGACACCTCTTTTAAAAAATCAAAACATGTGGAAATAGTT 120
QY 1164 TTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCCTTCTGTCACCTGTACTTTTGTGATGGT 1223
Db |||||||
121 TTTCCCAAATCGTTAGTGTGGCTTTTTCAGTCCCTTCTGTCACCTGTACTTTTGTGATGGT 180
QY 1224 ATTGCACAGGTCATGCAATTTAGAAAGATTTTAAATGAAGTGTCTTCATTTTCAAAATTTGACT 1283
Db |||||||
181 ATTGCACAGGTCATGCAATTTAGAAAGATTTTAAATGAAGTGTCTTCATTTTCAAAATTTGACT 240
QY 1284 GCAGGCCCATATCCTCTAATTTATTAACAATTATCATGCTCACACTTAATAGTATATCTAT 1343
Db |||||||
241 GCAGGCCCATATCCTCTAATTTATTAACAATTATCATGCTCACACTTAATAGTATATCTAT 300
QY 1344 GTCCTCTTGGCTGTCTATCTTGATCAAGTCATTTCCAGGSGAATTTGGCTTACGGAGATCA 1403
Db |||||||
301 GTCCTCTTGGCTGTCTATCTTGATCAAGTCATTTCCAGGSGAATTTGGCTTACGGAGATCA 360
QY 1404 TCTTTATATTTTCTGAAGCCTTCATATTTGGTCAAAGAGCAAAAGAAATTTATGAGGAGTTA 1463
Db |||||||
361 TCTTTATATTTTCTGAAGCCTTCATATTTGGTCAAAGAGCAAAAGAAATTTATGAGGAGTTA 420
QY 1464 TCAGAGGGCAATGTTAATGGAATATTTAGTTTTTAGTGAAATTTATGAGCCAGTTTCTTCA 1523
Db |||||||
421 TCAGAGGGCAATGTTAATGGAATATTTAGTTTTTAGTGAAATTTATGAGCCAGTTTCTTCA 480
QY 1524 GAATTTGTAGGAAAAGAGCCATAAGAAATTAGTGGTATTTCAGAGACATACAGAAAAGAG 1583
Db |||||||
481 GAATTTGTAGGAAAAGAGCCATAAGAAATTAGTGGTATTTCAGAGACATACAGAAAAGAG 540
QY 1584 GGTGAAAATGTGGAGGCTTTGAGAAAATTTGTCTATTGACATATATGAGGGTCAGATTACT 1643
Db |||||||
541 GGTGAAAATGTGGAGGCTTTGAGAAAATTTGTCTATTGACATATATGAGGGTCAGATTACT 600
QY 1644 GCCTTACTTGGCCACAGTCGAAACAGGAAAGAGTACATTGATGAATATTTCTTTTGGACTC 1703
Db |||||||
601 GCCTTACTTGGCCACAGTCGAAACAGGAAAGAGTACATTGATGAATATTTCTTTTGGACTC 660
QY 1704 TGCCACCTTCTGATGGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAA 1763
Db |||||||
661 TGCCACCTTCTGATGGGTTTGCATCTATATATGACACAGAGTCTCAGAAATAGATGAA 720
QY 1764 ATGTTTGAAGCAAGAAAATGATTTGGCATTTTGTCACAGTTAGATATACACTTTGATGTT 1823
Db |||||||
721 ATGTTTGAAGCAAGAAAATGATTTGGCATTTTGTCACAGTTAGATATACACTTTGATGTT 780
QY 1824 TTGACAGTAGAAGAAAATTTATCAATTTTGGCTTCAATCAAAGGGATACCAGCCAAACAAT 1883
Db |||||||

Db	781	TTGACAGTAGAAGAAAATTTATCAATTTTGGCTTCAATCAAAAGGGATACCAGCCAACAAT	840
QY	1884	ATAATACAAGAAGTGCAGAAGGTTTACTAGATTAGACATGCAGACTATCAAGATAAC	1943
Db	841	ATAATACAAGAAGTGCAGAAGGTTTACTAGATTAGACATGCAGACTATCAAGATAAC	900
QY	1944	CAAGCTAAAAAATTAACTGGTGGTCAAAAAAGAAAGCTGCTCATTAGGAATTCGTCTCTT	2003
Db	901	CAAGCTAAAAAATTAACTGGTGGTCAAAAAAGAAAGCTGCTCATTAGGAATTCGTCTCTT	960
QY	2004	GGGAACCCAAAGATACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGA	2063
Db	961	GGGAACCCAAAGATACTGCTGCTAGATGAACCAACAGCTGGAATGGACCCCTGTTCTCGA	1020
QY	2064	CATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACT	2123
Db	1021	CATATTGTATGGAATCTTTTAAATACAGAAAAAGCCAAATCGGGTGACAGTGTTCAGTACT	1080
QY	2124	CATTTCAATGGATGAAGCTGACATCTTTGCAGATAGGAAGAGCTGTGATATCAACAAGGAATG	2183
Db	1081	CATTTCAATGGATGAAGCTGACATCTTTGCAGATAGGAAGAGCTGTGATATCAACAAGGAATG	1140
QY	2184	CTGAATGTGTGGTTCCTTCAATGTTCTCAAAAGTAAATGGGGATCGGCTACCGCCTG	2243
Db	1141	CTGAATGTGTGGTTCCTTCAATGTTCTCAAAAGTAAATGGGGATCGGCTACCGCCTG	1200
QY	2244	AGCATGTACATAGACAAATATTGTGCCACAGAACTCTTTCTCACTGGTTAAACAACAT	2303
Db	1201	AGCATGTACATAGACAAATATTGTGCCACAGAACTCTTTCTCACTGGTTAAACAACAT	1260
QY	2304	ATACCTGGAGCTACTTTATTACAACAGAAATGACCAACAACTTGTGTATAGCTTGCCCTTC	2363
Db	1261	ATACCTGGAGCTACTTTATTACAACAGAAATGACCAACAACTTGTGTATAGCTTGCCCTTC	1320
QY	2364	AAGGACATGGACAAATTTTCAG-----GTTTG	2390
Db	1321	AAGGACATGGACAAATTTTCAGAAATGCTTGATAGACAAAAGGATGTTATGTATGTTG	1380
QY	2391	TTTTCTGCCCTAGACAGTCATCAAAATTTGGGTGTCATTTCTTATGGTGTTCATGACG	2450
Db	1381	TTTTCTGCCCTAGACAGTCATCAAAATTTGGGTGTCATTTCTTATGGTGTTCATGACG	1440
QY	2451	ACTTTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTAT	2510
Db	1441	ACTTTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTAT	1500
QY	2511	AGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATG	2570
Db	1501	AGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATG	1560
QY	2571	GAACAGAGCTTACTTATTTCTTGAAACCAAGCTTCTAGTGAGCACCATGAGCCTT	2630
Db	1561	GAACAGAGCTTACTTATTTCTTGAAACCAAGCTTCTAGTGAGCACCATGAGCCTT	1620
QY	2631	TGGAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCTTGAAACGTGAAAGT	2690
Db	1621	TGGAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTTACCTTGAAACGTGAAAGT	1680
QY	2691	AAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATG	2750
Db	1681	AAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATG	1740
QY	2751	TTTTTGTTTCATCACTCTTTTAAAAAATGCTGTGGTTCATCAAACTTGTTCAGACTTA	2810
Db	1741	TTTTTGTTTCATCACTCTTTTAAAAAATGCTGTGGTTCATCAAACTTGTTCAGACTTA	1800
QY	2811	TATTTCTAAAAACCTGGAGACAAAACCATATAATACAAAAAAGTCTGCTTCTTCAAAAT	2870
Db	1801	TATTTCTAAAAACCTGGAGACAAAACCATATAATACAAAAAAGTCTGCTTCTTCAAAAT	1860
QY	2871	TCTGCTG	2877
Db	1861	TCTGCTG	1867

RESULT 12	
ABK35706	
ID	ABK35706 standard; cDNA; 1548 BP.
XX	
AC	ABK35706;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	cDNA sequence #97 encoding novel human secreted protein.
XX	
KW	Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; allergic condition; neurodegenerative disorder; liver fibrosis; coagulation disorder; gene therapy; antimicrobial; tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
OS	Homo sapiens.
XX	
PN	WO200177289-A2.
XX	
PD	18-OCT-2001.
XX	
PF	29-MAR-2001; 2001WO-US010232.
XX	
PR	06-APR-2000; 2000US-0195605P.
XX	
PA	(GEMY) GENETICS INST INC.
XX	
PI	Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C; Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG; Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
XX	
DR	WPI; 2002-179322/23.
XX	
PT	Six hundred and twenty three polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders.
PT	
XX	
PS	Claim 1; Page 126; 393pp; English.
XX	
CC	The present invention relates to the isolation of novel cDNA sequences which encode human secreted proteins. The cDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polynucleotide sequences. The proteins are useful for identifying compounds that modulate their activity and production. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis), infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma), neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), and tumours. The polynucleotide sequences of the invention are also useful in gene therapy. ABK35610-CC ABK36232 represent the cDNA sequences of the invention that encode for novel human secreted proteins
XX	
SQ	Sequence 1548 BP; 466 A; 273 C; 268 G; 541 T; 0 U; 0 Other;

Query Match 28.2%; Score 1546.4; DB 6; Length 1548;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1547; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	2489	AGAAATTGACCAAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGA	2548
Db	1	AGAAATTGACCAAGCAGATTATAGTGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGA	60
QY	2549	TTCAAAATCTTTTGATGAATGGAACAGAGCTTACTTCTTCTGAAACCAAGGCTTC	2608
Db	61	TTCAAAATCTTTTGATGAATGGAACAGAGCTTACTTCTTCTGAAACCAAGGCTTC	120

QY 2609 TCTAGTGAGCACCATGAGCCCTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTCATTT 2668
Db 121 TCTAGTGAGCACCATGAGCCCTTTGGAAACAACAGATGTATACAATAGCAAAAGTTTCATTT 180
QY 2669 CTTTACCTTGAAACGCGTAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTT 2728
Db 181 CTTTACCTTGAAACGCGTAAAGTAAATCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTT 240
QY 2729 TTTACAGTTTCAGATTTTATGTTTTTGGTTTCATCCTCTTTTAAAAATGCTGCTGCTCC 2788
Db 241 TTTACAGTTTCAGATTTTATGTTTTTGGTTTCATCCTCTTTTAAAAATGCTGCTGCTCC 300
QY 2789 CATCAAACTTGTTCAGACTTATATTTTCTAAAAACCTGGAGACAAACCCACATAAATACAA 2848
Db 301 CATCAAACTTGTTCAGACTTATATTTTCTAAAAACCTGGAGACAAACCCACATAAATACAA 360
QY 2849 AACAAAGTCTGCTTCTTTCAAAATTCGCTGACTCAGATATCAGTGATCTTTATAGCTTTT 2908
Db 361 AACAAAGTCTGCTTCTTTCAAAATTCGCTGACTCAGATATCAGTGATCTTTATAGCTTTT 420
QY 2909 CACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCC 2968
Db 421 CACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCC 480
QY 2969 CCATAGTGGGCTTTTAAATGTGATGCATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTT 3028
Db 481 CCATAGTGGGCTTTTAAATGTGCTGCATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTT 540
QY 3029 CAACAGTACTATGGTTTTTATCTTTACCTATATTAGTGAATATCATTTAGTAACTACTATCT 3088
Db 541 CAACAGTACTATGGTTTTTATCTTTACCTATATTAGTGAATATCATTTAGTAACTACTATCT 600
QY 3089 TTATCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCITTCAGAAAT 3148
Db 601 TTATCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTCITTCAGAAAT 660
QY 3149 TACTGATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGT 3208
Db 661 TACTGATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGT 720
QY 3209 TACTGCAATGCCACCTTACTTTGCCATGGAAAATGCAGAGAATCATAGAATCAAAAGCTTA 3268
Db 721 TACTGCAATGCCACCTTACTTTGCCATGGAAAATGCAGAGAATCATAGAATCAAAAGCTTA 780
QY 3269 TACTCAACTTAAACTTTTCAGGCTTTTGGCCATCTGCATATTGGATTGGACAAGCTGTTGT 3328
Db 781 TACTCAACTTAAACTTTTCAGGCTTTTGGCCATCTGCATATTGGATTGGACAAGCTGTTGT 840
QY 3329 TGATATCCCTTATTTTTTATCATCTTATTTTGTAGTGAAGCTTATTTGGCATTTTCA 3388
Db 841 TGATATCCCTTATTTTTTATCATCTTATTTTGTAGTGAAGCTTATTTGGCATTTTCA 900
QY 3389 TTATGGATTATATTTTATAGTAAAGTTCCCTTGTGCTGTTTTTGGCTTATTTGGTTA 3448
Db 901 TTATGGATTATATTTTATAGTAAAGTTCCCTTGTGCTGTTTTTGGCTTATTTGGTTA 960
QY 3449 TGTTCATCAGTTATTCGTTCACCTTATATTTGCTTCTTTTACCTTTAAGAAAATTTTAAA 3508
Db 961 TGTTCATCAGTTATTCGTTCACCTTATATTTGCTTCTTTTACCTTTAAGAAAATTTTAAA 1020
QY 3509 TACCAAGAATTTTGGTCAATTTATCTATTCTGTGGCAGCGTTGGCTTGTATTGCAATCAC 3568
Db 1021 TACCAAGAATTTTGGTCAATTTATCTATTCTGTGGCAGCGTTGGCTTGTATTGCAATCAC 1080
QY 3569 TGAATAAATCTTTCTTTATGGGATACACAATTTGCACTATTTCTTCAATTTATGCTTTTGTAT 3628
Db 1081 TGAATAAATCTTTCTTTATGGGATACACAATTTGCACTATTTCTTCAATTTATGCTTTTGTAT 1140
QY 3629 CATCATTCCAATCTATCCACTCTAGGTTGCCTGATTTCTTTTCAAAAGATTTCTTTGAA 3688
Db 1141 CATCATTCCAATCTATCCACTCTAGGTTGCCTGATTTCTTTTCAAAAGATTTCTTTGAA 1200
QY 3689 GAATGTACGAAAAAATGTGGACACCTTATAATCCATGGGATAGGCTTTTCAGTAGCTGTTAT 3748

Db 1201 GAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTGTTAT 1260
QY 3749 ATCGCCTTACCTGCAGTGTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAATA 3808
Db 1261 ATCGCCTTACCTGCAGTGTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAATA 1320
QY 3809 TGGAGGCAGATCAATAAGAAAAGATCCCTTTTTCAGAAAACCTTTTCAACGAAGTCTAAAAA 3868
Db 1321 TGGAGGCAGATCAATAAGAAAAGATCCCTTTTTCAGAAAACCTTTTCAACGAAGTCTAAAAA 1380
QY 3869 TAGGAAGCTTCCAGAACCCAGACAATGAGGATGAAGATGTCAAAGCTCAAAG 3928
Db 1381 TAGGAAGCTTCCAGAACCCAGACAATGAGGATGAAGATGTCAAAGCTCAAAG 1440
QY 3929 ACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTTCAGGAGAAAACCATCCATTATGGT 3988
Db 1441 ACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTTCAGGAGAAAACCATCCATTATGGT 1500
QY 3989 CAGCAATTTGCATAAAGAAATATGATGACAAGAAAAGATTTTCTTTTTC 4036
Db 1501 CAGCAATTTGCATAAAGAAATATGATGACAAGAAAAGATTTTCTTTTTC 1548

RESULT 13
ABZ35938
ID ABZ35938 standard; cDNA; 2481 BP.

XX ABZ35938;

AC ABZ35938;

XX 10-FEB-2003 (first entry)

XX Human secretory polynucleotide SPTM SEQ ID NO 102.

XX Human; SPTM; autoimmune disorder; inflammatory disorder; AIDS; anaemia;
XX asthma; Crohn's disease; neurological disorder; epilepsy; cancer;
XX Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease;
XX multiple sclerosis; Parkinson's disease; cell proliferative disorder;
XX anti-inflammatory; immunosuppressive; neuroprotective; nootropic;
XX neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic;
XX antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus;
XX secretory polynucleotide; secretory protein; gene; ss.

OS Homo sapiens.

XX WO200283876-A2.

XX 24-OCT-2002.

XX 27-MAR-2002; 2002WO-US009921.

XX 29-MAR-2001; 2001US-0280067P.

XX 29-MAR-2001; 2001US-0280068P.

XX 16-MAY-2001; 2001US-0291280P.

XX 17-MAY-2001; 2001US-0291829P.

XX 17-MAY-2001; 2001US-0291849P.

XX 19-JUN-2001; 2001US-0299428P.

XX 20-JUN-2001; 2001US-0299776P.

XX 20-JUN-2001; 2001US-0300001P.

XX (INCY-) INCYTE GENOMICS INC.

XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

XX Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;

XX Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;

XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX MPI; 2003-075543/07.

XX P-PSDB; ABP75491.

XX New human secretory proteins and polynucleotides, useful for diagnosing,

XX treating or preventing autoimmune/inflammatory disorders (e.g. AIDS),

PT	neurological disorders (e.g. Alzheimer's), or cell proliferations or cancers.
PT	
XX	
PS	Claim 1; SEQ ID NO 102; 458pp + Sequence Listing; English.
XX	
CC	The invention relates to a secretory polynucleotide (designated sptm) comprising any of 567 polynucleotide sequences (AB235837-AB236403), a naturally occurring polynucleotide sequence at least 90 % identical to the polynucleotide sequence, a polynucleotide complementary to them or an RNA equivalent of them. The polypeptide or polynucleotide are useful for treating, preventing or diagnosing a disease or condition associated with the expression of functional SPTM. These are particularly useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's disease), neurological disorders (e.g. epilepsy, Huntington's disease, dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease, multiple sclerosis, cerebral palsy, Parkinson's disease, anxiety, schizophrenia or amnesia), or cell proliferative disorders (e.g. psoriasis, polycythemia vera, or cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma or cancers of the brain, breast, cervix or prostate). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SEQ	Sequence 2481 BP; 662 A; 452 C; 477 G; 889 T; 0 U; 1 Other;
	Query Match 25.6%; Score 1400; DB 7; Length 2481;
	Best Local Similarity 99.9%; Pred. No. 2.7e-295;
	Matches 1400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	97 AGGTTTATTTCAGAAAACATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 156
Db	
QY	1081 AGGTTTATTTCAGAAAACATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCA 1140
Db	
QY	157 GAACACCTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGG 216
Db	
QY	1141 GAACACCTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGG 1200
QY	217 AAATTCCTTTTCCACTATTTTTTTTTTTTGGTTAAATTAATAGCATGATGCATCCAA 276
Db	
QY	1201 AAATTCCTTTTCCACTATTTTTTTTTTTTGGTTAAATTAATAGCATGATGCATCCAA 1260
QY	277 ATAAGAAATATGAAGAAGTGCCTAAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 336
Db	
QY	1261 ATAAGAAATATGAAGAAGTGCCTAAATATAGAACTCAATCCTATGGACAAGTTTACTCTTT 1320
QY	337 CTAATCTAATCTTGGATATATCTCCAGTGACTAATATTACAAGCAGCATCATCAGAAAAG 396
Db	
QY	1321 CTAATCTAATCTTGGATATATCTCCAGTGACTAATATTACAAGCAGCATCATCAGAAAAG 1380
QY	397 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAAATATACAATGAAAGAAA 456
Db	
QY	1381 TGTCTACTGATCATCTACCTGATGTCATAATTACTGAAGAAATATACAATGAAAGAAA 1440
QY	457 TGTAAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGGTTTTTCAAGACTCCA 516
Db	
QY	1441 TGTAAACATCCAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGGTTTTTCAAGACTCCA 1500
QY	517 TGTCTATGAACCTTCGTTTTTTTCTCGATATGATCCAGTATCTTCTATTTATATGGATT 576
Db	
QY	1501 TGTCTATGAACCTTCGTTTTTTTCTCGATATGATCCAGTATCTTCTATTTATATGGATT 1560
QY	577 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 636
Db	
QY	1561 CAAGAGCTGGCTGTTCAAAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAG 1620
QY	637 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA 696
Db	
QY	1621 TTTTACAAGCATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGA 1680
QY	697 AGGAGCTGGAGTCAACTAAAGCTGTATTATTATGGAGAACTGCTGTTGTAGAAATAGATA 756
Db	
QY	1681 AGGAGCTGGAGTCAACTAAAGCTGTATTATTATGGAGAACTGCTGTTGTAGAAATAGATA 1740

QY	757 CCTTTCCCGAGAGTAATTTTAAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACT 816
Db	
QY	1741 CCTTTCCCGAGAGTAATTTTAAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACT 1800
Db	
QY	817 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAA 876
Db	
QY	1801 TTTTGGCAATTCATATCGTAGCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAA 1860
Db	
QY	877 TGGGACTTCATGATACTGCCCTTTTGGCTTTCTCTGGTTCCTCTATATACAAGTTTAAATT 936
Db	
QY	1861 TGGGACTTCATGATACTGCCCTTTTGGCTTTCTCTGGTTCCTCTATATACAAGTTTAAATT 1920
Db	
QY	937 TTCTTATGTCCTTCTTATGGCAGTCATTTGGCAGAGCTTCTTTGTTATTTCTCTCAAAGTA 996
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QY	1921 TTCTTATGTCCTTCTTATGGCAGTCATTTGGCAGAGCTTCTTTGTTATTTCTCTCAAAGTA 1980
Db	
QY	997 GCAGCATTTGATATTTCTGCTTTTCTCTTTTCTTTATGGATTCATCTGTATTTTTCCTT 1056
Db	
QY	1981 GCAGCATTTGATATTTCTGCTTTTCTCTTTTCTTTATGGATTCATCTGTATTTTTCCTT 2040
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QY	1057 TAATGCTGACACCTCTTTTAAATAAATCAAAACATGTTGGGAATAGTTGAATTTTGTGTTA 1116
Db	
QY	2041 TAATGCTGACACCTCTTTTAAATAAATCAAAACATGTTGGGAATAGTTGAATTTTGTGTTA 2100
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QY	1117 CTGTGGCTTTTGGATTTTATTTGGCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGT 1176
Db	
QY	2101 CTGTGGCTTTTGGATTTTATTTGGCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGT 2160
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QY	1177 TAGTGTGGCTTTTTCAGTCCCTTCTGTCACCTGTACTTTTGTGATTTGGTATTTGCACAGGTCA 1236
Db	
QY	2161 TAGTGTGGCTTTTTCAGTCCCTTCTGTCACCTGTACTTTTGTGATTTGGTATTTGCACAGGTCA 2220
Db	
QY	1237 TGCATTTAGAAGATTTTAAATGAAGTGTCTTCAATTTTCAAAATTTGACTGCAGGCCCATATC 1296
Db	
QY	2221 TGCATTTAGAAGATTTTAAATGAAGTGTCTTCAATTTTCAAAATTTGACTGCAGGCCCATATC 2280
Db	
QY	1297 CTCTAATTATTAACAATTATCATGCTCAGGGAATTTGGCTTACGGAGATCATCTTTATTTTC 1356
Db	
QY	2281 CTCTAATTATTAACAATTATCATGCTCAGGGAATTTGGCTTACGGAGATCATCTTTATTTTC 2340
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QY	1357 TCTATCTTCATCAAGTCATTCAGGGAATTTGGCTTACGGAGATCATCTTTATTTTC 1416
Db	
QY	2341 TCTATCTTCATCAAGTCATTCAGGGAATTTGGCTTACGGAGATCATCTTTATTTTC 2400
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QY	1417 TGAAGCCTTCATATTTGGTCAAGAGCAAAAGAAATTTATGAGAGTTATCAGAGGGCAATG 1476
Db	
QY	2401 TGAAGCCTTCATATTTGGTCAAGAGCAAAAGAAATTTATGAGAGTTATCAGAGGGCAATG 2460
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QY	1477 TTAATGGAATAATTAGTTTAA 1497
Db	
QY	2461 TTAATGGAATAATTAGTTTAA 2481
Db	
RESULT 14	
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ID	ABL64459 standard; DNA; 1346 BP.
XX	
AC	ABL64459;
XX	
DT	15-MAY-2002 (first entry)
XX	
DE	Stomach cancer related gene sequence SEQ ID NO:2796.
XX	
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX	gene; ds.
OS	Homo sapiens.
XX	
PN	WO200194629-A2.
XX	

Db 890 AGCCGTCA-GAAGAGTTTTCCTTCTATTTTGGCTTCTAAATTAATAAGGAAGATGTTTCAG 948
QY 4845 TCCCTTTTCAACAATCTTTTAAAGCTGGAAGAAAGCTAAACATGCTTTTGGCCATTGAAGAA 4904
Db 949 TCCCTTTTCCCAATCTTTTAAAGCTGGAAGAAAGCTAAACATGC-TTTGCCATTGAAGAA 1007
QY 4905 TATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTGTGTAGAACTCACTAAAGAAACAAGAG 4964
Db 1008 TATAGC-TTTTCTCAAGCAACATTTGGAACAGGTTTGTGTAGAACTCACTAAAGAAACAAGAG 1066
QY 4965 GAGGAAGATAATAGTTGTGGAACCTTTTAACAGCACACTTTGGTGGGAACGAACACAAGAA 5024
Db 1067 GAGGAAGATAATAGTTGTGGAACCTTTTAACAGCACACTTTGGT-GGAACGAACACAAGAA 1125
QY 5025 GATAGAGTAGTATTTTGAATTTGTATTTGCTCGGCTCTGCTTACTGGGACTTCTTTCTTTT 5084
Db 1126 GATAGAGTAGTATTTTGAATTTGTATTTGCTCGGCTCTGCTTACTGGGACTTCTTTCTTTT 1185
QY 5085 CACTTAATTTTAACTTTGGTTTAAAGTTTTTATTGGAATGTTAACTGGAGAACCAAG 5144
Db 1186 CACTTAATTTTAACTTTGGTTTAAAGTTTTTATTGGAATGTTAACTGGAGAACCAAG 1245
QY 5145 AACGCACCTTGAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTGTGTGTTTGCCTT 5204
Db 1246 AACGCACCTTGAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTGTGTGTTTGCCTT 1305
QY 5205 TTCTTTAAATAAAACGTATGTATATAATTAAGTCAA 5238
Db 1306 TTCTTTAAATAAAACGTATGTATATAATTAAGTCAA 1339

RESULT 15
ID ABL63763
XX ABL63763 standard; DNA; 1346 BP.
AC ABL63763;
XX
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:2100.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.

PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 2100; 44pp; English.
XX

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour

Sequence 1346 BP; 451 A; 206 C; 290 G; 395 T; 0 U; 4 Other;
Query Match 21.6%; Score 1182; DB 6; Length 1346;
Best Local Similarity 96.5%; Pred. No. 8.3e-248;
Matches 1306; Conservative 0; Mismatches 29; Indels 19; Gaps 9;

QY 3889 CAGACAATGAGGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTGA 3948
Db 1 CAGACAATGAGGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTGA 60
QY 3949 TGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAAT 4008
Db 61 TGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAAT 120
QY 4009 ATGATGACAAGAAAGATTTTCTTCTTCAAGAAAAGTAAAGAAAGTGGCACTAAATACA 4068
Db 121 ATGATGACAAGAAAGATTTTCTTCTTCAAGAAAAGTAAAGAGAGTGGCACTAAATACA 180

QY 4069 TCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCA 4128
Db |||||
181 TCTCTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCA 240
QY 4129 AAAGCACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTT 4188
Db |||||
241 AAAGCACAATTATTAATATTCTGGTTAGTGATATTGAACCAAGCTTCAGGCCAGGTATTTT 300
QY 4189 TAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGTGATGGTTACT 4248
Db |||||
301 TAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGTGATGGTTACT 360
QY 4249 GTCTCAGATAAAACCCCTTTGTGGCCAGATACATACATTGCAGGAACATTTTGAAATTTATG 4308
Db |||||
361 GTCTCAGATAAAACCCCTTTGTGGCCAGATACATACATTGCAGGAACATTTTGAAATTTATG 420
QY 4309 GAGCTGTCAAAGGAATGAGTGCAGAGTGACATGAAGAAGTCATAAGTCGAATAACACATG 4368
Db |||||
421 GAGCTGTCAAAGGAATGAGTGCAGAGTGACATGAAGAAGTCATAAGTCGAATAACACATG 480
QY 4369 CACTTGATTTAAAGAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAAAC 4428
Db |||||
481 CACTTGATTTAAAGAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAA 540
QY 4429 GAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGTAGATGAAC 4488
Db |||||
541 CGAAAGTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGTAGATGAAC 600
QY 4489 CATCTACAGGTATGGATCCCAA--GCCAAACAGCACATGTGGCGAGCAATTCGAACTGC 4546
Db |||||
601 CATCTACAGGTCTGGATCCCAAATGCCAAACATGCACATGTGGCATGCAATTCGAACTGC 660
QY 4547 ATTTAAAAACAGAAAGCGGGTGTCTATTCTGACCCTCACTATATGGAGGAGGCAGAGGC 4606
Db |||||
661 AT-----NNAAGCGGGTGTCTATTCTGACCCTCACTATATGGAGGAGGCAGAGGC 711
QY 4607 TGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGAGTTAAGATGTATCGGAACAGTACA 4666
Db |||||
712 TGTCTGTGATCGAGTAGCTATCATGGTGTCTGGGAGTTAAGATGTATCGGAACAGTACA 771
QY 4667 ACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAAATTGAA--GGACTGGA 4725
Db |||||
772 ACATCTAAAGAGTAAATTTGGAAAAG--NACTTTTGGAAATTAAATTGAA--CGGACTGGA 829
QY 4726 TAGAAAAACCTAGAG--TAGACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCA 4784
Db |||||
830 TAGAAAAACCTAGAGCTAGACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCA 889
QY 4785 AGCGTCTAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAG 4844
Db |||||
890 AGCGCTCA--GAAAGTTTTTCTTCTATTTTGGCTTCTAAAAATTAATAAGGAAGATGTTTCAG 948
QY 4845 TCCCTTTCAAACTTTTTTTAAGCTGGAAGAGTAAACATGCTTTTGGCCATTGAAGAA 4904
Db |||||
949 TCCCTTTCCCAATCTTTTTTAAAGCTGGAAGAGTAAACATGCT--TTTGGCCATTGAAGAA 1007
QY 4905 TATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACAATAAGAAACAAGAG 4964
Db |||||
1008 TATAGC--TTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACAATAAGAAACAAGAG 1066
QY 4965 GAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAGCAACAAGAA 5024
Db |||||
1067 GAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGT--GGAACGAACAACAAGAA 1125
QY 5025 GATAGAGTAGTATTTTGAATTTGTATTGTTTCGCTGCTTACTGGGACTTCTTTCTTTT 5084
Db |||||
1126 GATAGAGTAGTATTTTGAATTTGTATTGTTTCGCTGCTTACTGGGACTTCTTTCTTTT 1185
QY 5085 CACTTAATTTTAACTTTTGGTTTAAAGTTTTTATTTGGAATGGTAACTGGAGAACCAAG 5144
Db |||||
1186 CACTTAATTTTAACTTTTGGTTTAAAGTTTTTATTTGGAATGGTAACTGGAGAACCAAG 1245
QY 5145 AACGCACCTTGAAATTTTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGTGTTTGTGCTT 5204

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Job time : 1315 secs

Db 1246 AACGCACCTTGAAATTTTTCTAAGCTCCTTAATTGAATGCTGTGGTTGTGTGTTTGCTT 1305
QY 5205 TTCTTTAAATAAAACGTAATCTATAATTAAGTGAA 5238
Db 1306 TTCTTTAAATAAAACGTAATCTATAATTAAGTGAA 1339

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: April 12, 2004, 00:48:14 ; Search time 8463 Seconds
(without alignments)
19318.851 Million cell updates/sec

Title: US-10-090-458-4
Perfect score: 5475
Sequence: 1 gcgtccgcgcctcgacag.....cataaagcaatgtgaaagtt 5475

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2938.4	53.7	3950	11 AK047188	AK047188 Mus muscu
2	2811	51.3	3831	11 AK046203	AK046203 Mus muscu
3	1212.2	22.1	1529	11 AK034961	AK034961 Mus muscu
4	1182	21.6	1346	11 U66672	U66672 Homo sapien

5	837	15.3	850	14	CD250953	CD250953 AGENCOURT
6	797.6	14.6	809	11	BC029426	BC029426 Homo sapi
7	761.4	13.9	872	13	BQ722933	BQ722933 AGENCOURT
8	754.2	13.8	4620	29	AY414282	AY414282 Homo sapi
9	741.4	13.5	773	13	BQ441353	BQ441353 AGENCOURT
C 10	731	13.4	747	13	BU686259	BU686259 UI-CF-DUI
11	722.4	13.2	771	12	BG564439	BG564439 602584385
C 12	719.4	13.1	793	14	CB241963	CB241963 UI-CF-FNO
13	681.6	12.4	756	12	BG435656	BG435656 602506942
C 14	676.4	12.4	697	13	BQ774317	BQ774317 UI-H-EZ1-
15	668	12.2	926	13	BU146839	BU146839 AGENCOURT
C 16	661.6	12.1	728	13	BU623566	BU623566 UI-H-FG1-
17	652.4	11.9	800	13	BU750944	BU750944 CH3#036_H
18	641	11.7	664	14	CB044826	CB044826 NISC_gc06
19	637	11.6	670	12	BG570726	BG570726 602591840
20	634.4	11.6	4594	29	AY414284	AY414284 Mus muscu
21	633	11.6	633	14	CA773136	CA773136 im60b03.Y
22	630.4	11.5	768	13	BU853701	BU853701 AGENCOURT
23	628.6	11.5	724	14	CB962917	CB962917 AGENCOURT
24	627	11.5	4620	29	AY414283	AY414283 Pan trogl
25	625.2	11.4	694	10	BF969534	BF969534 602271862
26	623	11.4	623	14	CA773849	CA773849 im58a04.Y
27	621.6	11.4	3890	11	BC053340	BC053340 Mus muscu
28	617	11.3	642	14	CA773183	CA773183 im60g04.Y
C 29	612.4	11.2	614	14	CA771132	CA771132 io71b12.X
30	610.8	11.2	3357	11	BC037309	BC037309 Homo sapi
31	609.6	11.1	4119	11	AK029256	AK029256 Mus muscu
32	595.2	10.9	627	14	CD767029	CD767029 AGENCOURT
33	589.6	10.8	898	12	BG192651	BG192651 RST11768
34	586.8	10.7	961	14	CD242938	CD242938 AGENCOURT
C 35	583.8	10.7	589	12	BG149983	BG149983 nad50a05.
C 36	583.6	10.7	678	10	BE220217	BE220217 hv69f11.X
37	577.2	10.5	713	14	CF745072	CF745072 UI-M-GV0-
C 38	573.6	10.5	581	14	CA941420	CA941420 ir34h12.X
C 39	573.2	10.5	578	13	BU069128	BU069128 im58a04.X
C 40	565.8	10.3	608	10	AW131017	AW131017 xe68f06.X
41	565.2	10.3	744	9	AL700140	AL700140 DKF2p686H
C 42	561.2	10.3	622	13	BU952395	BU952395 io74a05.X
43	559.4	10.2	769	14	CD349566	CD349566 UI-M-FY0-
44	559.2	10.2	3300	11	AK085555	AK085555 Mus muscu
45	556.6	10.2	606	14	CD704485	CD704485 EST21012

ALIGNMENTS

RESULT 1	AK047188	AK047188	3950 bp	mRNA	linear	HTC 20-SEP-2003
LOCUS	Mus musculus	10 days neonate cerebellum cDNA, RIKEN full-length				
DEFINITION	enriched library, clone:B930033A02	product:ATP-BINDING CASSETTE				
	PROTEIN homolog [Homo sapiens], full insert sequence.					
ACCESSION	AK047188					
VERSION	AK047188.1	GI:26338625				
KEYWORDS	HTC; CAP trapper.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
REFERENCE	1					
AUTHORS	Carninci, P. and Hayashizaki, Y.					
TITLE	High-efficiency full-length cDNA cloning					
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)					
MEDLINE	99279253					
PUBMED	10349636					
REFERENCE	2					
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,					
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.					
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to					
JOURNAL	prepare full-length cDNA libraries for rapid discovery of new genes					
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)					
PUBMED	20499374					
	11042159					

REFERENCE

AUTHORS

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3950)

TITLE

JOURNAL

REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE

JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers

FEATURES

source

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/db_xref="GI:26338626"

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KTCDAAYWSLFTVLAQSIDAAIIQLKTNVSWSELESTKAVIMGEAAVEIDTFPR
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MSLMVIAATASSLFPSSIVIFELFLYGLSSVFFALMLTFLFKSKHGVVEFFV
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ORIGIN

Query Match 53.7%; Score 2938.4; DB 11; Length 3950;
Best Local Similarity 86.4%; Pred. No. 0;
Matches 3245; Conservative 0; Mismatches 511; Indels 0; Gaps 0;
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QY 467 CAGTCTCTTAAGCCGAGCAACTTTGTAGGTGTGGTTTTCAGAACTCCATGTCTCTATGA 526
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Db 614 ACTTCGTTTTTTTCTCTGATATGATTTCCAGTATCTTCTATTTATATGATTTCAAGAGAGG 673
QY 587 CTGTTCAAAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTTCAGATTTTACAAGC 646
Db 674 CTGTTCAAAAGACATGTGATGCTGCTCAGTACTGCTTCTTTGGGGTTTACAGTTCTGCAGGC 733
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QY 707 GTCAACTAAAGCTGTTTATATGGGAGAAACGCTGTGTGTAGAAATAGATACCTTTCCCGC 766
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QY 767 AGGAGTAATTTTAAATATACCTAGTTATAGCATTTTTCACCTTTTGGGATACTTTTGGCAAT 826

Db 854 AGGGTCATCCTCATCTACCTCGTCATAGCCCTTCTGCGCCCTCGGCTACTTTCCTGGCAAT 913
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Db 3674 GCAATATGCAGTTACGGCTGTCTTTTCAATACACCTTCTGTCATAGCCATTCCAATCTACCC 3733
|||
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Db 3734 TCTCCTGGGTTGTCTGATTTCTTTTCAATAAGGTTCTTGGAGAAGATATGCCAAAAAATGA 3793
|||
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RESULT 2
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DEFINITION Mus musculus adult male corpora quadrigemina cDNA, RIKEN
full-length enriched library, clone:B230352G14 product:ATP-BINDING
CASSETTE PROTEIN homolog [Homo sapiens], full insert sequence.
ACCESSION AK046203
VERSION AK046203.1 GI:26091381
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS

TITLE

JOURNAL
AUTHORS

TITLE

JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT

FEATURES
source

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 3831)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

Location/Qualifiers

1. 3831

/organism="Mus musculus"

/mol_type="mRNA"

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/db_xref="FANTOM DB:B230352G14"
/db_xref="MGI:2411591"
/db_xref="taxon:10090"
/clone="B230352G14"
/sex="male"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
misc_feature
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/note="ATP-BINDING CASSETTE PROTEIN homolog [Homo sapiens]
(SPTR|CAB93535, evidence: FASTY, 89.4%ID, 76.5%length,
match=3750)"

ORIGIN

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QY	107	AGAAAACATGTCCACTGCAATTAAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCT	166	
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QY	167	ACTGAAGAATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATCTTTT	226	
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QY	347	TCCTGGATATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGCTACTGA	406	
Db	480	TCCTGGATACACTCCCGTGACTAACATTACAAGCAGCATTATGCAGAGGGTTTCTACCGA	539	
QY	407	TCATCTACCTGATGTCATAATTACTGAAGAATATACAATGAAAAAGAAATGTTAAACATC	466	
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QY	467	CAGTCTCTCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTCAAAGACTCCATGTCTCTATGA	526	
Db	600	AAGTCTTTCTAAGTCCAGCAACTTCGTAGGTGTGGTTTTCAAAGACACCATGTCTCTATGA	659	
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Db	660	ACTTCGTTTTTTTTCCTGAAATGATTCAGTGTCTTCTATTTATATGAAATCAAGAGAAGG	719	
QY	587	CTGTTCAAATCATGTGAGGCTGCTCAGTACTGGTCCCTCAGGTTTTCACAGTTTACAAGC	646	
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QY	647	ATCCATAGATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAGGAGCTGGA	706	
Db	780	ATCGATAGATGCTGCCATTATACAGCTGAAGACCAATGTTTCTGTGTGGAGCGAGCTGGA	839	
QY	707	GTCAACTAAAGCTGTTATTATGGGAGAAACTGCTGTGTGTAGAAATAGATACTTTCCCGG	766	
Db	840	GTCGACCAAAGCTGTGATCATGGGAGAGGCCGCTGTTGTGGAGATTGACACCTTCCCGCG	899	
QY	767	AGGAGTAATTTTAATATACCTAGTTATAGCAATTTTCACTTTTGGATACCTTTTGGCAAT	826	
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QY	827	TCATATCTGAGCAGAAAAAGAAAAATAAAAGAAATTTTAAAGATAAATGGGACTTCA	886	
Db	960	CCACATCGTGGCAGAAAAAGAAAGAAAGTTAAAGGAATTTTAAAGATAAATGGGACTTCA	1019	
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Db	1080	CCTGCTTATGGCTGTTCATCGCAACAGCTTCTTCGTTATTCCTCAGAGTAGCAGCAATTGT	1139	
QY	1007	GATATTTCTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTCCTTTTAAATGCTGAC	1066	
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QY	1187	TTTCAGTCCCTTCTGTCACTGTACTTTTGTGATTGGTATTGCACAGGTCATGCAATTTAGA	1246	
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QY	1247	AGATTTTAAATGAAGGTGCTTCATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAATTTAT	1306	
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Db	1500	CCAAGTCATTTCCAGGGGAATTTGGCTTGAGGAGGTCACTTTGTATTTTGAAGCCATC	1559	
QY	1427	ATATTGCTC-AAAGAGCAAAAGAAATTTATGAGGAGTTTATCAGAGGGCAATGTTAATGGAA	1485	
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Db	1680	TAAGAAATAGTGGTATTTCAGAAATCTCTATAGAAAGAAACTGAGAAACGTGGAGGCTTTGA	1739	
QY	1606	GAAATTTGTTCATTGACATATATGAGGGTCAGATTACTGCTTACTTGGCCACAGTGGAA	1665	
Db	1740	GAAATTTGTTCATTGACATATATGAGGGTCAGATTACTGCTTACTTGGCCACAGTGGAA	1799	
QY	1666	CAGGAAAGAGTACATTGATGAATATTTTGTGGACTCTGCCCCACCTTCTGATGGGTTTG	1725	
Db	1800	CAGGAAAGAGTACATTGATGAATATTTTGTGGACTCTGTGTGGACTGTGCTCACCCCTCTGATGGGTTTG	1859	
QY	1726	CATCTATATATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAAATGA	1785	
Db	1860	CTTCTATATATGGACACAGAGTCTCTGAAATAGATGAATGTTTGAAGCAAGAAAAATGA	1919	
QY	1786	TTGGCAATTTGTCCACAGTTAGATATACACTTTTGATGTTTTCAGAGTAGAAGAAAAATTTAT	1845	
Db	1920	TTGGCAATATGTCCGAGTCAGATATAAACTTTTGATGTTTCTGACAGTAGAAGAAAAATTTAT	1979	
QY	1846	CAATTTTGGCTTCAATCAAAGGGATACAGCCCAACAATATAATAACAAGAGTGCAGAAAG	1905	
Db	1980	CAATTTTGGCTTCAATCAAAGGGATACAGCCCAACAATATAATAACAAGAGTGCAGAAAG	2039	
QY	1906	TTTTTACTAGATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAATTAAGTGGTG	1965	
Db	2040	TGTTGCTGGATCTGGACATGCAAGCCCATCAAAGATAATCAAGCGAAAAAGTTAAGCGGTG	2099	
QY	1966	GTCAAAAAAGAAAGCTGTCAATTAGGAATTTGCTGTTCTTGGGAACCCAAAGATACTGCTGC	2025	
Db	2100	GTCAGAAAAAGGAAGCTGTCTGTAGGAATTCAGTTTCTCGGGAATCCAAAGATACTCCTGC	2159	

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2160 TAGACGAGCTACAGCAGGAATGGACCCCTGCTCTCGCATATTGTTTGGAACTCTCTAA 2219
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Db |||||
2220 AGTATAGAAAGGCTAACAGAGTACCGTGTCTTAGTACTCACTTCATGGATGAGGCTGACA 2279
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Db |||||
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Db |||||
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QY 2266 GTGCCACAGAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTAC 2325
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Db |||||
2520 GCTTGTCTTCTGCTCTAGACATTCATTCAACCTGGGTGTATTTCTTATGGTGTTCGA 2579
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Db |||||
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RESULT 3
AK034961
LOCUS

DEFINITION
AK034961 1529 bp mRNA linear HTC 18-SEP-2003
Mus musculus 12 days embryo embryonic body between diaphragm region
and neck CDNA, RIKEN full-length enriched library, clone:9430067009
product:ATP-BINDING CASSETTE PROTEIN homolog [Homo sapiens], full
insert sequence.

ACCESSION
AK034961
VERSION
AK034961.1 GI:26330331
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
1 Carninci,P. and Hayashizaki,Y.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS
Carninci,P. and Hayashizaki,Y.
TITLE
High-efficiency full-length cDNA cloning
JOURNAL
Meth. Enzymol. 303, 19-44 (1999)
MEDLINE
99279253
PUBMED
10349636

REFERENCE
2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL
MEDLINE
20499374
PUBMED
11042159

REFERENCE
3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Db 901 CCTGCAAAATTTCTTGCTGTGGTGTTCCTCATTTGCTTATGTGCCCTCCGTCATCTG 960
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QY 3588 GGATACACAATTTGCAACTATTCTTCATATATGCTTTTGTATCATCTCCAAATCTATCCA 3647
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Db 1321 AAGGATCCATTTTTCAGGGCCCTTTCACAAAAGGCCAAAAAATAAGAAAGTTTCCAGAACCA 1380
QY 3888 CCAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTG 3947
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QY 3948 ATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAAGCAATTTGCATAAAGAA 4007
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Db 1501 TATGATGACAAGAAAGATTTTCTTCTCATTC 1529

RESULT 4
U66672 LOCUS U66672 1346 bp mRNA linear HTC 23-JUL-2001
DEFINITION Homo sapiens clone EST90625 mRNA sequence.
ACCESSION U66672
VERSION U66672.1 GI:1906557
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Allikmets,R., Gerrard,B., Hutchinson,A. and Dean,M.
TITLE Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed sequence tags database
JOURNAL Hum. Mol. Genet. 5 (10), 1649-1655 (1996)
MEDLINE 97049974
PubMed 8894702
REFERENCE 2 (bases 1 to 1346)
AUTHORS Allikmets,R., Gerrard,B. and Dean,M.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1996) Human Genetics Section, National Cancer Institute, NCI-FCRDC, Frederick, MD 21702, USA
FEATURES
Location/Qualifiers
1..1346
/organism="Homo sapiens"
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/clone="EST90625"

ORIGIN
Query Match 21.6%; Score 1182; DB 11; Length 1346;
Best Local Similarity 96.5%; Pred. No. 4.4e-198;
Matches 1306; Conservative 0; Mismatches 29; Indels 19; Gaps 9;
/note="similar to ATP-binding cassette transporter"
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QY 3949 TGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGTCATAAAGAA 4008
Db 61 TGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGTCATAAAGAA 120
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Db 181 TCTCTTCTGTGTGAAAAAAGAGAGATCTTTAGGACTATTTGGGTCCAAATGGTCTGGCA 240
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Db 241 AAAGCACAATTATTATATTCTGGTTAGTGATATTGAACCACTTCAGGCCAGGTATTTT 300
QY 4189 TAGGAGATTATTCTTCAGAGACAAAGTGAAGATGATGATTCACTGAAGTGTATGGGTACT 4248
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QY 4249 GTCTCTCAGATAAAACCCCTTTGTGGCCAGATACATACTATGCAGGAACATTTTGAATTTATG 4308
Db 361 GTCTCTCAGATAAAACCCCTTTGTGGCCAGATACATACTATGCAGGAACATTTTGAATTTATG 420
QY 4309 GAGCTGTCAAAGGAATGAGTCAAGTGACATGAAGAGAGTCAAGTCAAGTCAAGTCAAGTCAAG 4368
Db 421 GAGCTGTCAAAGGAATGAGTCAAGTGACATGAAGAGAGTCAAGTCAAGTCAAGTCAAGTCAAG 480
QY 4369 CACTTGATTTAAAGAAACATCTTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAAAAC 4428
Db 481 CACTTGATTTAAAGAAACATCTTTCAGAAAGACTGTAAAGAAACTACCTGCNAGGAATCAAAA 540
QY 4429 GAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAAC 4488
Db 541 CGAAAGTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAAC 600
QY 4489 CATCTACAGGTATGGATCCCAAA--GCCAAACAGACACATGTGGCGAGCAATTCGAACTGC 4546
Db 601 CATCTACAGGTCTGGATCCCAATGCCAAACATGCATCATGTGGCATGTGCAATTCGAACTGC 660
QY 4547 ATTTAAAAAACAGAAAGCGGGTCTATTCTGACCCTCACTATATGGAGGAGGCAGAGGC 4606
Db 661 AT-----NNAAGCGGGTCTATTCTGACCCTCACTATATGGAGGAGGCAGAGGC 711
QY 4607 TGCTGTGATCGAGTAGCTATCATGGTGTCTGGGCACTTAAGATGTATCGGAACAGTACA 4666
Db 712 TGCTGTGATCGAGTAGCTATCATGGTGTCTGGGCACTTAAGATGTATCGGAACAGTACA 771
QY 4667 ACATCTAAAGAGTAAATTTGGAAGAGGCTACTTTTGGAAAAATTAAATTGAA--GGACTGGA 4725
Db 772 ACATCTAAAGAGTAAATTTGGAAGAG--NACTTTTGGAAAAATTAAATTGAACCGGACTGGA 829
QY 4726 TAGAAAAACCTAGAAG--TAGACCGCCCTTCAAAGAGAAAAATTCAGTATATTTTCCCAATGCA 4784
Db 830 TAGAAAAACCTAGAAGCTAGACCGCCCTTCAAAGAGAAAAATTCAGTATATTTTCCCAATGCA 889
QY 4785 AGCGCTCAGGAAAGTTTTTCTTCTATTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCA 4844
Db 890 AGCGCTCA--GAAAGTTTTTCTTCTATTATTTTGGCTTCTAAAAATTAATAAGGAAGATGTTTCA 948
QY 4845 TCCCTTTCACAATCTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGGCATTGAAGAA 4904

Db 949 TCCCTTCCCAATCTTTTAAAGCTGGAAGAAGCTAAACATGC-TTTGCCATTGAAGAA 1007

Qy 4905 TATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCAGTAAAGAACAAAGAG 4964

Db 1008 TATAGC-TTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCAGTAAAGAACAAAGAG 1066

Qy 4965 GAGGAAGATAAATAGTTGTGGAACCTTTAAACAGCACACCTTTGGTGGGAACGACGACAAAGAA 5024

Db 1067 GAGGAAGATAAATAGTTGTGGAACCTTTAAACAGCACACCTTTGGT-GGAACGACGACAAAGAA 1125

Qy 5025 GATAGAGTAGTATTTTGAATTTGTATTGTTTCGGTCTGCTTACTGGGACTTCTTCTTTT 5084

Db 1126 GATAGAGTAGTATTTTGAATTTGTATTGTTTCGGTCTGCTTACTGGGACTTCTTCTTTT 1185

Qy 5085 CACTTAATTTTAACTTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGGAGAACCAAG 5144

Db 1186 CACTTAATTTTAACTTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGGAGAACCAAG 1245

Qy 5145 AACGCACCTTGAAATTTTCTAAGCTCCTTAATTGAATGCTGTGGTTGTGTGTTTTCCTT 5204

Db 1246 AACGCACCTTGAAATTTTCTAAGCTCCTTAATTGAATGCTGTGGTTGTGTGTTTTCCTT 1305

Qy 5205 TTTCTTAAATAAAACGATGATGATATAATTAAGTGAA 5238

Db 1306 TTTCTTAAATAAAACGATGATGATATAATTAAGTGAA 1339

RESULT 5

CD250953

LOCUS CD250953 850 bp mRNA linear EST 22-MAY-2003

DEFINITION AGENCOURT 14214041 NIH MGC_179 Homo sapiens cDNA clone

IMAGE:30385589 5', mRNA sequence.

ACCESSION CD250953

VERSION CD250953.1 GI:31011419

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 850)

TITLE NIH-MGC <http://mgc.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM452 row: o column: 06

High quality sequence stop: 719.

FEATURES

source

1..850

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:30385589"

/tissue_type="Pituitary"

/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"

/clone_lib="NIH MGC 179"

/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV (destroyed); Site_2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 15.3%; Score 837; DB 14; Length 850;

Best Local Similarity 99.8%; Pred. No. 2.6e-137;

Matches 848; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 4117 ATGTCCTCGGCAAAAGCACAAATTATTAAATA-TTCTGTTGGTGATATTGAACCAACTTCA 4175

Db 1 ATGTCCTCGGCAAAAGCACAAATTATTAAANTTCTGTTGGTGATATTGAACCAACTTCA 60

Qy 4176 GGCCAGGTATTTTGGAGATTTATTTCTTCAGAGACAAAGTGAAGATGATGATTCACCTGAAG 4235

Db 61 GGCCAGGTATTTTGGAGATTTATTTCTTCAGAGACAAAGTGAAGATGATGATTCACCTGAAG 120

Qy 4236 TGTAATGGGTTACTGTCTCAGATAAAACCCCTTTGTGGCCAGATACATGATTCGAGGAACAT 4295

Db 121 TGTAATGGGTTACTGTCTCAGATAAAACCCCTTTGTGGCCAGATACATGATTCGAGGAACAT 180

Qy 4296 TTTGAAATTTATGGAGCTGTCAAAAGGAATGAGTGCAAGTGAATGCAATGAAAGAAAGTCATAAGT 4355

Db 181 TTTGAAATTTATGGAGCTGTCAAAAGGAATGAGTGCAAGTGAATGCAATGAAAGAAAGTCATAAGT 240

Qy 4356 CGAATAACACATGCACCTTGATTTAAAGAAACATCTTCAGAAAGACTGTAAAGAAACTACCT 4415

Db 241 CGAATAACACATGCACCTTGATTTAAAGAAACATCTTCAGAAAGACTGTAAAGAAACTACCT 300

Qy 4416 GCAGGAATCAAAACGAAAGTTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTACT 4475

Db 301 GCAGGAATCAAAACGAAAGTTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTACT 360

Qy 4476 TTGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCAAAACAGCACATGTGGCGAGCA 4535

Db 361 TTGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCAAAACAGCACATGTGGCGAGCA 420

Qy 4536 ATTGCAACTGCATTTTAAAGAAAGCGGGCTGCTATTCTGACCACCTCAGTATATGGAG 4595

Db 421 ATTGCAACTGCATTTTAAAGAAAGCGGGCTGCTATTCTGACCACCTCAGTATATGGAG 480

Qy 4596 GAGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGTGTCTGGCAGTTAAGATGATC 4655

Db 481 GAGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGTGTCTGGCAGTTAAGATGATC 540

Qy 4656 GGAACAGTACAACATCTAAAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAATG 4715

Db 541 GGAACAGTACAACATCTAAAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAATG 600

Qy 4716 AAGCACTGGATAGAAAACCTAGAAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTT 4775

Db 601 AAGCACTGGATAGAAAACCTAGAAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTT 660

Qy 4776 CCAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGAA 4835

Db 661 CCAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGAA 720

Qy 4836 GATGTTCAGTCCCTTTTCAAAATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCC 4895

Db 721 GATGTTCAGTCCCTTTTCAAAATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCC 780

Qy 4896 ATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAA 4955

Db 781 ATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAA 840

Qy 4956 GAACAAGAGG 4965

Db 841 GAACAAGAGG 850

RESULT 6

BC029426

LOCUS BC029426

DEFINITION Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 5, mRNA (cDNA clone IMAGE:4723522), containing frame-shift errors.

ACCESSION BC029426

VERSION BC029426.1 GI:20809520

BC029426 809 bp mRNA linear HTC 19-NOV-2003

KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 809)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 809)
Strausberg, R.
Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 41 Row: 1 Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27262625
This clone has the following problem: frame shifted.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4723522"
/tissue_type="Liver"
/clone_lib="NIH MGC_76"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"
ORIGIN
Query Match 14.6%; Score 797.6; DB 11; Length 809;
Best Local Similarity 99.5%; Pred. No. 2.3e-130;
Matches 800; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 60 CGCGTCCAGGCTGACAGCTCTGCGGCTCGGGCCCTGAGGTTATTTCAGAAAACATGTCC 119
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Db 1 CGCGTCCAGGCTGACAGCTCTGCGGCTCGGGCCCTGAGGTTATTTCAGAAAACATGTCC 60
QY 120 ACTGCAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACCTTCTACTGAGAAATTAC 179
Db 61 ACTGCAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACCTTCTACTGAGAAATTAC 120
QY 180 TTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCACTATTTT 239
Db 121 TTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCACTATTTT 180
QY 240 TTAATTTGGTTAAATTAATTAGCATGATGCATCCAAATAAGAAATATGAGAAAGTGCCT 299
Db 181 TTAATTTGGTTAAATTAATTAGCATGATGCATCCAAATAAGAAATATGAGAAAGTGCCT 240
QY 300 AATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTCTGGATATACT 359
Db 241 AATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTCTGGATATACT 300
QY 360 CCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTACCTGAT 419
Db 301 CCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTACCTGAT 360
QY 420 GTCATAATTACTGAAGAATATACAAATGAAAGAAATGTTAACAATCCAGTCTCTCTAAG 479
Db 361 GTCATAATTACTGAAGAATATACAAATGAAAGAAATGTTAACAATCCAGTCTCTCTAAG 420
QY 480 CCGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGTCCTATGAACCTTCGTTTTT 539
Db 421 CCGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGTCCTATGAACCTTCGTTTTT 480
QY 540 CCTGATATGATTCAGTATCTTCTATTTATATGGAATCAAGAGCTGGCTGTTCAAAATCA 599
Db 481 CCTGATATGATTCAGTATCTTCTATTTATATGGAATCAAGAGCTGGCTGTTCAAAATCA 540
QY 600 TGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTCAAGGTTTCAAGCATCCATAGATGCT 659
Db 541 TGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTCAAGGTTTCAAGCATCCATAGATGCT 600
QY 660 GCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACTAAAGCT 719
Db 601 GCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACTAAAGCT 660
QY 720 GTTATTATGGAGAAACTGCTGTGTAGAAATAGATACCTTTCCCGAGGAGTAATTTA 779
Db 661 GTTATTATGGAGAAACTGCTGTGTAGAAATAGATACCTTTCCCGAGGAGTAATTTA 720
QY 780 ATATACCTAGTTATAGCATTTTACCTTTTGGATACCTTTTGGCAATTCATATCGTAGCA 839
Db 721 ATATACCTAGTTATAGCATTTTACCTTTTGGATACCTTTTGGCAATTCATATCGTAGCA 780
QY 840 GAAAAAGAAAAAATAAAGAA 863
Db 781 AAAAAAATAAAGAAAAA 804
RESULT 7
BQ722933
LOCUS
DEFINITION
AGENCOURT_8100461 Lupeki_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6190464 5', mRNA sequence.
ACCESSION
BQ722933
VERSION
BQ722933.1 GI:21861819
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 872)
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAX13589 row: f column: 01
High quality sequence stop: 717.
Location/Qualifiers
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/clone="IMAGE:6190464"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site 2: SalI; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5'-TCGACCCCGCTCCG-3' and
5'-GACTAGTTCAGATCGGAGCGGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.9 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine); available through Life
Technologies."

ORIGIN

Query Match 13.9%; Score 761.4; DB 13; Length 872;
Best Local Similarity 97.9%; Pred. No. 5.2e-124;
Matches 825; Conservative 0; Mismatches 11; Indels 7; Gaps 5;

QY 4073 TTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAG 4132
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Db 1 TTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAG 60
|||||

QY 4133 CACAATTATTAATATTCTGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGG 4192
|||||
Db 61 CACAATTATTAATATTCTGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGG 120
|||||

QY 4193 AGATTATCTTCAGAGACAAGTGAAGATGATGATCACTGAAGTGATGGTTACTGTCC 4252
|||||

Db 121 AGATTATCTTCAGAGACAAGTGAAGATGATGATCACTGAAGTGATGGTTACTGTCC 180
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QY 4253 TCAGATAAACCCCTTTGTGGCCAGATACTACATTGCAGGAACATTTTGAATTTATGGAGC 4312
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Db 181 TCAGATAAACCCCTTTGTGGCCAGATACTACATTGCAGGAACATTTTGAATTTATGGAGC 240
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QY 4313 TGTCAAAGGAATGAGTGCAGTACATGAAAGAGTCATAAGTCGAATAACACATGCACT 4372
|||||

Db 241 TGTCAAAGGAATGAGTGCAGTACATGAAAGAGTCATAAGTCGAATAACACATGCACT 300
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QY 4373 TGATTTAAAGAACATCTTTCAGAAGACTGTAAAGAACTACCTGCAGGAATCAAAACGAA 4432
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Db 301 TGATTTAAAGAACATCTTTCAGAAGACTGTAAAGAACTACCTGCAGGAATCAAAACGAA 360
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QY 4433 GTTGTTGTTTGTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGTAGAACCATC 4492
|||||

Db 361 GTTGTTGTTTGTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGTAGAACCATC 420
|||||

QY 4493 TACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAA 4552
|||||

Db 421 TACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAA 480
|||||

QY 4553 AAACAGAAAGCGGGCTGCTATTCTGACCACCTACATATATGGAGGAGGCGAGGCTGTCTG 4612
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Db 481 AAACAGAAAGCGGGCTGCTATTCTGACCACCTACATATATGGAGGAGGCGAGGCTGTCTG 540
|||||

QY 4613 TGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCT 4672
|||||

Db 541 TGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCT 600
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QY 4673 AAAGAGTAAATTTGGAAAGCGCTACTTTTGGAAATTAAATTGAAGGACTGGATAGAAA 4732
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Db 601 AAAGAGTAAATTTGGAAAGCGCTACTTTTGGAAATTAAATTGAAGGACTGGATAGAAA 660
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QY 4733 CCTAGAAGTAGACCGCCCTTCAAAGAGAAATTCAGTATATTTTCCCAATGCAAG-CCGTC 4791
|||||

Db 661 CCTAGAAGTAGACCGCCCTTCAAAGAGAAATTCAGTATATTTTCCCAATGCAAGCCGTC 720
|||||

QY 4792 AGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATT-CCTAAGGAAGATGTTTCAGT-CCCT 4849
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Db 721 AGGAAAGTTTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCT 780
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QY 4850 TTCACAATCTTTTTTAA---GCTGGAAGAAGCTAAACAT-GCTTTTGCCATTGAAGAA 4905
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Db 781 TTCACAATCCTTTTTTTAAGCCTGGAAGAAGCTAAACATGGCTTTTGCCATTGGAAGAA 840
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QY 4906 ATA 4908
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Db 841 ATA 843
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RESULT 8
AY414282
LOCUS
DEFINITION
AY414282 4620 bp DNA linear GSS 17-DEC-2003
Homo sapiens ABCA9 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY414282
VERSION
AY414282.1 GI:39770244
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 4620)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302
REFERENCE
2 (bases 1 to 4620)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1. .4620
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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ORIGIN
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Best Local Similarity 50.2%; Pred. No. 5e-123;
Matches 2435; Conservative 0; Mismatches 2069; Indels 346; Gaps 19;

QY 150 CAGACCAGAACACTTCTACTGAAGAATTACTTAATTAATGCAGAACCAAAAAGAGTAGT 209
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Db 31 CAAACATGGGCTCTTCTCTGCAAGAACTGTCTCAAAAAAATGGAGAATGAAAAGACAGACC 90
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Db 2071 TATATTTTGCCTTTGGAAAGGACAAACAAATTTCCAGNNNNNNNNNNNNNNNNNNNNNNNN 2130

QY 2409 CATTCAAATTTGGGTGTCAATTTCTTTATGGTGTCTTCCATGACGACTTTTGGAAAGACGTAATTT 2468

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QY 2469 TTAAAGCTAGAAAGTTGAAGCAGAAATTCACCAAGCAGATTATAGTGTATTTACTCAGCAG 2528

Db 2191 CTGAAATTTAGAAAGAAATCAACTATTGATGAATCAGATATTGGAATTTGGGGACAATTA 2250

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Db 2251 CAAACTGATGGGCAAAAGATATAGGAAGCCTTGTGAGCTGGAAACAAGTTTGTCTCTCC 2310

QY 2589 CTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATTGAGCCTTTTGGAAACAACAGATGTAT 2648

Db 2311 TTCCACGAAACAAAGAAAC---AATCAGTGGCGTGGCGCTCTGAGGCAGCAGGCTGT 2367

QY 2649 ACAATAGCAAAGTTTCATTTCTTTACCTTGAAACGTTGAAGTAAATCAGTGAGATCAGTG 2708

Db 2368 GCAATAGCAAAGTTTCGCTTCTCTAAAGTTAAAGAAAGAAAGAAAGCCTGTGGACTATA 2427

QY 2709 TTGCTTCTGCTTTTAATTTTTCACAGTTCAGATTTTATGTTTGTGTTTTCATCACTCT 2768

Db 2428 TTATTGCTTTTGTGTTATAGCTTTATCCCTCAACTTTTGGAAACATCTATTCTACGAGTCA 2487

QY 2769 TTTAAAAATGCTGTGGTTCCCATCAAACTGTGTTCCAGACTTATATTTTCTAAACCTTGA 2828

Db 2488 TATCAGAAAGT---TACCCTGGGAACTGTCTCCTCAAAATACATACTTCTCTCACCAGGA 2544

QY 2829 GACAAACCAATATAAATACAAACAAAGTCTGCTTCTTCAAAATTTCTGCTGACTCAGATATC 2888

Db 2545 CAACAACCAACAGGATCCTCTGACCCATTACTGGTCTATCAATAAGACAGGGTCAACCAAT 2604

QY 2889 AGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGACGATGATTATGACAGT 2948

Db 2605 GATAACTTTTACATTCACATGAGCGACAGAACATAGCTATAGAAGTGGATGCCTTTGA 2664

QY 2949 GACTATGTATCCGTGGCTCCCCATAGTGGCGCTTTAAATGTGATGCATTCAGAAAAGGAC 3008

Db 2665 ACTAGAAATGGCACAGATGACCCATCTTACAATGGTGCTATCATTTGTGTCAGGTGATGAA 2724

QY 3009 TATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTATTCTTTACCTATATTAGTGAAT 3068

Db 2725 AAGNN 2784

QY 3069 ATCATTAGTAACACTACTATCTTTATCATTTAAATGTGACTGAACCATCCAGATCTGGAGT 3128

Db 2785 NNN 2844

QY 3129 ACCCCATTTCTTCAAGAAATTAAGTATAGTATAGTATGGTACCGAAGTAACACC 3188

Db 2845 NNN 2904

QY 3189 GCTTTGCTTGGATCATTTGTTACTGCAATGCCACCTTACTTTGCCATGGAAATGCAGAG 3248

Db 2905 TTCTTCTGGATACCGATGGCAGCCTCTTTCACTCCATACATTGCAATGAGCAGCATTTGGT 2964

QY 3249 AATCATAAGATCAAAGCTTATACCTCAACTTAACTTTTTCAGGTCTTTTGGCCATCTGCATAT 3308

Db 2965 GACTACAAAAAAGCTCATTTCCAGCTACGGATTTTCAGGCTCTACCCCTTCTGCAATAC 3024

QY 3309 TGGATTGGACAAGCTGTTGTGATATCCCTTATTTTTTATCACTCTTATTTTGTATGC-- 3366

Db 3025 TGGTTTGGCCAAAGCACTGGTGGATGTTTCCCTGTACTTTTGTATCCTCTCTGCTAATGCAA 3084

QY 3367 --TAGGAAGCTTATTTGGCATTTCATTTAGGATATATTTTTTATCTGTAAAGTTCCCTGC 3424

Db 3085 ATAATGGATTATATTTTATAGCCAGAGGAGATATATTTATA-ATTCAAAAACCTGTTAAT 3143

QY 3425 TGTGGTTTTTGGCCTTATTTGTTTATGTTCCATCAGTTATTTCTGTTCACTTATATTTGCTTC 3484

Db 3144 TCAAACTCTGTAGTATTTGGCTATGTTCTCATCTCTTGTGTTTCTTGACATATGTGATTC 3203

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Db 3204 ATTCAATTTTTCGCAATGGGAGAAAAAATAGTGGCATTTTGGTCATTTTCTTCT--- 3256

QY 3545 AGCGTTGGCTTGTATTTGCAATCACTGAAATAAATTTCTTTATGGGATPACACAATTTGCAAC 3604

Db 3257 -----TAATTTGGTTCATCTTCTCGATAGTTGCTAC 3287

QY 3605 TATTCTTCATTTATGCTCTTTTGTATCATCATTTCCAATCTATCCACTTCTAGGTTGCCTGAT 3664

Db 3288 TGATCTAAATGA----- 3299

QY 3665 TTCTTTTCATAAAGATTTCTTTGGAAGAAATGTACGAAAAAATGTGGACACCTATAATCCATG 3724

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QY 3725 GGATAGGCTTTTCAGTAGCTGTTATATC-GCCTTACCTGCAGTGTGTACTGTGGATTTTCC 3783

Db 3353 TGATTGGCTCTCTATTTCTATTTTCTGAGCCTTACCTTCATTTTCTCATTTTCTTTTCA 3412

QY 3784 TCTTACAATACTATGAGAAAAAATATGAGGCGAGATCAATAAGAAAAAGATCCCTTTTCA 3843

Db 3413 TTCTGCGATGCTTAGAAATGAATGCACTGCAGGAAGAACTAATGAGAAAGGATCCTGTGTTCA 3472

QY 3844 GAAACCTTTCAACGAAGTCTAAAAAATAGGAAGCTTCCAGAACCCACGACACAATGAGGATG 3903

Db 3473 GAATTTCTCCAA-----GAAGCAACGCTATTTTCCAAACCCAGAGAGCCTGAAGGAG 3526

QY 3904 AAGATGAAGATGTCAAAGCTGAAAGACTTAAAGGTCAAAGAGCTGATGGTTGCCAGTGT 3963

Db 3527 AGGAGGAAGATATCCAGATGGAAGAAATGAGAACAGTGAATGCTATGGCTGTGCGAGACT 3586

QY 3964 GTGAGGAGAAACCATCCATTATGGTCAACCAATTTGCATAAAGAAATATGATGACAAGAAAG 4023

Db 3587 TTGATGAGACACCCGTCATCATTTGCCAGCTGTCTACGGAAGGAATATGAGGCAAAAAGA 3646

QY 4024 ATTTTCTTCTTTCAAGAAAGTAAAGAAAGTGGCAACTTAAATACATCTCTTTCTGTGTGA 4083

Db 3647 AAAATTGCTTTTCTAAAGGAAGAAAAAATTTGCCACAAGAAATGTCTTTTTTGT---- 3702

QY 4084 AAAAAGGAGAGATCTTTAGGACTATTGGGTCCAAATGGTGTGCTGGCAAAAGCACAATTTA 4143

Db 3703 -----GAAGTTATAGGACTGTTAGGACACAATGGAGCTGGTAAAGTACAACATA 3754

QY 4144 ATATTCTGGTTGCTGATATTGAACCAACTTCAGGCCAGGTATTTTATAGGAGATTTCTT 4203

Db 3755 AGATGATAACTGGAGACACAAAACCAACTGCAGGACAGGTGATTTTGAAAGGG----- 3807

QY 4204 CAGAGACAAGTGAAGATGATGATTCACGTGAAGTGTATGGTTACTGTCTCTCAGATAAAC 4263

Db 3808 -----AGCGGTGGAGGGGAAACCCCTGGGCTTCTGGGTACTGCCCTCAGGAGAATG 3859

QY 4264 CTTTGTGGCCAGATACTACATTCAGGAAACATTTTGAATTTTATGGAGCTGTCAAAGGAA 4323

Db 3860 CGCTGTGGCCCAACCTGACAGTGAAGGACACCTGCAGGTGTACCGTCCGTGAAAGGTC 3919

QY 4324 TGAGTGCAAGTGAATGAAAGAAAGTCAATAAGTCAATAACACATGCATTTGATTTTAAAG 4383

Db 3920 TCAGGAAAGGGGAGCAATGATCGCCATCACACGGTTAGTGGATGCGCTCAAGCTGCAGG 3979

QY 4384 AACATCTTCAGAAGACTGTAAAGAAACTTACCTGCAGGAATCAAAACGAAAGTTGTGTTTG 4443

Db 3980 ACCAGCTGAAGGCTCCCGTGAAGACCTTGTGAGAGGGAATAAAGCGAAAGCTGTGCTTTG 4039

QY 4444 CTCTAAGTATGCTAGGGAATCCTCAGATTTACTTTGCTAGATGAACCATCTACAGGTATGG 4503

Db 4040 TGCTGAGCATCTCTGGGAAACCCGTGAGTGGTGTCTTCTGGATGAGCCGTGACCCGGGATGG 4099

QY 4504 ATCCCAAAGCCAAACAGACACATGTGGCGAGCAATTCGAACTGCAATTTAAAAACAGAAAGC 4563

Db 4100 ACCCGAGGGGCGACGACCAATGTGGCAGGTGATTCGGGCCACCTTTAGAAAAACACGGAGA 4159

QY	4564	GGGCTGCTATTCTGACCACTCACTATATGGAGAGGCAGAGGCTGCTGTGATCGAGTAG	4623
Db	4160	GGGGCGCCCTCCTGACCACTACATGGCAGAGGCTGAGGCGGTGTGTGACCGAGTGG	4219
QY	4624	CTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAAACAGTACAACATCTAAAGAGTAAAT	4683
Db	4220	CCATCATGGTGTGAGGAAGGCTGAGATGTATTGGTTCCATCCAAACACCTGAAAAGCAAAAT	4279
QY	4684	TTGGAAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAACCTAGAAAGTAG	4743
Db	4280	TTGGCAAAGACTACCTGCTGGAGATGAAGCTGAAGAAACCTGGCACAA-----TGG	4330
QY	4744	ACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAGGAAAAGTTTIT	4803
Db	4331	AGCCCTCCATGCAGAGATCCTGAGGCTTTTCCCCAGGCTGCTCAGCAGGAAAGTTTCT	4390
QY	4804	CTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCAGTCCCTTTTCACAAATCTTTT	4863
Db	4391	CCTCCCTGATGGTCTATAAGTTGCCCTGTTGAGGATGTGCGACCTTTATCACAGGCTTTCT	4450
QY	4864	TTAAGCTGGAAGAGCTAAACATGCTTTTGGCATTTGAAGAAATATAGCTTTTCTCAAGCAA	4923
Db	4451	TCAAAATTAGAGATAGTTAAACAGAGTTTCGACCTGGAGGAGTACAGCCTCTCACAGTCTA	4510
QY	4924	CATTGGAACAGGTTTTTGTAGAACTCACTAAAGAAACAGAGGAGGAAGAT	4973
Db	4511	CCCTGGAGCAGGTTTTCTGGAGCTCTCCAAGGAGCAGGAGCTGGGTGAT	4560

RESULT 9
BQ441353
LOCUS
DEFINITION
BQ441353 773 bp mRNA linear EST 24-MAY-2002
AGENCOURT_7838430 NIH_MGC_82 Homo sapiens cdna clone IMAGE:6101304
5', mRNA sequence.

ACCESSION BQ441353
 VERSION BQ441353.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

SOURCE	ORGANISM	REFERENCE
Homo sapiens (human)	Homo sapiens	1 (bases 1 to 773)
Eukaryota; Metazoa	Eukaryota; Metazoa	
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
	Chordata; Craniata; Vertebrata; Euteleostomi;	

REFERENCE	1 (bases 1 to 775)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: CLONTECH cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

FEATURES
SOURCE

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1. /organism="Homo sapiens"
2. /mol_type="mRNA"
3. /db_xref="taxon:9606"
4. /clone="IMAGE:6101304"
5. /lab_host="DH10B (T1 phage-resistant)"
6. /clone_lib="NH MGC 82"

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/clone_lib="Nin_MGC_02"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site:1:
SfiI (ggcgccctcgcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCGATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo

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ORIGIN		Alto, CA)."				
		Query Match	13.5%;	Score 741.4;	DB 13;	Length 773;
		Best local Similarity	98.4%;	Pred. No. 1.8e-120;		
		Matches 759;	Conservative	0;	Mismatches 11;	Indels 1; Gaps 1;
QY	4426	AACGAAAGTTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATG	4485			
DB	3	AACGAAAGTTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATG	62			
QY	4486	AACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTG	4545			
DB	63	AACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTG	122			
QY	4546	CATTTAAAAACAGAAAGCGGGCTGCTATTCTTGACCACCTCACTATATGGAGGAGGCAGAGG	4605			
DB	123	CATTTAAAAACAGAAAGCGGGCTGCTATTCTTGACCACCTCACTATATGGAGGAGGCAGAGG	182			
QY	4606	CTGTCGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTAC	4665			
DB	183	CTGTCGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTAC	242			
QY	4666	AACATCTAAAGAGTAAATTTTGGAAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGA	4725			
DB	243	AACATCTAAAGAGTAAATTTTGGAAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGA	302			
QY	4726	TAGAAAACCTAGAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAA	4785			
DB	303	TAGAAAACCTAGAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAA	362			
QY	4786	GCCGTCAGGAAAGTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGT	4845			
DB	363	GCCGTCAGGAAAGTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGT	422			
QY	4846	CCCTTTCAAACTCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCATTTGAAGAAT	4905			
DB	423	CCCTTTCAAACTCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCATTTGAAGAAT	482			
QY	4906	ATAGCTTTTCTAAGCAACATTGGAAACAGGTTTTTGTAGAACTCACTAAGAACAAAGAGG	4965			
DB	483	ATAGCTTTTCTAAGCAACATTGGAAACAGGTTTTTGTAGAACTCACTAAGAACAAAGAGG	542			
QY	4966	AGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAACACAAGAAG	5025			
DB	543	AGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAACACAAGAAG	602			
QY	5026	ATAGAGTAGTATTTTGAATTTGTATTGTTCCGTCCTTACTGGGACTTCTTTCTTTTTC	5085			
DB	603	ATAGAGTAGTATTTTGAATTTGTATTGTTCCGTCCTTACTGGGACTTCTTTCTTTTTC	662			
QY	5086	ACTTAATTTTAACTTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACTGGAGAACCAAGA	5145			
DB	663	ACTTAATTTT-AACTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACTGGAGAACCCAGA	721			
QY	5146	ACGCACCTTGAAATTTTCTAAGCTCCTTAATTTGAATTCGTGTTGTGTG 5196				
DB	722	ACGCACCTTGAAATTTTCTAAGCTCCTTAATTTGAATTCGTGTTGTGTG 772				

RESULT 10	ACCESSION	REFERENCE
BU686259/c	VERSION	
LOCUS	KEYWORDS	
DEFINITION	SOURCE	
	ORGANISM	

sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN		Query Match		Score 722.4; DB 12; Length 771;		Best Local Similarity 99.4%; Pred. No. 4e-117;		Matches 767; Conservative 0; Mismatches 1; Indels 4; Gaps 4;	
QY	3824	AAGAAAGATCCCTTTTTCAGAAACCTTTCACGAAAGTCTAAAAATAGGAAGCTTCCAGA	3883						
Db	1	AAGAAAGATCCCTTTTTCAGAAACCTTTCACGAAAGTCTAAAAATAGGAAGCTTCCAGA	60						
QY	3884	ACCACCAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAGACTAAAGGTCAAAGA	3943						
Db	61	ACCACCAGCAATGAGGATGAAGATGAAGATGTCAAAGCTGAAGACTAAAGGTCAAAGA	120						
QY	3944	GCTGATGGTGTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAA	4003						
Db	121	GCTGATGGTGTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAA	180						
QY	4004	AGAATATGATGACAAGAAAGATTTTCTTTCAAGAAAGTAAAGAAAGTGGCAACTAA	4063						
Db	181	AGAATATGATGACAAGAAAGATTTTCTTTCAAGAAAGTAAAGAAAGTGGCAACTAA	240						
QY	4064	ATACATCTCTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGTCCAAATGGTGC	4123						
Db	241	ATACATCTCTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGTCCAAATGGTGC	300						
QY	4124	TGGCAAAAGCACAAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCAGGT	4183						
Db	301	TGGCAAAAGCACAAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCAGGT	360						
QY	4184	ATTTTATGAGATATTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGTGTATGGG	4243						
Db	361	ATTTTATGAGATATTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGTGTATGGG	420						
QY	4244	TTACTGTCTCAGATAAACCCCTTTGGGCCAGATACTACATTGCAGGAACATTTTGAAT	4303						
Db	421	TTACTGTCTCAGATAAACCCCTTTGGGCCAGATACTACATTGCAGGAACATTTTGAAT	480						
QY	4304	TTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAGAAGTCATAAGTCGAATAAC	4363						
Db	481	TTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAGAAGTCATAAGTCGAATAAC	540						
QY	4364	ACATGCACITGATTTAAAGAACAATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAAT	4423						
Db	541	ACATGCACITGATTTAAAGAACAATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAAT	600						
QY	4424	CAAA-CGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAG	4482						
Db	601	CAAAACCGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAG	660						
QY	4483	ATGAACCATCTACAGGTATGG-ATCCCAAAGCCAAACACAGCAC-ATGTGGCGAGCAATTGG	4540						
Db	661	ATGAACCATCTACAGGTATGGATCCCAAAGCCAAACACAGCACATGTGGCGAGCAATTGG	720						
QY	4541	AACTGCATTTAAAAACAGAAAGCGGCTGCTATTCTGCACCACTCACTATATG	4592						
Db	721	AACTGCATTTAAAAACAGAAAGC-GGCTGCTATTCTGCACCACTCACTATATG	771						

RESULT 12
CB241963/c
LOCUS
DEFINITION
UI-CF-FN0-aga-m-08-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
793 bp mRNA linear EST 12-FEB-2003
UI-CF-FN0-aga-m-08-0-UI 3', mRNA sequence.
CB241963
ACCESSION
CB241963.1 GI:28363607
VERSION

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 793)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library prepared by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..793
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FN0-aga-m-08-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FN0"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-CF-FN0 is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DU1) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FN0
TAG_SEQ=GGCTGTAGGC"

ORIGIN

Query Match		13.1%; Score 719.4; DB 14; Length 793;		Best Local Similarity 99.3%; Pred. No. 1.3e-116;		Matches 731; Conservative 0; Mismatches 4; Indels 1; Gaps 1;	
QY	4503	GATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTCGAAGTCAATTTAAAAACAGAAAG	4562				
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QY	4563	CGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGAGAGCTGTCTGTGATCGAGTA	4622				
Db	691	CGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGAGAGCTGTCTGTGATCGAGTA	632				
QY	4623	GCTATCATGGTGTCTGGCAGTTAAGATGTATCGGAACAGTACCAATCTAAAGAGTAA	4682				
Db	631	GCTATCATGGTGTCTGGCAGTTAAGATGTATCGGAACAGTACCAATCTAAAGAGTAA	572				
QY	4683	TTTGGAAAAGGCTACTTTTTTGGAAATTAATTTGAAGGACTGGATAGAAAACCTAGAAGTA	4742				
Db	571	TTTGGAAAAGGCTACTTTTTTGGAAATTAATTTGAAGGACTGGATAGAAAACCTAGAAGTA	512				
QY	4743	GACCGCCTTCAAAGAGAAATTCAGTATATTTTCCAAATGCAAGCCGTGAGGAAAGTTTT	4802				
Db	511	GACCGCCTTCAAAGAGAAATTCAGTATATTTTCCAAATGCAAGCCGTGAGGAAAGTTTT	452				

QY 4803 TCTTCTATTGCTTATATAAATTCCTAAGGAAGATGTTTCTAGTCCCTTTTCACAAATCTTTT 4862
Db 451 TCTTCTA-TTTGGCTTATAAATTCCTAAGGAAGATGTTTCTAGTCCCTTTTCACAAATCTTTT 393
QY 4863 TTTAAGCTGGAAGAAAGCTAAACATCTCTTTTGCCTATTGAAGAAATATAGCTTTTCTCAAGCA 4922
Db 392 TTTAAGCTGGAAGAAAGCTAAACATCTCTTTTGCCTATTGAAGAAATATAGCTTTTCTCAAGCA 333
QY 4923 ACATTGGAACAGGTTTTTTGTAGAACTCACTAAAGAACACAGAGGAGGAAGATATAGTTGT 4982
Db 332 ACATTGGAACAGGTTTTTTGTAGAACTCACTAAAGAACACAGAGGAGGAAGATATAGTTGT 273
QY 4983 GGAACITTTAAACAGCACACTTTTGTGGGAACGAAACACAGAAAGATAGAGTAGTATTTTGA 5042
Db 272 GGAACITTTAAACAGCACACTTTTGTGGGAACGAAACACAGAAAGATAGAGTAGTATTTTGA 213
QY 5043 ATTTGTAATGTTTCGGTCTGCTTACTGGGACTTCTTTTCTTTTCACTTAATTTTAACTTTG 5102
Db 212 ATTTGTAATGTTTCGGTCTGCTTACTGGGACTTCTTTTCTTTTCACTTAATTTTAACTTTG 153
QY 5103 GTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGGAGAACCAAGAACGCACCTTGAATTTT 5162
Db 152 GTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGGAGAACCAAGAACGCACCTTGAATTTT 93
QY 5163 CTAAGCTCCTTAATGAAATGCTGTGGTGTGTGTTTTGCTTTTCTTTAAATAAAACGTA 5222
Db 92 CTAAGCTCCTTAATGAAATGCTGTGGTGTGTGTTTTGCTTTTCTTTAAATAAAACGTA 33
QY 5223 TGTATAATTAAGTGAA 5238
Db 32 TGTATAATTAAGTGAA 17

RESULT 13
BG435656
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

756 bp mRNA linear EST 14-MAR-2001
602506942F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4604099 5',
mRNA sequence.
BG435656
BG435656.1 GI:13342162
EST.
Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 756)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCN1339 row: c column: 12
High quality sequence stop: 706.

FEATURES
Source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:4604099"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_79"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgcc); Site 2: SfiI
(ggcgattggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'

and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.3
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.4%; Score 681.6; DB 12; Length 756;
Best Local Similarity 97.1%; Pred. No. 6e-110;
Matches 726; Conservative 0; Mismatches 19; Indels 3; Gaps 3;
QY 4290 GAACATTTTGAATTTATGGAGCTGTCAAAGGAATGAGTGCAGTGCATGAAAGAGTC 4349
Db 1 GAACATTTTGAATTTATGGAGCTGTCAAAGGAATGAGTGCAGTGCATGAAAGAGTC 60
QY 4350 ATAAAGTCGAATAACACATGCACCTTGATTTAAAGAACATCTTCAGAAAGACTGTAAAGAA 4409
Db 61 ATAAAGTCGAATAACACATGCACCTTGATTTAAAGAACATCTTCAGAAAGACTGTAAAGAA 120
QY 4410 CTACCTGCAGGAATCAAACGAAAGTTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAG 4469
Db 121 CTACCTGCAGGAATCAAACGAAAGTTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAG 180
QY 4470 ATTACTTTGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTG 4529
Db 181 ATTACTTTGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTG 240
QY 4530 CGAGCAATTCGAACTGCATTTAAAAACAGAAAGCGGGTCTGCTATTCTGACCACCTCAT 4589
Db 241 CGAGCAATTCGAACTGCATTTAAAAACAGAAAGCGGGTCTGCTATTCTGACCACCTCAT 300
QY 4590 ATGGAGGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGTTGTTCTGGGAGTTAAGA 4649
Db 301 ATGGAGGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGTTGTTCTGGGAGTTAAGA 360
QY 4650 TGTATCGGAACAGTACAACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATT 4709
Db 361 TGTATCGGAACAGTACAACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATT 420
QY 4710 AAATTGAAGGACTGGATAGAAAACCTAGAAAGTAGACCGCCCTTCAAAGAGAAATTCAGTAT 4769
Db 421 AAATTGAAGGACTGGATAGAAAACCTAGAAAGTAGACCGCCCTTCAAAGAGAAATTCAGTAT 480
QY 4770 ATTTTCCCAAATGCAAGCCGTCAGGAA-AGTTTTTCTTCTATTTTGGCTTATAAAATTC 4828
Db 481 ATTTTCCCAAATGCAAGCCGTCAGGAAACAGTTTTTCTTCTATTTGGCTTATAAAATTC 540
QY 4829 TAAGGAAGATGTTTCACTCCCTTTCAAAATCTTTTTTAAGCTGGAAGAAAGCT-AAACATG 4887
Db 541 TAAGGAAGATGTTTCACTCCCTTTCAAAATCTTTTATTAAGCTGGAAGAAAGCTAAACATG 600
QY 4888 CTTTGGCAATTGAAGAAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAAC 4947
Db 601 CTTTGGCAATTGAAGAAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAAC 660
QY 4948 TCAC-TAAAGAACAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGG 5006
Db 661 TCAC-TAAAGAACAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGG 720
QY 5007 TGGGAACGAACACAAAGAGATAGTAG 5034
Db 721 GGGAAACGAACACAAAGAGATAGTAG 748

RESULT 14
BQ774317/c
LOCUS
DEFINITION
ACCESSION
VERSION

697 bp mRNA linear EST 26-JUL-2002
BQ774317
UI-H-EZ1-bca-d-17-0-UI.s1 NCI CGAP Ch2 Homo sapiens cDNA clone
UI-H-EZ1-bca-d-17-0-UI 3', mRNA sequence.
BQ774317
BQ774317.1 GI:21982793

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 697)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopaedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-25, >AT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..697
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZ1-bca-d-17-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ch2"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCT.
TAG TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ1
TAG_SEQ=ATCTAATATG

ORIGIN
Query Match 12.4%; Score 676.4; DB 13; Length 697;
Best Local Similarity 99.1%; Pred. No. 5.1e-109;
Matches 680; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4553 AAACAGAAAGCGGCGTCTATTCTGACCACTCACTATATGGAGGAGGAGGCTGTCTG 4612
DB 697 AAACAGAAAGCGGCGTCTATTCTGACCACTCACTATATGGAGGAGGAGGCTGTCTG 638
QY 4613 TGATCGAGTAGCTATCATGTGTCTGGGAGTTAAGATGTATCGGAACAGTACAACATCT 4672
DB 637 TGATCGAGTAGCTATCATGTGTCTGGGAGTTAAGATGTATCGGAACAGTACAACATCT 578
QY 4673 AAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAAATTAATTAAGGAGCTGGATAGAAAA 4732
DB 577 AAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAAATTAATTAAGGAGCTGGATAGAAAA 518
QY 4733 CCTAGAAGTAGACCGCCTTCAAGAGAGAAATTCAGTATATTTCCAAATGCAAGCCGTCA 4792
DB 517 CCTAGAAGTAGACCGCCTTCAAGAGAGAAATTCAGTATATTTCCAAATGCAAGCCGTCA 458
QY 4793 GGAAAAGTTTTTCTTCTATTTTGGCTTATAAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTC 4852

DB 457 GGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTC 398
QY 4853 ACAATCTTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTT 4912
DB 397 ACAATCTTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTT 338
QY 4913 TTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCACTAAAGAAACAAGAGGAGGAAGA 4972
DB 337 TTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCACTAAAGAAACAAGAGGAGGAAGA 278
QY 4973 TAATAGTTGTGGAACCTTTAAACAGCACACACTTTTGGTGGGAACGAACACAAAGAGATAGAGT 5032
DB 277 TAATAGTTGTGGAACCTTTAAACAGCACACACTTTTGGTGGGAACGAACACAAAGAGATAGAGT 218
QY 5033 AGTATTTTGAATTTGTATTGTTTCGCTCTGCTTACTGGGACTTCTTTTTCACCTTAAT 5092
DB 217 AGTATTTTGAATTTGTATTGTTTCGCTCTGCTTACTGGGACTTCTTTTTCACCTTAAT 158
QY 5093 TTTAACTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGAGAAACCAAGAACGCACCT 5152
DB 157 TTTAACTTTGGTTTAAAAAGTTTTTTTATTGGAATGGTAACCTGAGAAACCAAGAACGCACCT 98
QY 5153 TGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGCTGTTTGTCTTTTCTTTAA 5212
DB 97 TGAAATTTTCTAAGCTCCTTAATTGAAATGCTGTGGTTGCTGTTTGTCTTTTCTTTAA 38
QY 5213 ATAAACCGTATGTATATAATTAAAGTGAA 5238
DB 37 ATAAACCGTATGTATATAATTAAAAAAA 12

RESULT 15
BU146839
LOCUS AGENCOURT 7978475 Lupski_dorsal_root_ganglion Homo sapiens cDNA
DEFINITION clone IMAGE:6185202 5', mRNA sequence.
ACCESSION BU146839
VERSION BU146839.1 GI:22660371
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 926)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLMI3575 row: j column: 19
High quality sequence stop: 657.

FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6185202"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 Yr"
/lab_host="DH10B"
/clone_lib="Lupski_dorsal_root_ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:

5'-TCGACCCACGGTCCG-3' and
5'-GACTAGTTCTAGATCGGAGCGCCGCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
technologies."

ORIGIN

Query Match		12.2%;	Score 668;	DB 13;	Length 926;
Best Local Similarity		95.8%;	Pred. No. 1.4e-107;		
Matches	731;	Conservative	0;	Mismatches	21;
		Indels	11;	Gaps	4;
QY	3618	GCCTTTTGTATCATCTCCAAATCTATCCACTTCTAGGTGCTGATTTCTTTTCATAAAG	3677		
Db	1	GCCTTTTGTATCATCTCCAAATCTATCCACTTCTAGGTGCTGATTTCTTTTCATAAAG	60		
QY	3678	ATTTCTTGGAGAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCA	3737		
Db	61	ATTTCTTGGAGAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCA	120		
QY	3738	GTAGCTGTATATCGCCCTTACCTGCGAGTGTACTGTGGATTTTCCCTTTACAATACTAT	3797		
Db	121	GTAGCTGTATATCGCCCTTACCTGCGAGTGTACTGTGGATTTTCCCTTTACAATACTAT	180		
QY	3798	GAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTCAACG	3857		
Db	181	GAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTCAACG	240		
QY	3858	AAGTCTAAAAATAGGAAGCTTCCAGAACCCAGACATGAGGATGAAGATGAAGATGTC	3917		
Db	241	AAGTCTAAAAATAGGAAGCTTCCAGAACCCAGACATGAGGATGAAGATGAAGATGTC	300		
QY	3918	AAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTGTGAGGAGAAACCA	3977		
Db	301	AAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGTTGCCAGTGTGTGTGAGGAGAAACCA	360		
QY	3978	TCCATTATGTCAGCAATTTGCATAAAGAAATATGATGACAAGAAAGATTTTCTTTTCA	4037		
Db	361	TCCATTATGTCAGCAATTTGCATAAAGAAATATGATGACAAGAAAGATTTTCTTTTCA	420		
QY	4038	AGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGAAAAA----	4093		
Db	421	AGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGAAAAAAGGTGGAGA	480		
QY	4094	GATCTTAGGACTATTGGGTCCAAATGGTGGTGGCAAAACACAATATTATTAATTTCTGGT	4153		
Db	481	GATCTTAGGACTATTGGGTCCAAATGGTGGTGGCAAAACACAATATTATTAATTTCTGGT	540		
QY	4154	TGGTGATATTGAACCAACTTCAGGCCAGGTATTTTGGAGATTTATCTTTCAGAGACAAG	4213		
Db	541	TGGTGATATTGAACCAACTTCAGGCCAGGTATTTTGGAGATTTATCTTTCAGAGACAAG	600		
QY	4214	TGAAGATGATGATTCACCTGAAAGTGTATGGGTTACTGTCTCTCAGATAAACCCCTTGTGGCC	4273		
Db	601	TGAAGATGATGATTCACCTGAAAGTGTATGGGTTACTGTCTCTCAGATAAACCCCTTGTGGCC	660		
QY	4274	AGATACTACATTGCAGG---AACATTTTGAATTTTATGGAGCTGTCAAAGGAA---TGAG	4327		
Db	661	AGATACTACATTGCANGGAACATTTTGAATTTTATGGAGCTGTCAAAGGAAATGAGTG	720		
QY	4328	TGCAAGTGACATGAAAGAGTCAAT-AAGTCGAATAACATGC	4369		
Db	721	CACAGTGACCATGAAAGAGTCAATAAATTCGAATAACACCTGC	763		

Search completed: April 12, 2004, 07:51:37
Job time : 8479 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 12, 2004, 18:02:58 ; Search time 9482 Seconds
(without alignments)
7505.723 Million cell updates/sec

Title: US-10-090-458-5
Perfect score: 8426
Sequence: 1 MSTAIREVGWVRQTRTLK.....CGTLNSTLWERTQEDRVVF 1642

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2 1/USPTO spool/US10090458/runat 08042004 121552 25470/app query.fasta_1.1799
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10090458 @CGN 1 1 6133 @runat 08042004 121552 25470 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	8426	100.0	5475	6	AX537473	AX537473 Sequence
2	8422	100.0	6369	6	AX392931	AX392931 Sequence
3	8422	100.0	6525	6	AX473847	AX473847 Sequence
4	8422	100.0	6525	9	AY028897	AY028897 Homo sapi
5	8421	99.9	5096	9	HSA275973	AJ275973 Homo sapi
6	8395	99.6	4929	6	AX417824	AX417824 Sequence
7	8395	99.6	5262	6	AX417828	AX417828 Sequence
8	8309	98.6	4917	6	AX537472	AX537472 Sequence
9	8309	98.6	5463	6	AX537470	AX537470 Sequence
10	8112	96.3	4785	6	AX417826	AX417826 Sequence
11	7774	92.3	5170	10	RNO426052	AJ426052 Rattus no
12	7737.5	91.8	4945	10	RNO550165	AJ550165 Rattus no
13	7729	91.7	4929	10	AB097675	AB097675 Mus muscu
14	7674	91.1	5347	10	AF491842	AF491842 Mus muscu
15	6477	76.9	4078	9	HSN806823	BX640746 Homo sapi
16	4930.5	58.5	3347	6	AX833036	AX833036 Sequence
17	4930.5	58.5	3347	9	AK094416	AK094416 Homo sapi
18	4847.5	57.5	3268	6	AX714300	AX714300 Sequence
19	4847.5	57.5	3268	9	AK056533	AK056533 Homo sapi
20	4663	55.3	2845	9	HSA512612	AJ512612 Homo sapi
21	3829	45.4	3112	9	AB067475	AB067475 Homo sapi
22	3481	41.3	5243	9	HSN807592	BX647447 Homo sapi
23	3234	38.4	6181	6	AX473850	AX473850 Sequence
24	3234	38.4	6181	9	AY028900	AY028900 Homo sapi
25	3229	38.3	5722	6	AX657703	AX657703 Sequence
26	3228	38.3	6333	9	AY247065	AY247065 Homo sapi
27	3215.5	38.2	4875	9	AF423307	AF423307 Homo sapi
28	3200.5	38.0	4875	6	AX535877	AX535877 Sequence
29	3200.5	38.0	5018	6	AX535879	AX535879 Sequence
30	3197.5	37.9	5981	6	AX473849	AX473849 Sequence
31	3197.5	37.9	5981	9	AY028899	AY028899 Homo sapi
32	3195	37.9	5335	10	AF498362	AF498362 Mus muscu
33	3192	37.9	5680	6	AX657701	AX657701 Sequence
34	3169	37.6	6268	10	AF491299	AF491299 Mus muscu
35	3148	37.4	6141	9	HSN803311	AL832004 Homo sapi
36	3137.5	37.2	1964	9	AK122803	AK122803 Homo sapi
37	3124	37.1	4984	9	AF373290	AF373290 Homo sapi
38	3124	37.1	5211	6	AX575480	AX575480 Sequence
39	3124	37.1	5296	6	AX473848	AX473848 Sequence
40	3124	37.1	5296	9	AY028898	AY028898 Homo sapi
41	3117	37.0	4854	6	AX538009	AX538009 Sequence
42	3117	37.0	5332	6	AX538007	AX538007 Sequence
43	3108	36.9	5677	9	AB020629	AB020629 Homo sapi
44	3065	36.4	5149	6	AX392958	AX392958 Sequence
45	3044	36.1	5622	6	AX392940	AX392940 Sequence

ALIGNMENTS

RESULT 1

AX537473
LOCUS AX537473 5475 bp DNA linear PAT 23-NOV-2002
DEFINITION Sequence 4 from Patent WO02070690.
ACCESSION AX537473
VERSION AX537473.1 GI:25269282
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Chen,H., Kilinski,L. and le Bihan,S.
TITLE Abca5 transporter and uses thereof
JOURNAL Patent: WO 02070690-A 4 12-SEP-2002;
Active Pass Pharmaceuticals, Inc. (CA)
FEATURES
source location/Qualifiers
1..5475
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 5475
Score: 8426.00 Matches: 1642
Percent Similarity: 100.00% Conservative: 0
Best local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-090-458-5 (1-1642) x AX537473 (1-5475)
QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys 20
Db 114 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 173
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 174 AATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCACTA 233
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 234 TTTTITTTTATTTGGTTAATTAATTAATAGCATGATGCATGCCAAATAGAAATATGAAGAA 293
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 294 GTGCCTAATATAGAACTCAATCCTATGGCAAGTTTACTCTTCTTAATCTAATCTTGA 353
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 354 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGCTACTGATCATCTA 413
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 414 CCTGATGTCATAATTACTGAAGATATACAAATGAAAAGAAAATGTTAACAATCCAGTCTC 473
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 474 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTCAAAGACTCCATGCTCTATGAACTTCGT 533
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 534 TTTTITTCCTGATATGATTCAGTATCTCTATTATATGGATTCAAGAGCTGGCTGTTC 593
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 594 AAATCATGTGAGGCTGCTCAGTACTGTCCTCAGGTTTCAGATTTCAGATTTTACAAGCATCCATA 653
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
Db 654 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTTGAAGGAGCTGGAGTCAACT 713
QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220

Db 714 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCCGAGGAGTA 773
QY 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db 774 ATTTAATATACCTAGTATAGCAATTTTCACCTTTGGATACATTTTGGCAATTCATATC 833
QY 241 ValAlaGluLysGluLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
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RESULT 2

AX392931
LOCUS AX392931 6369 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 33 from Patent WO0212340.
ACCESSION AX392931
VERSION AX392931.1 GI:19700978
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Yue,H., Thornton,M., Ramkumar,J., Tang,Y.T., Azimzai,Y.,
Baughn,M.R., Yang,J., Yao,M.G., Lal,P., Wallia,N.K., Gandhi,A.R.,
Hafalia,A.J., Nguyen,D.B., Patterson,C., Elliott,V.S.,
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Sanjanwala,M.S., Raumann,B.E., Burford,N., Ison,C.H., Lee,E.A.,
Ding,L., Das,D., Kallick,D.A., Khan,F.A. and Seilhamer,J.J.
JOURNAL Patent: WO 0212340-A 33 14-FEB-2002;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 2798241CB1"
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VERSION AX473847.1 GI:22208006
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Denefle,P., Rosier-Montus,M.F., Prades,C., Arnould-Reguigne,I.,
Duverger,N., Allikmets,R. and Dean,M.
TITLE Nucleic acids of the human abca5, abca6, abca9, and abca10 genes,
vectors containing such nucleic acids and uses thereof
JOURNAL Patent: WO 0246458-A 1 13-JUN-2002;
Aventis Pharma S.A. (FR) ; The Secretary, Department of Health and
Human Services (US)
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DEFINITION Homo sapiens ATP-binding cassette A5 mRNA, complete cds.
ACCESSION AY028897
VERSION AY028897.1 GI:17223619
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 6525)
AUTHORS Schriml,L.M., Arnould,I., Prades,C., Lachtermacher-Rocha,M.,
Schneider,T., Maintoux,C., Lemoine,C., Debono,D., Devaud,C.,
Naudin,L., Bauche,S., Annat,M., Alikmets,R., Denefle,P., Rosier,M.
and Dean,M.
TITLE Identification and characterization of a cluster of five new
ATP-binding cassette transporter genes on human chromosome 17q24: a
novel sub-group within the ABCA sub-family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 6525)
AUTHORS Schriml,L.M., Arnould,I., Prades,C., Lachtermacher-Rocha,M.,
Schneider,T., Maintoux,C., Lemoine,C., Debono,D., Devaud,C.,
Naudin,L., Bauche,S., Annat,M., Alikmets,R., Denefle,P., Rosier,M.
and Dean,M.
TITLE Direct Submission
JOURNAL Submitted (20-MAR-2001) Evry Genomics Center, Aventis Pharma, 2 Rue
Gaston Cremieux, Evry 91057, France
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ORIGIN

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Score: 8422.00 Matches: 1641
Percent Similarity: 99.94% Conservative: 0
Best Local Similarity: 99.94% Mismatches: 1
Query Match: 99.95% Indels: 0
DB: 9 Gaps: 0

US-10-090-458-5 (1-1642) x AY028897 (1-6525)

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Db	1071	AAATTAATAATTAATGCAGAACCAAAAAGAGTAGTGTTTCAGGAAATCTCTTTCCACTA	1130
QY	41	PhePheLeuPheTyrLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu	60
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QY	1401	VallYsGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu	1420
Db	5211	GTCAAAGGAATGAGTGCAGATGACATGAAGAAGTCATAAGTCGAATAACACATGCACCT	5270
QY	1421	AspLeuLysGluHisLeuGlnLysThrVallYsLysLeuProAlaGlyIleLysArgLys	1440
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QY	1461	ThrGlyMetAspProLysAlaLysGlnHisMetTyrArgAlaIleArgThrAlaPheLys	1480
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QY	1481	AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys	1500
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QY	1501	AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu	1520
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QY	1601	SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp	1620
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QY	1621	AsnSerCysGlyThrLeuAsnSerThrLeuTyrTrpGluArgThrGlnGluAspArgVal	1640
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Db	5931	GTATTT	5936
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LOCUS		5096 bp mRNA linear	PRI 31-JUL-2002
DEFINITION		Homo sapiens mRNA for ATP-binding cassette protein of the (ABCA subfamily).	
ACCESSION		AJ275973	
VERSION		AJ275973.3	GI:22080663
KEYWORDS		ABCA subfamily; ATP-binding cassette protein.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1	
AUTHORS		Petry,F., Kotthaus,A. and Hirsch-Ernst,K.I.	
TITLE		Molecular cloning and tissue distribution of a novel ATP-binding cassette (ABC) transporter belonging to the subfamily ABCA	
JOURNAL		Unpublished	

REFERENCE	2		
AUTHORS		Hirsch-Ernst,K.I.	
TITLE		Direct Submission	
JOURNAL		Submitted (02-MAR-2000) Hirsch-Ernst K.I., Department of Toxicology, University of Goettingen, Robert-Koch-Strasse 40, Lowery Saxony, D-37075, GERMANY revised by [3]	
REMARK		3 (bases 1 to 5096)	
REFERENCE			
AUTHORS		Hirsch-Ernst,K.I.	
TITLE		Direct Submission	
JOURNAL		Submitted (20-NOV-2001) Hirsch-Ernst K.I., Department of Toxicology, University of Goettingen, Robert-Koch-Strasse 40, Lowery Saxony, D-37075, GERMANY	
COMMENT		On Aug 1, 2002 this sequence version replaced gi:17046099.	
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CDS			
ORIGIN			
Alignment Scores:			
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Percent Similarity:	100.00%	Conservative:	2
Best Local Similarity:	99.88%	Mismatches:	0
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DEFINITION Sequence 1 from Patent WO0231147.
ACCESSION AX417824
VERSION AX417824.1 GI:21522942
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Hu,Y. and Nepomnichy,B.
TITLE Human transporter proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0231147-A 1 18-APR-2002;
LEXICON GENETICS INC (US)
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Score: 8395.00 Matches: 1637
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Best Local Similarity: 99.70% Mismatches: 5
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US-10-090-458-5 (1-1642) x AX417824 (1-4929)

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AX417828 LOCUS AX417828 5262 bp DNA linear PAT 18-JUN-2002

DEFINITION Sequence 5 from Patent WO0231147.

ACCESSION AX417828

VERSION AX417828.1 GI:21522944

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Hu, Y. and Nepomnichy, B.

AUTHORS Human transporter proteins and polynucleotides encoding the same

TITLE Patent: WO 0231147-A 5 18-APR-2002;

JOURNAL LEXICON GENETICS INC (US)

FEATURES Location/Qualifiers

source

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VERSION AX537472.1 GI:25269279
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Chen,H., Kilinski,L. and le Bihan,S.
TITLE Abca5 transporter and uses thereof
JOURNAL Patent: WO 02070690-A 3 12-SEP-2002;
Active Pass Pharmaceuticals, Inc. (CA)
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Best Local Similarity: 98.79% Mismatches: 2
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AX537470

LOCUS AX537470 5463 bp DNA linear PAT 23-NOV-2002

DEFINITION Sequence 1 from Patent WO02070690.

ACCESSION AX537470

VERSION AX537470.1 GI:25269277

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Chen,H., Kilinski,L. and le Bihan,S.

TITLE Abca5 transporter and uses thereof

JOURNAL Patent: WO 02070690-A 1 12-SEP-2002;

Active Pass Pharmaceuticals, Inc. (CA)

FEATURES

source 1. 5463

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

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Score: 8309.00 Matches: 1629

Percent Similarity: 98.85% Conservative: 1

Best Local Similarity: 98.79% Mismatches: 2

Query Match: 98.61% Indels: 18

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QY 1274 sValLysGluLeuMetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAs 1294
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Qy	1494	uGluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIl	1514
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Qy	1514	eGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLe	1534
Db	4643	CGGAACAGTACAACTCTAAAGAGTAAATTGGAAAAAGGCTACTCTTTTGGAAATTAAT	4702
Qy	1534	uLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePh	1554
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VERSION	AX417826.1	GI:215222943	
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ORGANISM	Homo sapiens		
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AUTHORS	Hu, Y. and Nepomnichy, B.		
TITLE	Human transporter proteins and polynucleotides encoding the same		
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Best Local Similarity:	99.69%	Mismatches:	5
Query Match:	96.27%	Indels:	0
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Qy	41	PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu	60
Db	121	TTTTTTTATTTTGGTTAATATTAATTAGCATGATGATCCAAATAAGAAATAAGAA	180
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Qy	81	TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu	100
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Qy	101	ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu	120
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RESULT 11

RNO426052 LOCUS RNO426052 5170 bp mRNA linear ROD 08-JAN-2003

DEFINITION Rattus norvegicus mRNA for Abca5 protein.

ACCESSION AJ426052

VERSION AJ426052.2 GI:27368658

KEYWORDS abca5 gene; ATP-binding cassette protein.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

1 Petry, F., Kotthaus, A. and Hirsch-Ernst, K.I.

Cloning of human and rat ABCA5/Abca5 and detection of a human

splice variant

Biochem. Biophys. Res. Commun. 300 (2), 343-350 (2003)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

FEATURES

source

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ORIGIN

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Score: 95.19% Conservative: 80
Percent Similarity: 90.32% Mismatches: 79
Best Local Similarity: 92.26% Indels: 0
Query Match: 10 Gaps: 0
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US-10-090-458-5 (1-1642) x RNO426052 (1-5170)

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RESULT 12
RNO550165 4945 bp mRNA linear ROD 24-MAR-2003
LOCUS Rattus norvegicus mRNA for ATP-binding cassette protein 5 (Abca5
DEFINITION gene), splice variant V+16.
ACCESSION AJ550165
VERSION AJ550165.1 GI:29170395
KEYWORDS Abca5 gene; alternative splicing; ATP-binding cassette protein 5.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Petry, F. and Hirsch-Ernst, K.I.
TITLE Identification of novel highly conserved splice variants of rat
Abca5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4945)
AUTHORS Petry, F.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-2003) Petry F., Toxicology, University of
Goettingen, Robert-Koch-Strasse 40, Goettingen, Lower Saxony,
D-37075, GERMANY
FEATURES
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US-10-090-458-5 (1-1642) x RNO550165 (1-4945)

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QY	61	ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly	80
Db	189	GTATCTGATATAGAACTCAGCCCTATGGACAAATCCATCTCTTCCAACTTATCTCTGGGG	248
QY	81	TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu	100
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QY	101	ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu	120
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QY	121	SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg	140
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QY	141	PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer	160
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QY	161	LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle	180
Db	489	AAGTCATGTGATGCTGCTCAGTACTGGTCTTTCAGGGTTTACAGCTTTACAGGCCTCAATA	548
QY	181	AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTyrLysGluLeuGluSerThr	200
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QY	201	LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal	220
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QY	221	IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle	240
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Db	789	GCTTTTGGCTGTCTCGGTCTTCTGTACACGAGTTTGATCTTCTCTATATGTCCTCTCTT	848
QY	281	MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe	300
Db	849	ATGGCCGTCATTGCAACACCGCTCTCGTTATTCCCTCAGAGTAGCAGCATCGTGATTTT	908
QY	301	LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu	320
Db	909	CTGCTCTCTTCTGTCAGGATTGTCATCTGTGTTTTTTTGTCTTAAATGTTGACGCGCTCTT	968
QY	321	PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe	340
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QY	461	PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle	480
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VERSION AB097675.1 GI:29420876
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Kubo,Y., Satsuma,Y., Sekiya,S., Nada,S. and Yamaguchi,A.
TITLE Molecular cloning of mABCA5, the mouse homologue of ABCA5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 4929)
AUTHORS Kubo,Y., Satsuma,Y., Sekiya,S., Nada,S. and Yamaguchi,A.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2002) Yoshiyuki Kubo, I.S.I.R., Osaka Univ.; Mihogaoka 8-1, Ibaraki City, Osaka 567-0047, Japan
(E-mail:kubo37@sanaken.osaka-u.ac.jp, Tel:81-06-6879-8546, Fax:81-06-6879-8549)
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ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 4929
Score: 7729.00 Matches: 1480
Percent Similarity: 94.88% Conservative: 78
Best Local Similarity: 90.13% Mismatches: 84
Query Match: 91.73% Indels: 0
DB: 10 Gaps: 0

US-10-090-458-5 (1-1642) x AB097675 (1-4929)

QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys 20
|||:::|||||
Db 1 ATGGCTACTGCAATTAGGGATGTGGGAGTTTGGAGACAGACCAGAACACTTCTTACTGAAA 60
|||
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
|||
Db 61 AATTACCTAATTAATGCAGGACTAAAAAAGTAGTGTTCAGGAAATTCCTTTTCTCTTA 120
|||
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
|||
Db 121 TTTTCTTATTTTGGCTGATATTAGTTAGCATGATGATGATCCAAATAAGAAATATGAAGAG 180
|||
QY 61 ValProAsnIleGluLeuAsnProMetMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
|||:::|||||
Db 181 GTATCTGATATAGAGCTCAGCCCTATGGACAAATTCAGCCTTTCACACGTTATTCTTCTGA 240
|||
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
|||
Db 241 TACACTCCCGTGACTAACATTACAAGCAGCATTTATGACAGAGGGTTTCTACCGATCATCTT 300
|||
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
|||
Db 301 CCCAAGGTTATAGTTACTGAAGAATACGCAAAATGAGAAAGAACTGGTAGCCGCACTCTT 360
|||

QY	121	SerLysProSerAsn	PheValGlyValValPheLysAspSerMetSerTyrGluLeuArg	140
DB	361	TCTAAGTCCAGCA	ACTTCGTAGGTGTGGTTTTCAAGACACACCATGTCTTATGAACCTCGT	420
QY	141	PhePheProAspMet	IleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer	160
DB	421	TTTTTTCCTGAA	ATGATTCCAGTGTCTTCTATTATATGAATTCAAGAGAGGCTGTTC	480
QY	161	LysSerCysGluAla	AlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle	180
DB	481	AAGACATGTGAT	GTCTGTCTTTGGGGTTTACAGTTCTGCAGGCATCGATA	540
QY	181	AspAlaAlaIle	IleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr	200
DB	541	GATGCTGCCATT	ATATACAGCTGAAGACCAATGTTTTCTGTGTGGAGCGAGCTGGAGTCGACC	600
QY	201	LysAlaValIle	MetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal	220
DB	601	AAAGCTGTGAT	CATCGGAGAGCCGCTGTTGTGTGGAGATTGACACCTTCCCGCGAGGGGTC	660
QY	221	IleLeuIleTyr	LeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle	240
DB	661	ATCCTCATCTAC	CTCGTATAGCCTTCTCGCCCTTCGGCTACTTCTCTGGCAATCCACATC	720
QY	241	ValAlaGluLys	GluLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr	260
DB	721	GTGGCAGAAA	AAAGAAAGTTAAAGGAATTTTAAAGATAATATGGGACTTCATGACACT	780
QY	261	AlaPheTrpLeu	SerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu	280
DB	781	GCTTTTGGCT	TTTCCGGTCTTCTGTACGCAAGCTTGATTTTCCTTATGTCCCTGCTT	840
QY	281	MetAlaValIle	AlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe	300
DB	841	ATGGCTGTCT	ATCGCAACAGCTTCTTCGTTATTTCCCTCAGAGTAGCAGCATTTGTGATCTTT	900
QY	301	LeuLeuPhePhe	LeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu	320
DB	901	CTACTGTTCT	TCTTATATGGATTGTCACTGTGTTTTTGTCTTAAATGCTGACGCCCTCTT	960
QY	321	PheLysLysSer	LysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe	340
DB	961	TTTAAAAAAT	CAAAACACGTGGGAGTCGTTGAGTTTTTGTCAACCGTGTGTTGGATTT	1020
QY	341	IleGlyLeuMet	IleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer	360
DB	1021	GTTGGCCTGCT	GATTGTCTCATAGAAAGTTTCCCCAGGTGGTGGTGTGGCTCTTCAGT	1080
QY	361	ProPheCysHis	CysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe	380
DB	1081	CCTTTGTGTC	AGTGTGCTTTCTGATTGGGATTGCACAGGTCATGCATTTAGAAGATTTT	1140
QY	381	AsnGluGlyAla	SerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle	400
DB	1141	AATGAGGTGCT	TATTCTTAATTGACTGAAGGTCCTATCCTCTAATTATTACTATT	1200
QY	401	IleMetLeuThr	LeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal	420
DB	1201	ATCATGCTAG	CTCTTGACAGTGTGTTCTATGTCTCTTGGCTGTGTATCTCGACCAAGTC	1260
QY	421	IleProGlyGlu	PheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp	440
DB	1261	ATTCCAGGGGA	ATTTGGCTTGAGGAGGTCACTCTTTGTATTTTGAAGCCATCGTATTGG	1320
QY	441	SerLysSerLys	ArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer	460
DB	1321	TCAAAAAACA	AAAGAACTATAAGGAGCTATCGGAGGGCAACATTAAATGGCAATATTAGT	1380
QY	461	PheSerGluIle	IleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle	480
DB	1381	CTCAATGAA	ATTGTTGAGCCCGTTTCTTCAGAAATTTATAGGGAAGAAGCTATAAGATA	1440
QY	481	SerGlyIleGln	LysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu	500

Db	1441	AGTGGTATTTCAGAAATCCTATAGAAAGAAAACTGAGAACGTGGAGGCTTTGAGAAATTTG	1500
QY	501	SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys	520
Db	1501	TCATTTGACATATATGAAGTTCAGATTACTGCACCTGCTGGGCCACAGTGGAAACAGGAAAA	1560
QY	521	SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle	540
Db	1561	AGCACACTGATGAATATTCTGTGTGGACTGTGTCCACCCCTCTGATGGGTTGCTTCTATA	1620
QY	541	TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle	560
Db	1621	TATGGACACAGAGTCTCTGAAATAGATGAATGTTTGAAGCAAGAAAAATGATTGGCATA	1680
QY	561	CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu	580
Db	1681	TGTCGCGCAGTCAGATATAAACTTTTGATGTTCTGCAGTAGAAGAAAAATTTATCAATTTTG	1740
QY	581	AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu	600
Db	1741	GCTTCAATCAAAGGAATACCAGCCCAACAATATAATTTCAAGAAAGTGCAGAAAGTGTGTGCTG	1800
QY	601	AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys	620
Db	1801	GATCTGGACATGCAAGCCCATCAAAGATAATCAAAGCGAAAAAGTTAAGCGGTGTCAGAAA	1860
QY	621	ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu	640
Db	1861	AGGAAGCTGTCTGTAGGAATTGCAGTTCTCGGGAATCCAAAGATACTCTCTGTAGACGAG	1920
QY	641	ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg	660
Db	1921	CCTACAGCAGGAATGACCCCTGCTCTCGCCATATTGTTTGAATCTTCTAAAGTATAGA	1980
QY	661	LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla	680
Db	1981	AAGGCTAACAGACTGACCGTGTTAGTACTCACTTCATGGATGAGGCTGACATTCTTGCC	2040
QY	681	AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu	700
Db	2041	GACAGGAAAGTGTCTATATCAAGGAATGCTGAAGTGTGTGTTCTTCAATTTTCCCTA	2100
QY	701	LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr	720
Db	2101	AAGAGTAAATGGGAATCGCTACCGCCTGAGCATGTATATAGACAGATACTGTGCCACA	2160
QY	721	GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn	740
Db	2161	GAGTCACTGTCGTCGTTAGGCAGCACATACCCGACGCCGCTACTGTGAGCAGAAT	2220
QY	741	AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe	760
Db	2221	GACCAGCAGCTCGTGTAAGCCTGCCCTTCAAAGACATGGACAAAATTTTCAGGCTTGT	2280
QY	761	SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr	780
Db	2281	TCTGCTCTAGACATTCAATTCAAACCTGGGTGTATTCTTATGGTGTTCCTCATGACAACA	2340
QY	781	LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer	800
Db	2341	TTGGAAGATGTATTCTTTAAAGCTAGAAAGTTGAAGCAGAAAATTGACCAAGCAGACTATAGT	2400
QY	801	ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu	820
Db	2401	GTATTTACACAGCAGCCGCGGAGGAAGAAACAGATTCAAATTCCTTTGATGAAATGGAA	2460
QY	821	GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp	840
Db	2461	CAGAGTTTACTTATTCTCTCTGAAACGAAAGCTTCTTCAGTGAGCACCATGAGCCTCTGG	2520
QY	841	LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys	860

Db 930 GTGGCAGAAAAAGAAAGAGTTAAAGGAATTTTAAAGATAATGGGACTTCATGACACT 989

Qy 261 AlapheTlpLeuSerTlpValleuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280

Db 990 GCTTTTGGCTTTCCCTGGGTCTTCTGTACGCAAGCTTGATTTTCCCTTATGTCCCTGCTT 1049

Qy 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300

Db 1050 ATGGCTGTCAATCGCAACAGCTTCTTCGTTATTCCTCAGAGTAGCAGCATGTGATCTTT 1109

Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320

Db 1110 CTACTGGTCTTCTTATATGATGTTCATCTGTGTTTTTGTCTTTAATGCTGACGCTCTT 1169

Qy 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340

Db 1170 TTTAAAAAATCAAAACACCTGGAGTCGTTGAGTTTTTGTCAACCGTGGTGTGGATTT 1229

Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTlpLeuPheSer 360

Db 1230 GTTGGCCTGCTGATTTCTCTCATAGAAAGTTTTCCCAAGTTCGCTGGTGGCTCTTCAGT 1289

Qy 361 PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380

Db 1290 CCTTTGTGTCAGTGTGCTTTCTGATTGGGATTGCACAGGTCATGCATTTAGAAGATTTT 1349

Qy 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400

Db 1350 AATGAGGGTGCTTATTTCTAATTTTGACTGAAGTCCCTATCCTCTAATATTACTATT 1409

Qy 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420

Db 1410 ATCATGCTAGTCTCTTGACAGTGTGTTCTATGTCCTCCTGGCTGTGTATCTCGACCAAGTC 1469

Qy 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTlp 440

Db 1470 ATTCCAGGGGAATTTGGCTTGAGGAGGTTCATCTTTGTATTTTGAAGCCATCGTATTGG 1529

Qy 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460

Db 1530 TCAAAAAACAAAAGAACTATAAGGAGCTATCGAGGGCAACATTAAATGGCAATATTAGT 1589

Qy 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480

Db 1590 CTCAAATGAATTTGTGACCCGCTTCTTCAGAATTTATAGGGAAGAGCTATAAGAATA 1649

Qy 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500

Db 1650 AGTGGTATTTCAGAAATCCTATAGAAAGAAAACCTGAGAACGTGGAGGCTTGAGAAATTTG 1709

Qy 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520

Db 1710 TCATTTGACATATATGAAGGTCAGATTACTGCACTGCTGGGCCACAGTGAACAGGAAAA 1769

Qy 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540

Db 1770 AGCACACTGATGAATATTCTGTGTGGACCGGTGCCACCTCTGATGGGTTTGCTTCTATA 1829

Qy 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560

Db 1830 TATGGACACAGAGTCTCTGAATAGATGAATATTGAAGCAAGAAAAATGATTGGCATA 1889

Qy 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580

Db 1890 TGTCCGCAGTCAGATATAAACTTTGTATGTTCTGACAGTAGAAGAAATTTATCAATTTTG 1949

Qy 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600

Db 1950 GCTTCAATCAAAGGAATACCAGCCCAACAATATAATTCAGAAGTGCAGAAAGTGTGCTG 2009

Qy 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlnLys 620

Db 2010 GATCTGGACATGCAAGCCATCAAAGATAATCAAGCGAAAAAGTTAAGCGGTGGTTCAGAAA 2069

Qy 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640

Db 2070 AGGAAGCTGTCTGTAGGAATTGCAGTTCTCGGGAATCCAAAGATACTCCTGCTAGACGAG 2129

Qy 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTlpAsnLeuLeuLysTyrArg 660

Db 2130 CCTACAGCAGGAATGGACCCCTGCTCTCGCCATATTGTTTGAATCTTCTAAAGTATAGA 2189

Qy 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680

Db 2190 AAGGCTAACAGAGTGACCGTGTTTAGTACTCTCATGATGAGGCTGACATTTCTTGCC 2249

Qy 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700

Db 2250 GACAGGAAAAGCTGTCAATATCAAAAGGAATGCTGAAGTGTGTTGTTCTTCAATTTCTTA 2309

Qy 701 LysSerLysTlpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720

Db 2310 AAGAGTAAATGGGAATCGGCTACCGCTAGGCAGCACATACCGCAGCCGCTACTGCAGCAGAAT 2369

Qy 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsn 740

Db 2370 GAGTCACTGTGCTCGCTGGTTAGGCAGCACATACCGCAGCCGCTACTGCAGCAGAAT 2429

Qy 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760

Db 2430 GACCAGCAGCTCGTGTACAGCCTGCCTTTCAAGACATGGACAAATTTTCAGGCTGTTT 2489

Qy 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780

Db 2490 TCTGCTCTAGACATTCAATTCAAACCTGGGTGTATTCTTATGGTGTTCATGACAACA 2549

Qy 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800

Db 2550 TTGGAAGATGTATTCTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGACTATAGT 2609

Qy 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820

Db 2610 GTATTTACACAGCAGCCGCGGGAGGAGAAACAGATTCAAAATCCTTTGATGAATGGAA 2669

Qy 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTlp 840

Db 2670 CAGAGTTTACTTATTCTCTGAAACGAAAGCTTCTTCAGTGAGCACCATGAGCCCTGG 2729

Qy 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860

Db 2730 AAGCAGCAAGTGTCTACGATTGCAAAAGTTTCATTTCTCTCATTTGAACCGAGAAAGCAA 2789

Qy 861 SerValArgSerValleuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880

Db 2790 TCAGTGGCGCTGTGTGCTTCTGCTTTTAAATTTTTTTTGCAGTTTCAGATTTTATGGTT 2849

Qy 881 LeuValHisHisSerPheLysAsnAlaValProIleLysLeuValProAspLeuTyr 900

Db 2850 TTTCTCCATCATTCTTTAAAAATGCTGTGTTCCCATCAAACTCGTTCCAGACTTGTAT 2909

Qy 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSer 920

Db 2910 TTCCTAAAGCCTGGAGATAAACCTCATATAATACAAAAACAAGCCTGCTGCTTCAAAAATCT 2969

Qy 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940

Db 2970 ACTGACTCAGATATCAATGGTCTTATTGAGTTTTTTTGCACACCAGAACATAATGGTGCA 3029

Qy 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960

Db 3030 ATGTTTAATGACAGTGACTATGTGTCTGCTGCTCTCACAGTGGGCTCTCAATGTGGTG 3089

Qy 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980

Db 3090 CGTTCTGAAAAGGACTATGTTTTTTCTGCTGTTTTTCAACAGTACTATGTTTATTGTTG 3149

QY 981 ProileLeuValAsnIleileSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
Db 3150 CCAGTCATGATGAACATCATAGTAACACTACTATCTTTATCATTTAATGTGACTGAAGCC 3209
QY 1001 IleGlnIleTyrSerThrProphePheGlnGluIleThrAspIleValPheLysIleGlu 1020
Db 3210 ATCCAGACCTGGAGTACCCGTTTCATTCAAGAAATTAAGTACATGTTTAAATTTGAG 3269
QY 1021 LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040
Db 3270 CTATATTTTCAAGCAGCTTTGCTTGGAAATCATGTTACTGCAATGCCACCTTACTTTGCC 3329
QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
Db 3330 ATGGAAATGCAGAGAAATCATAGATCAAGCTTATATACTCAACTTAAACTTTTCGGTCTT 3389
QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIle 1080
Db 3390 TTGCCATCAGCCTATTGGGTGGACAAGCTGTGTGGATATTCCCTTGTTTTGTGTGTT 3449
QY 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
Db 3450 CTGATTTTGATGCTGGGAAGTTTATTGCAATTCATCATGGACTGTAATTTTATCCTGCA 3509
QY 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
Db 3510 AAATTTCTTGTGTGTGTTTTCCTTCATTTGTTATGTCCTCCCTCCGTCATCTGTTTCA 3569
QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheThrPheIle 1140
Db 3570 TACATAGCTTCGTTCACTTTCAAGAAATTTTAAATACCAAGGAATTTTGTGTCATTTATC 3629
QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
Db 3630 TATTCGTGACCCGATTTGGCTTGTGTGGCAATCACGGAACCAACTTCTTCTGCAATAT 3689
QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
Db 3690 GCAGTTACGGCTGCTTTCATTACACCTTCTGCATAGCCATTCCCAATCTACCTCTCCTG 3749
QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
Db 3750 GGTGCTCTGATTTCTTTCAAAAGGTTCTTGGAAAGATATGCCAAAAAATGAGAATACC 3809
QY 1201 TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220
Db 3810 TACAATCCCTGGGATAGACTTTTAGTTGCTGTAATCATGCCCTACCTCAGTGATACCTG 3869
QY 1221 TrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp 1240
Db 3870 TGGATTTTCTCTTACAACACTATGAGAAATACATGGAGGCAGATCTATAAGAAAGGAT 3929
QY 1241 ProphePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
Db 3930 CCATTTTTCAGGGCCCTTTCACAAAGGCCCAAAATAAGAAAGTTTCCAGAACCCCATC 3989
QY 1261 AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280
Db 3990 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAGACTGAAGTTTAAAGAGCTGATGGGT 4049
QY 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
Db 4050 TGCCAGTGTGTGAGGAGAGCCAGCCATTATGTTATGTCATTTGCAATAAGATATGAT 4109
QY 1301 AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer 1320
Db 4110 GACAAGAAAGATTTTCTTTCATTCAAGAAACCAACAAAGTAGCAACAAATACATCTCT 4169
QY 1321 PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340
Db 4170 TTCTGTGTGAAAAAGGAGAGATCTTGGGACTGTGGGTCCAAATGGAGCTGGCAAAAGC 4229
QY 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360

Db 4230 ACAGTCATTAACACTCTGGTTGGGACGTTGAGCCAACTTCAGGCAAGATCTTTCTAGGA 4289
QY 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380
Db 4290 GATTATGTTTCACTTCAAGTGAAGATGACCAATCCATTAAAGTGTATGGGTACTGCCCC 4349
QY 1381 GlnIleAsnProLeuTrpProAspThrThrIleuGlnGluHisPheGluIleTyrGlyAla 1400
Db 4350 CAGACAAACCCACTGTGGCCAGATCTCACTCTACAGGAACATTTTGAATTTACGGAGCT 4409
QY 1401 VallysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
Db 4410 GTGAAAGGAATGAGTCTCTGGTGACATGAGGAAGTCATCAGTCGAATAACAAAGCCCTT 4469
QY 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
Db 4470 GATTTGAAAGAACATCTTCAGAAAGACTGTAAAGAAAGCTACCTGCAGGGATCAAGCGAAAG 4529
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db 4530 CTGTGTTTGTCTCTCAGCATGCTGGGAACCCCTCAGGTGACGCTGCTGGATGAGCCGTCC 4589
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
Db 4590 ACAGGCATGGACCCCAAGAGCCAAAGCAGCACATGTGGAGAGCTATTTCGAACCTGATTAAA 4649
QY 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
Db 4650 AACAAAAGCGGGCCCTCTCTGACTACTCTACATACATGGAAGAGGCAGAGCTGTCTGT 4709
QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
Db 4710 GACAGAGGGGCCCATCATGTTATCTGGGCAGCTAAGATGTATTGGAACAGTACAAACATCTA 4769
QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540
Db 4770 AAGAGTAAGTTTGTAAAGGCTACTTTTGTGAAATTAATAATTAAAGGACTGGATAGAAAC 4829
QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
Db 4830 CTGGAATAGATCGCTTCAAGAGAAATTCATATATATTTTCCCAATGCAAGCCGCAA 4889
QY 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
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QY 1641 ValPhe 1642
Db 5130 GTATTT 5135

RESULT 15
HSM806823
LOCUS
DEFINITION Homo sapiens mRNA; cDNA DKFZp686K07118 (from clone DKFZp686K07118).
ACCESSION BX640746
VERSION BX640746.1 GI:34364843
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 4078) Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weill,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
CONSRSTM	The German Human cDNA Consortium
TITLE	Direct Submission
JOURNAL	Submitted (26-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp686K07118) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/ .

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ORIGIN

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ORIGIN

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Best Local Similarity:	95.64%	Mismatches:	1
Query Match:	76.87%	Indels:	57
DB:	9	Gaps:	3
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Search completed: April 13, 2004, 00:30:47
Job time : 9921 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 12, 2004, 17:58:28 ; Search time 902 Seconds
(without alignments)
7733.416 Million cell updates/sec

Title: US-10-090-458-5
Perfect score: 8426
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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10: geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	8422	100.0	6525	6 ABN89594	Abn89594 Human ATP
4	8395	99.6	4929	6 AAD37618	Aad37618 Human tra
5	8395	99.6	5262	6 AAD37620	Aad37620 Human tra
6	8309	98.6	4917	7 ABS57750	Abs57750 Coding se
7	8309	98.6	5463	7 ABS57749	Abs57749 cDNA enco
8	8112	96.3	4785	6 AAD37619	Aad37619 Human tra

9	4847.5	57.5	3268	7	ADA53416	Ada53416 Human cod
10	4282	50.8	2723	9	ADC51606	Adc51606 Human mac
11	3259	38.7	5797	8	ADA20300	Ada20300 Human ATP
12	3234	38.4	6181	6	ABN89597	Abn89597 Human ATP
13	3229	38.3	5722	7	ABZ22923	Abz22923 Human ABC
14	3200.5	38.0	4875	7	ABS57519	Abs57519 Human ABC
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18	3192	37.9	5680	7	ABZ22922	Abz22922 Human ABC
19	3124	37.1	5211	7	AAD47363	Aad47363 Human tra
20	3124	37.1	5296	6	ABN89595	Abn89595 Human ATP
21	3117	37.0	5332	6	ABQ77736	Abq77736 Human ABC
22	3108	36.9	4743	8	ACC47571	Acc47571 Drug tran
23	3108	36.9	5677	6	ABT10141	Abt10141 Human bre
24	3107.5	36.9	3928	6	ABK35707	Abk35707 cDNA sequ
25	3065	36.4	5149	6	AAD33675	Aad33675 Human TRI
26	3044	36.1	5622	6	AAD33657	Aad33657 Human TRI
27	2991.5	35.5	5065	6	AAD33650	Aad33650 Human TRI
28	2982	35.4	4798	6	ABV99425	Abv99425 Human NOV
29	2971	35.3	5846	7	AAD49503	Aad49503 Human TRI
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38	1677	19.9	1346	6	ABL63763	Ab163763 Breast ca
39	1677	19.9	1346	6	ABN96909	Abn96909 Gene #340
40	1674	19.9	2645	7	ADA53722	Ada53722 Human cod
41	1637	19.4	5971	5	AAS70348	Aas70348 DNA encod
42	1555.5	18.5	6470	4	AAH57445	Aah57445 Human lun
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44	1553.5	18.4	6491	6	ABL66808	Ab166808 Lung canc
45	1553.5	18.4	6491	6	ABK84439	Abk84439 Human cDN

ALIGNMENTS

RESULT 1

ABS57751
ID ABS57751 standard; cDNA; 5475 BP.

XX
AC ABS57751;

XX
DT 04-FEB-2003 (first entry)

XX
DE cDNA encoding novel human ATP binding cassette ABCA5 transporter #2.

XX
KW Human; ATP binding cassette; ABC; ABCA5; transporter;
KW neurotoxin transport; beta-amyloid peptide; chromosome mapping;
KW blood brain barrier transport; tissue typing; predictive medicine;
KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

FT CDS 114..5042

FT /*tag= a

FT /product= "ABCA5"

FT /note= "ATP binding cassette (ABC) A5 transporter"

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PN US2002123107-A1.

XX
PD 05-SEP-2002.

XX
PF 01-MAR-2002; 2002US-00090458.

XX
PR 02-MAR-2001; 2001US-0272885P.

XX
PA (ACTI-) ACTIVE PASS PHARM INC.

XX Chen H, Kilinski L, Le Bihan S;
PI
XX WPI; 2003-066798/06.
DR P-PSDB; ABG72424.
DR
XX
PT Novel isolated ATP binding cassette transporter family polypeptide,
PT ABCA5, useful for treating disorders associated with aberrant or unwanted
PT ABCA5 transporter expression or activity.
XX
PS Claim 2; Page 39-42; 52pp; English.
XX
CC The invention describes an isolated ATP binding cassette (ABC)
CC transporter family polypeptide (I), designated ABCA5. (I) or the
CC polynucleotide encoding it (II) are useful as targets for developing
CC modulating agents to regulate a variety of cellular processes,
CC particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC (BBB), as targets for developing modulating agents of multi-drug
CC resistance, as diagnostic and therapeutic tools, or to treat disorders
CC associated with aberrant or unwanted ABCA5 transporter expression or
CC activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC screening assays, detection assays (e.g., chromosomal mapping, tissue
CC typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC (III) are useful as reagents or targets in assays applicable to treatment
CC and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC -hybrid or three-hybrid assay; and to identify other proteins which bind
CC to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC activity; to locate gene regions associated with genetic disease or to
CC associate ABCA5 with the disease, to identify an individual from a minute
CC biological sample (tissue typing), and to aid in forensic identification
CC of the biological sample. This sequence encodes a novel human ATP binding
CC cassette (ABC) A5 transporter
XX
SQ Sequence 5475 BP; 1705 A; 917 C; 1048 G; 1804 T; 0 U; 1 Other;

Alignment Scores:
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Score: 8426.00 Matches: 1642
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-090-458-5 (1-1642) x ABS57751 (1-5475)

QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys 20
DB 114 ATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGACACTTCTACTGAAG 173
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGlnIleLeuPheProLeu 40
DB 174 AATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTCCTTTCCACTA 233
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
DB 234 TTTTCTTATTTTGGTTAATATTAAATAGCATGATGCATCCCAATAAGAAATATGAAGAA 293
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
DB 294 GTGCCTAATATAGAACTCAATCCTATGACCAAGTTTACTCTTTCTAATCTAATCTTGGAA 353
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
DB 354 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTCTCTACTGATCATCTA 413
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120

DB 414 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC 473
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
DB 474 TCTAAGCCGAGCAACTTTTGTAGTGTGGTTTTCAAAGACTCCCATGTCTATGAACCTCGT 533
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
DB 534 TTTTCTCTGATATGATTCAGTATCTTCTATTTATATGGATTCAGAGCTGGCTGTTCA 593
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
DB 594 AAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTTCACAGTTTTCACAGCATCCATA 653
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
DB 654 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 713
QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
DB 714 AAAGCTGTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 773
QY 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240
DB 774 ATTTTAAATATACCTAGTTATAGCAATTTTCACCTTTTGGATACTTTTGGCAATTATATC 833
QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
DB 834 GTAGCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT 893
QY 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
DB 894 GCCTTTGGCTTCTCTGGGTTCTCTATATACAAAGTTTAAATTTTCTTATGTCCCTTCTT 953
QY 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
DB 954 ATGGCAGTCATTCGACAGCTTCTTGTATTTCCTCAAAGTAGCAGCATTTGTGATATTT 1013
QY 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
DB 1014 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTCGTTTAAATGCTGACACCTCTT 1073
QY 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
DB 1074 TTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTGTACTGTGGCTTTTGGATTT 1133
QY 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
DB 1134 ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTAGTGTGGCTTTTCAGT 1193
QY 361 PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
DB 1194 CCTTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253
QY 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
DB 1254 AATGAAGGTGCTTCATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAAT 1313
QY 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
DB 1314 ATCATGCTCACACTTAATAGTATATTCTATGTCCTCTTGGCTGTCTATCTTGATCAAGTC 1373
QY 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
DB 1374 ATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1433
QY 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
DB 1434 TCAAAGAGCAAAAGAAATATGAGGAGTTATGAGGAGTATCAGAGGGCAATGTTAATGGAAATATTAGT 1493
QY 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
DB 1494 TTTAGTGAAATTTATTGAGCCAGTTTCTTCTCAGAAATTTGTAGGAAAAAGAACCCATAAGAATT 1553

QY 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
| | | | |
Db 1554 AGTGGTATTCAGAAGACATACAGAAAGAAGGGTGAAATGTGGAGGCTTTGAGAAATTTG 1613

QY 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
| | | | |
Db 1614 TCATTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAAAG 1673

QY 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
| | | | |
Db 1674 AGTACATTGATGAATATCTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATA 1733

QY 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
| | | | |
Db 1734 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATAATGATTGGCATT 1793

QY 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
| | | | |
Db 1794 TGTCCACAGTTAGATATACACTTTTGATGTTTTTGACAGTAGAAGAAATTTATCAATTTTG 1853

QY 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
| | | | |
Db 1854 GCTTCAATCAAAGGGATACCAGCCAACAATATAATACAAGAAGTGCAGAAGGTTTTACTA 1913

QY 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
| | | | |
Db 1914 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTTAAAAAATTAAGTGGTGCATAAAA 1973

QY 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
| | | | |
Db 1974 AGAAAGCTGTCTATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 2033

QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660
| | | | |
Db 2034 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTCTATGGAATCTTTTAAAAATACAGA 2093

QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
| | | | |
Db 2094 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTCTTGCA 2153

QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
| | | | |
Db 2154 GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGTTGTTCTTCAATGTTTCCTC 2213

QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
| | | | |
Db 2214 AAAAGTAAATGGGGATCGGGTACCGCCTGAGCATGTACATAGACAAATATGTGCCACA 2273

QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
| | | | |
Db 2274 GAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTAACAACAGAAT 2333

QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
| | | | |
Db 2334 GACCAACAACCTTGTGTATAGCTTGCCTTTCAGGACATGGACAAATTTTCAGGTTTGTIT 2393

QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
| | | | |
Db 2394 TCTGCCCTAGACAGTCAATTCAAATTTGGGTGTCAATTTCTATGGTGTTCATGCCAGCT 2453

QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
| | | | |
Db 2454 TTGGAAGACGTAATTTTAAAGCTAGAAGTTTGAAGCAGAAATTGACCAAGCAGATTATAGT 2513

QY 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
| | | | |
Db 2514 GTATTTACTCAGCAGCCCTGGAGGAAGAAATGGATTCAAAATCTTTTGTGATGAATGGAA 2573

QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
| | | | |
Db 2574 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGG 2633

QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860
| | | | |
Db 2634 AAACAACAGATGTATACAATAGCAAGTTTTCATTTCTTTACCTTGAAACGTTGAAAGTAAA 2693

QY 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
| | | | |
Db 2694 TCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTTTTTCACAGTTCAGATTTTATGTTT 2753

QY 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
| | | | |
Db 2754 TTGGTTCACTCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATAT 2813

QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSer 920
| | | | |
Db 2814 TTTCTAAAAACCTGGAGACAAACACATAAATACAAAACAAGTCTGCTTCTTCAAAATCT 2873

QY 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
| | | | |
Db 2874 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTTACAAGCCAGAACATAATGGTGACG 2933

QY 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960
| | | | |
Db 2934 ATGATTAAATGACAGTGACTATGATCCGTGGCTCCCATAGTGGCGCTTTAAATGTGATG 2993

QY 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
| | | | |
Db 2994 CATTAGAAAAAGGACTATGTTTGTGAGCTGTTTCAACAGTACTATGGTTTATTCTTTA 3053

QY 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
| | | | |
Db 3054 CCTATATTAGTGAATATCAITAGTAACACTACTATCTTTATCATTTAAATGTGACTGAAACC 3113

QY 1001 IleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGlu 1020
| | | | |
Db 3114 ATCCAGATCTGGAGTACCCCATCTCTTCAAGAAATTTACTGATATAGTTTTTAAAAATTGAG 3173

QY 1021 LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040
| | | | |
Db 3174 CTGTATTTTCAAGCAGCTTGTGCTTGGAAATCATTTGTTACTGCAATGCCACCTTACTTTGCC 3233

QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
| | | | |
Db 3234 ATGGAATAATGCAGAGAAATCAATAAGATCAAAGCTTAACTCAACTTAAACTTTCAGGCTCT 3293

QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIle 1080
| | | | |
Db 3294 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTGTGATATCCCTTATTTTTTATCAT 3353

QY 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
| | | | |
Db 3354 CTTATTTTGATGCTAGGAAGCTTATTGGCATTTTCATTATGGAATTATATTTTATACTGTA 3413

QY 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
| | | | |
Db 3414 AAGTTCCTTGTGCTGGTTTTTCCTTATTTGGTTATGTTCCATCAGTTATTTCTGTTCACT 3473

QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
| | | | |
Db 3474 TATATTGCTTCTTTTCACCTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCATTTATC 3533

QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
| | | | |
Db 3534 TATCTGTGGCAGCGGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATAC 3593

QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
| | | | |
Db 3594 ACAATTGCAACTATTCTTCATTATGCCTTTTGTATCATCATCTCCAATCTATCCACTTCTA 3653

QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
| | | | |
Db 3654 GGTTGCCCTGATTTCTTTTCATAAAGATTTCTTGGAGAATGTACGAAAAAATGTGGACACC 3713

QY 1201 TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220
| | | | |

Db 3714 TATAATCCATGGGATAGCGTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTACTG 3773
QY 1221 TrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp 1240
Db 3774 TGGATTTTCCTCTTACATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAGAT 3833
QY 1241 ProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
Db 3834 CCCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACGAC 3893
QY 1261 AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280
Db 3894 AATCAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGT 3953
QY 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
Db 3954 TGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAAATATGAT 4013
QY 1301 AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer 1320
Db 4014 GACAAAGAAAGATTTTCTTCTTCAAGAAAGATAAGAAAGTGGCAACTAAATACATCTCT 4073
QY 1321 PheCysValLysLysGlyGluIleLeuGlyLeuGlyProAsnGlyAlaGlyLysSer 1340
Db 4074 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGCGAAAGC 4133
QY 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360
Db 4134 ACAATTATTAATATTCTGTGTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 4193
QY 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380
Db 4194 GATTATTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGTGTATGGGTACTGTCTCT 4253
QY 1381 GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400
Db 4254 CAGATAAACCCCTTTGTGGCCAGATACTACATTGCAGGAACATTTTGAATTTATGGAGCT 4313
QY 1401 ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
Db 4314 GTCAAAGGAATGAGTGCAGTGACATGAAAGAGTCAAGTCAAGTCAATACACATGCACCT 4373
QY 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
Db 4374 GATTTAAAGAAACATCTTCAGAGACTGTAAAGAACTACCTGCAGGAATCAAAACGAAAG 4433
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db 4434 TTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4493
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTyrArgAlaIleArgThrAlaPheLys 1480
Db 4494 ACAGGTATGGATCCCAAGCCCAACAGCACATGTGGCGAGCAATTCGAACCTGCATTAAA 4553
QY 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluAlaGluAlaValCys 1500
Db 4554 AACAGAAACGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGGTGTCTGT 4613
QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
Db 4614 GATCGAGTAGCTATCATGTTGTTGGGAGTTAAGATGTATCGGAACAGTACACATCTA 4673
QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTyrIleGluAsn 1540
Db 4674 AAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAAC 4733
QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
Db 4734 CTAGAAAGTAGACCGCCTTCAAAGAGAAAATTCAGTATATTTTCCCAATGCAAGCCGTCAG 4793
QY 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580

Db 4794 GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA 4853
QY 1581 GlnSerPhePheLysLeuGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600
Db 4854 CAATCTTTTTTTAAGCTGGAAGAAAGCTAAACATGCTTTTGCCATTGAAGAAATATAGCTTT 4913
QY 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620
Db 4914 TCTCAAGCAACATTGGAACAGGTTTGTGTAGAACTCACTAAAGAACAAAGAGAGGAAGAT 4973
QY 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
Db 4974 AATAGTTGTGGAACCTTTAAACAGCACACACTTTGGTGGGAAACGAACACAGATAGAGTA 5033
QY 1641 ValPhe 1642
Db 5034 GTATTT 5039
RESULT 2
AAD33648
ID AAD33648 standard; cDNA; 6369 BP.
XX
AC AAD33648;
XX 01-JUL-2002 (first entry)
XX Human TRICH-3 cDNA.
DE
XX Human; transporter and ion channel; TRICH-3; transport disorder; angina;
KW amyotrophic lateral sclerosis; cystic fibrosis; neuromuscular disorder;
KW cardiac disorder; polymyositis; diabetes; neurological disorder; cancer;
KW depression; schizophrenia; anaemia; Wilson's disease; Cushing's disease;
KW cell proliferated disorder; infertility; arteriosclerosis; gene therapy;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; allergy;
KW myasthenia gravis; multiple sclerosis; metabolic disorder; hypertension;
KW acquired immune deficiency syndrome; immunological disorder; scleroderma;
KW endocrine disorder; autoimmune thyroiditis; rheumatoid arthritis; goitre;
KW cardiac myopathy; amnesia; toxic myopathy; Addison's disease; infection;
KW epilepsy; mental disorder; myocarditis; Crohn's disease; Grave's disease;
KW muscle disorder; stroke; dementia; anxiety; asthma; cirrhosis;
KW gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1238..6166
FT /*tag= a
FT /product= "Human TRICH-3 protein"
XX
PN WO200212340-A2.
XX 14-FEB-2002.
XX 01-AUG-2001; 2001WO-US024217.
XX 03-AUG-2000; 2000US-0223269P.
PR 10-AUG-2000; 2000US-0224456P.
PR 18-AUG-2000; 2000US-0226410P.
PR 25-AUG-2000; 2000US-0228140P.
PR 31-AUG-2000; 2000US-0230067P.
PR 08-SEP-2000; 2000US-0231434P.
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Yue H, Thornton M, Ramkumar J, Tang YT, Azimzai Y, Baughn MR;
PI Yang J, Yao MG, Lal P, Wallia NK, Gandhi AR, Hafalia AJA, Nguyen DB;
PI Patterson C, Elliott VS, Tribouley CM, Lu DAM, Xu Y, Reddy R;
PI Hernandez R, Borowsky ML, Lo TP, Lu Y, Policky JL, Greene BD;
PI Sanjanwala MS, Raumann BE, Burford N, Ison CH, Lee EA, Ding L;
PI Das D, Kallick DA, Khan FA, Seilhamer JJ;
XX
DR WPI; 2002-206330/26.
DR P-PSDB; AAE21159.

XX New human transporters and ion channels polypeptides and polynucleotides
PT for diagnosing, preventing or treating transport, neurological, muscle,
PT immunological and cell proliferative disorders.
XX

PS Claim 77; Page 203-205; 230pp; English.
XX

CC The invention relates to human transporter and ion channel polypeptides
CC designated TRICH and nucleic acid molecules encoding such polypeptides.
CC TRICH sequences are useful for diagnosis, treatment and prevention of
CC transport, muscle, neurological, immunological and cell proliferative
CC disorders. Transport disorders include akinesia, amyotrophic lateral
CC sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular
CC dystrophy, diabetes mellitus, diabetes insipidus, myasthenia gravis,
CC myocardiitis, prostate cancer, cardiac disorders associated with transport
CC e.g. polymyositis, bradyarrhythmia, dermatomyositis, angina, neurological
CC disorders associated with transport e.g. amnesia, bipolar disorder,
CC depression, Tourette's disorder, schizophrenia, other disorders
CC associated with transport e.g. neurofibromatosis, sickle cell anaemia,
CC Wilson's disease, cataracts, infertility, hyperglycaemia, hypoglycaemia,
CC goitre, Cushing's disease, hypercholesterolaemia and cystinuria. Cell
CC proliferated disorders include cancer, actinic keratosis, cirrhosis,
CC arteriosclerosis, atherosclerosis, bursitis, hepatitis and psoriasis.
CC Neurological disorders include Alzheimer's, Pick's and Parkinson's
CC disease, amyotrophic lateral sclerosis, epilepsy, stroke, Huntington's
CC disease, multiple sclerosis, dementia and other extrapyramidal disorder,
CC motor neuron disorder, prion disease, metabolic disease of the nervous
CC system and other developmental disorders of the central nervous system,
CC neuromuscular disorders, metabolic, endocrine and toxic myopathies,
CC periodic paralysis, mental disorders including mood, anxiety; and
CC immunological disorders include acquired immune deficiency syndrome
CC (AIDS), adult respiratory distress syndrome, Addison's disease,
CC allergies, asthma, atherosclerosis, osteoporosis, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, Crohn's disease, atopic dermatitis,
CC Grave's disease, glomerulonephritis, rheumatoid arthritis, scleroderma,
CC systemic lupus erythematosus, systemic sclerosis, ulcerative colitis,
CC haemodialysis, uveitis; viral, bacterial, fungal, parasitic, protozoal,
CC helminthic infections and trauma; and muscle disorders include cardiac
CC myopathy, myocardiitis, polymyositis, arrhythmias and hypertension. The
CC TRICH polynucleotides are used in gene therapy. The present sequence is
CC human TRICH-3 cDNA

XX
SQ Sequence 6369 BP; 1893 A; 1112 C; 1246 G; 2118 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 6369
Score: 8422.00 Matches: 1641
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.94% Mismatches: 0
Query Match: 99.95% Indels: 0
DB: 6 Gaps: 0

US-10-090-458-5 (1-1642) x AAD33648 (1-6369)

QY	1	MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLys	20
DB	1238	ATGTCCTGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG	1297
QY	21	AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu	40
DB	1298	AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA	1357
QY	41	PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu	60
DB	1358	TTTTTTTATTTGGTTAATTAATTAGCATGATGCATCCCAATAAGAAATATGAAGAA	1417
QY	61	ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly	80
DB	1418	GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGA	1477
QY	81	TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu	100
DB	1478	TATACTCCAGTACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA	1537

QY	101	ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu	120
DB	1538	CCTGATGTCATAATTACTGAAGAATATACAATGAAAAAGAAATGTTAAACATCCAGTCTC	1597
QY	121	SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg	140
DB	1598	TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTTCAAAGACTCCATGTCTTAACTTCGT	1657
QY	141	PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer	160
DB	1658	TTTTTTTCTGATATGATCCAGTATCTTCTATTTATATGATTCAAGAGCTGGCTGTTCA	1717
QY	161	LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle	180
DB	1718	AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTTCACAGTTTTTACAAGCATCCATA	1777
QY	181	AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr	200
DB	1778	GATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTTGAAGGAGCTGGAGTCAACT	1837
QY	201	LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal	220
DB	1838	AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAAATAGATACCTTTCCCGAGGAGTA	1897
QY	221	IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle	240
DB	1898	ATTTTAATATACCTAGTTATAGCATTTTCACTTTTGGATACTTTTTGGCAATTCATATC	1957
QY	241	ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr	260
DB	1958	GTAGCAGAAAAGAAAAATAAAAGAAATTTTAAAGATAATATGGGACTTCATGATACT	2017
QY	261	AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu	280
DB	2018	GCCTTTTGGCTTCTCTGGGTTCTTCTATATACAAAGTTTAAATTTTCTATGTCCCTTCTT	2077
QY	281	MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe	300
DB	2078	ATGGCAGTCATTGGACAGCTTCTTTTGTATTCTCTCAAAGTAGCAGATTTGTGATATT	2137
QY	301	LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu	320
DB	2138	CTGCTTTTTCCTTTATGGATTATCATCTGTATTATTTTGTCTTTAATGCTGACACCTCTT	2197
QY	321	PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe	340
DB	2198	TTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTT	2257
QY	341	IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer	360
DB	2258	ATTGGCCTTATGATAATCCTCATAGAAAGTTTTCCTCAAATCGTTAGTGGCTTTTCAGT	2317
QY	361	PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe	380
DB	2318	CCTTTCTGTCACTGTACTTTTGTGATTGTTGATTTGCACAGGTCATGCATTTAGAAGATTTT	2377
QY	381	AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle	400
DB	2378	AATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCTCTTAATATTACAATT	2437
QY	401	IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal	420
DB	2438	ATCATGCTCACACTTAATAGTATATTTCTATGTCCTCTTTGGCTGTCTATCTTGTATCAAGTC	2497
QY	421	IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp	440
DB	2498	ATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTTCATATTGG	2557
QY	441	SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer	460
DB	2558	TCAAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT	2617

Db 4778 GGTTGCCTGATTCTTTTCATAAAGATTCTTTGGAAGAAATGTACGAAAAAATGTGGACACC 4837

Qy 1201 TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220

Db 4838 TATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTACTG 4897

Qy 1221 TrpIlePheLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp 1240

Db 4898 TGGATTTCCTCTTACAATACTATGAGAAAAAATATGAGGCGAGATCAATAAGAAAAGAT 4957

Qy 1241 ProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260

Db 4958 CCCTTTTTCAGAAACCTTTTCACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACAGAC 5017

Qy 1261 AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280

Db 5018 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAAGGTCAAAGAGCTGATGGGT 5077

Qy 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300

Db 5078 TGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGATATGAT 5137

Qy 1301 AspLysLysAspPheLeuLeuSerArgLysValLysValLysValAlaThrLysTyrIleSer 1320

Db 5138 GACAGAAAGATTCTTCTTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 5197

Qy 1321 PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340

Db 5198 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTCTGGCAAAAGC 5257

Qy 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360

Db 5258 ACAATTATTAAATTTCTGGTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 5317

Qy 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380

Db 5318 GATTATTCTTCAGAGACAAGTGAAGATGATGATTCTCACTGAAGTGTATGGGTACTGTCCT 5377

Qy 1381 GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400

Db 5378 CAGATAAACCCCTTTGTGGCCAGATACTACATTGCAGGAACATTTTGAAATTTATGGAGCT 5437

Qy 1401 ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420

Db 5438 GTCAAAGGAATGAGTGCAGATGACATGAAGAAGTCAATGAAGTCGAATAACACATGCACCT 5497

Qy 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440

Db 5498 GATTAAAAGAACAATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAAACGAAAG 5557

Qy 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460

Db 5558 TTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 5617

Qy 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480

Db 5618 ACAGTATGGATCCCAAAGCCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTAAA 5677

Qy 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500

Db 5678 AACAGAAAGCGGGCTGCTATTCTGACCCTCACTATATGAGGAGGCGAGAGCTGTCTGT 5737

Qy 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520

Db 5738 GATCAGTAGCTATCATGTGCTCTGGCAGTTAAGATGTATCGGAACAGTACAAACATCTA 5797

Qy 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540

Db 5798 AAGAGTAAATTTGAAAAAGGCTACTTTTGGAAATTAATTAAGGACTGGATAGAAAAC 5857

Qy 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560

Db 5858 CTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAATGCAAGCCGTCAG 5917

Qy 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580

Db 5918 GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCCAGTCCCTTCA 5977

Qy 1581 GlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600

Db 5978 CAATCTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTGCATTGAAGAATATAGCTTT 6037

Qy 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620

Db 6038 TCTCAAGCAACATTGGAAACAGGTTTTTGTAGAACTCACTAAAGAACAGAGGAGGAGAT 6097

Qy 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640

Db 6098 AATAGTTGTGGAACCTTTTAAACAGCACACTTTGGTGGGAACCAACAGAAAGATAGAGTA 6157

Qy 1641 ValPhe 1642

Db 6158 GTATTT 6163

RESULT 3

ABN89594

ID ABN89594 standard; cDNA; 6525 BP.

XX AC ABN89594;

XX 18-SEP-2002 (first entry)

XX Human ATP-binding cassette transporter ABCA5 cDNA SEQ ID NO:1.

XX Human; ABCA5; ABCA6; ABCA9; ABCA10; ATP-binding cassette transporter;

KW chromosome 17; chromosome 17q; chromosome 17q24; antiarteriosclerotic;

KW gene therapy; cholesterol; lipophilic molecule; inflammation;

KW prostaglandin; prostacyclin; arteriosclerosis; transport; gene; ss.

OS Homo sapiens.

XX WO200246458-A2.

PN 13-JUN-2002.

XX 07-DEC-2001; 2001WO-EP015401.

XX 07-DEC-2000; 2000EP-00403440.

PR 23-JAN-2001; 2001US-0263231P.

XX (AVET) AVENTIS PHARMA SA.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Denefle P, Rosier-Montus M, Prades C, Arnould-Reguigne I;

PI Duverger N, Allikmets R, Dean M;

XX WPI; 2002-557584/59.

DR P-PSDB; ABB81574.

XX A novel nucleic acid corresponding to ATP-binding cassette transporter genes and the encoded polypeptide, useful for preventing or treating a dysfunction in reverse transport of cholesterol.

PS Claim 1; Page 151-153; 216pp; English.

XX The present invention describes human ATP-binding cassette transporters (ABC). Specifically described are the human ABCA5, ABCA6, ABCA9 and ABCA10 genes (see ABN89594 to ABN89597) which encode the proteins given in ABB81574 to ABB81577). ABN89598 to ABN89715 represent ABCA5, ABCA6, ABCA9 and ABCA10 nucleotide fragments; and ABN89716 to ABN89806 represent primers for ABCA5, ABCA6, ABCA9 and ABCA10 genes which are used in the exemplification of the present invention. The ABC sequences have antiarteriosclerotic activities and can be used in gene therapy. ABC sequences can be used in the manufacture of a medicament intended for the prevention and/or treatment of a subject affected by a dysfunction in the reverse transport of cholesterol. The ABC proteins are involved in the

CC reverse transport of cholesterol, in membrane transport of lipophilic
CC molecules, in particular inflammation mediating substance such as
CC prostaglandins and prostacyclins, or in any pathology whose candidate
CC chromosomal region is situated on chromosome 17. They are also useful for
CC the manufacture of a medicament intended for prevention of
CC arteriosclerosis in various forms. The ABCA5, ABCA6, ABCA9 and ABCA10
CC genes are located to chromosome 17, more specifically to the 17q24 locus
xx
SQ Sequence 6525 BP; 1973 A; 1108 C; 1258 G; 2185 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 0 Length: 6525
Score: 8422.00 Matches: 1641
Percent Similarity: 99.94% Conservative: 0
Best Local Similarity: 99.94% Mismatches: 1
Query Match: 99.95% Indels: 0
DB: 6 Gaps: 0

US-10-090-458-5 (1-1642) x ABN89594 (1-6525)

Qy 1 MetSerThrAlaIleArgGluValTyrArgGlnThrArgThrLeuLeuLeuLys 20
Db 1011 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 1070
Qy 21 AsnTyrLeuIleLysCysArgThrLysLysSerValGlnGluIleLeuPheProLeu 40
Db 1071 AATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATCTCTTTTCCACTA 1130
Qy 41 PhePheLeuPheTyrLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 1131 TTTTTTTTATTTTGGTTAATAATTAATAGCATGATGCATCCAAATAAGAAATATGAAGAA 1190
Qy 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 1191 GTGCCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTCTAATCTAATCTTGA 1250
Qy 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 1251 TATACTCCAGTGACTAATATTACAGCAGCATCATGCAGAAAGTGCTACTGATCATCTA 1310
Qy 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 1311 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAGAAATGTTAACATCCAGTCTC 1370
Qy 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 1371 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTCAAGAGCTCCATGTCCTATGAATTCGT 1430
Qy 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 1431 TTTTTTCTTGATATGATTCAGTATCTTCTATTTATATGGATTCAAGAGCTGGCTGTTC 1490
Qy 161 LysSerCysGluAlaAlaGlnTyrTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 1491 AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTTCAGAGTTTACAGATCCATA 1550
Qy 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTyrLysGluLeuGluSerThr 200
Db 1551 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 1610
Qy 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 1611 AAAGCTGTTATTATGGGAGAAACTGCTGTGTGTAGAAATAGATACCTTTCCCGAGGAGTA 1670
Qy 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240
Db 1671 ATTTTAATATACCTAGTTATAGCATTTTCACCTTTTGGATACTTTTGGCAATTCATATC 1730
Qy 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisaspThr 260
Db 1731 GTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTTCATGATACT 1790
Qy 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280

Db 1791 GCCTTTTGGCTTTCCTGGGTCTTCTATATACAGTTTAAATTTTCTTAATGTCCTTCTT 1850
Qy 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
Db 1851 ATGGCAGTCATTGCGACAGCTTCTTTGTTATTCTCTCAAGTAGCAGCATTTGTGATATT 1910
Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 1911 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTCGCTTAAATGCTGACACCTCTT 1970
Qy 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 1971 TTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTT 2030
Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 2031 ATTGGCTTATGATAATCCTCATAGAAAGTTTTCGAAATCGTTAGTGTGGCTTTTCAGT 2090
Qy 361 ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 2091 CCTTCTGTCTACTGTACTTTTGTGATTGGTATTGCAGGTCATGCATTTAGAGATTTT 2150
Qy 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 2151 AATGAAGGTGCTTTCATTTTCAAAATTTGACTGCAGGCCCATATCTCTAATTATTACAAT 2210
Qy 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 2211 ATCATGCTCACACTTAATAGTATATTCTATGTCTCTTGGCTGTCTATCTTGTATCAAGTC 2270
Qy 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 2271 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTG 2330
Qy 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db 2331 TCAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGCAATGTTAATGGAATATATTAGT 2390
Qy 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db 2391 TTTAGTGAAATTTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAGCCATAAGAATT 2450
Qy 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 2451 AGTGGTATTCAGAAAGACATACAGAAAGAGGGTGAATTTGTGAGGCTTTGAGAAATTTG 2510
Qy 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
Db 2511 TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAAACAGGAAAG 2570
Qy 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 2571 AGTACATTGATGAATATTCTTTGTGGACTCTGCCCACCTTCTGTATGGGTTTGCATCTATA 2630
Qy 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 2631 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCATT 2690
Qy 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
Db 2691 TGTCCACAGTTAGATATACACTTTTGATGTTTTTGACAGTAGAAGAAAAATTTATCAATTTTG 2750
Qy 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 2751 GCTTCAATCAAGGGGATACCAGCCAAATATATACAGAGGTGCAGAGGTTTTTACTA 2810
Qy 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
Db 2811 GATTTAGACATGCAGACTATCAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 2870
Qy 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640

Db 2871 AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATATACTGCTGCTAGATGAA 2930
Qy 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660
Db 2931 CCAACAGCTGGAATGGAACCCCTGTTCTCGACATATTGTATGGAATCTTTAAATACAGA 2990
Qy 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Db 2991 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCA 3050
Qy 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 3051 GATAGGAAAGCTGTGATATCACAGGAATGCTGAAATGTGTGGTTCTTCAATGTTCCCTC 3110
Qy 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 3111 AAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 3170
Qy 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
Db 3171 GAAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAT 3230
Qy 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuphe 760
Db 3231 GACCAACAACCTTGTGTATAGCTTGCCTTTCAGGACATGGACAAATTTTCAGGTTTGT 3290
Qy 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 3291 TCTGCCCTAGACAGTCATTCAAATTTGGGTGTCAATTTCTTATGGTGTTCATGACGACT 3350
Qy 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 3351 TTGGAAGACGTATTTTAAAGCTAGAGGAAAGAAATGGATTCAAAATCTTTTGATGAAATGGAA 3410
Qy 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 3411 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAA 3470
Qy 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 3471 CAGAGCTTACTTATTCTTTCTGAACCAAGGCTTCTTAGTGAGCACCATGAGCCTTTGG 3530
Qy 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860
Db 3531 AAACAACAGATGTATACAAATAGCAAGTTTCTATTCTTACCTTGAACGTGAAGTAAA 3590
Qy 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 3591 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 3650
Qy 881 LeuValHisHisSerPheLysAsnAlaValProIleLeuLysLeuValProAspLeuTyr 900
Db 3651 TTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACCTTGTTCAGACTTATAT 3710
Qy 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
Db 3711 TTTCTAAAACCTGGAGACAACCAACACATAAATACAAAACAAGTCTGCTTCTCAAAATTCT 3770
Qy 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
Db 3771 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAAATGGTGACG 3830
Qy 941 MetIleAsnAspSerAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 960
Db 3831 ATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCATAGTCGGCTTTAAATGTGATG 3890
Qy 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
Db 3891 CATTGAAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTATCTTTA 3950
Qy 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
Db 3951 CCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCATTTAATGTGACTGAAACC 4010

Qy 1001 IleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGlu 1020
Db 4011 ATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATTAATGATATAGTTTTTAAATTTGAG 4070
Qy 1021 LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040
Db 4071 CTGTATTTTCAAGCAGCTTGTCTTGGAAATCATTTACTGCAATGCCACCTTACTTTGCC 4130
Qy 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
Db 4131 ATGGAATAATGCAGAGAATCATAAGATCAAAGCTTATACTCAACTTAAACTTTCAGGTCTT 4190
Qy 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIle 1080
Db 4191 TTGCCATCTGCATATTGGATTGGACAAAGCTGTGTGATATCCCTTATTTTATCAT 4250
Qy 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheThrVal 1100
Db 4251 CTTATTTTGATGCTAGGAAGCTTACTGGCAATTCATATGGAATATATTTTATACTGTA 4310
Qy 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
Db 4311 AAGTTCCTTGTGCTGGTTTTTTCCTTATTGGTTATGTTCCATCAGTTATTCTGTCTCACT 4370
Qy 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
Db 4371 TATATTGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC 4430
Qy 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
Db 4431 TATTCTGTGGCAGCGTTGNCTTGTATTGCAATCACTGAAATAAATTTCTTTATGGGATAC 4490
Qy 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
Db 4491 ACAATTGCAACTATTCTTTCATTTATGCCTTTTGTATCATCATTTCCAATCTATCCACTTCTA 4550
Qy 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
Db 4551 GGTGCTCTGATTTCTTTCATAAAGATTTCTTGGAGAATGTACGAAAAAATGTGGACACC 4610
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Db 5931 GTATTT 5936

RESULT 4

AAD37618
ID AAD37618 standard; cDNA; 4929 BP.

XX AAD37618;

AC AAD37618;

XX 10-SEP-2002 (first entry)

DE Human transporter protein cDNA #1.

XX Human; novel human protein; NHP; transporter protein; mental disorder;

KW cancer; gene therapy; drug screening; nutraceutical application; gene;

KW cosmetic application; polymorphism; ss.

XX Homo sapiens.
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XX
FH Key
CDS
Location/Qualifiers
1..4929
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2878
misc_feature
/*tag= d
/note= "This degenerate base represents a polymorphic site"
WO200231147-A2.
18-APR-2002.
04-OCT-2001; 2001WO-US031113.
10-OCT-2000; 2000US-0239629P.
XX (LEXI-) LEXICON GENETICS INC.
XX Hu Y, Nepomnichy B;
XX WPI; 2002-454552/48.
DR P-PSDB; AAE23656.
XX Novel nucleic acid molecule encoding novel human proteins, useful for therapeutic, diagnostic and pharmacogenomic applications.
PT Claim 1; Page 34-35; 46pp; English.
XX The present sequence is a cDNA coding for novel human protein (NHP), human transporter protein. NHPs shares structural similarity with the mammalian ATP-binding cassette (ABC) transporters and multidrug resistance transporters. NHP polynucleotides are useful for the therapeutic, diagnostic and pharmacogenomic applications. They are used for detecting and treating mental disorders and cancers. They are also used in gene therapy. NHP polypeptides are useful for diagnosis, drug screening, clinical trial monitoring, treatment of diseases and disorders, and cosmetic or nutraceutical applications
XX
SQ Sequence 4929 BP; 1544 A; 827 C; 950 G; 1604 T; 0 U; 4 Other;

Alignment Scores:

Pred. No.: 0 Length: 4929
Score: 8395.00 Matches: 1637
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 5
Query Match: 99.63% Indels: 0
DB: 6 Gaps: 0

US-10-090-458-5 (1-1642) x AAD37618 (1-4929)

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QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerValGlnGluIleLeuPheProLeu 40

Db 61 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAATCTTTTCCACTA 120

QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
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 QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
 Db 181 GTGCCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAACTCTAATTTCTGGA 240
 QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
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 QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
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 QY 121 SerLysProSerAsnPheValGlyValPheLysAspSerMetSerTyrGluLeuArg 140
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 Db 601 AAAGCTGTATATATGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 660
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QY 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
|||
Db 4861 AATAGTGTGGAACTTTTAAACAGCACACTTTGGTGGGAACGAACACAGAGATAGAGTA 4920
|||
QY 1641 ValPhe 1642
||||
Db 4921 GTATTT 4926
||||

RESULT 5
AAD37620
ID AAD37620 standard; cdna; 5262 BP.
XX
AC AAD37620;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human transporter protein cDNA #3.
XX
KW Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application;
KW cosmetic application; polymorphism; ss.
XX
OS Homo sapiens.
XX
PN WO200231147-A2.
XX
PD 18-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031113.
XX
PR 10-OCT-2000; 2000US-0239629P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B;
XX
PI WPI; 2002-454552/48.
DR
XX
PT Novel nucleic acid molecule encoding novel human proteins, useful for
PT therapeutic, diagnostic and pharmacogenomic applications.
XX
PS Disclosure; Page 45-46; 46pp; English.
XX
CC The present sequence is a cDNA coding for novel human protein (NHP),
CC human transporter protein. NHPs shares structural similarity with the
CC mammalian ATP-binding cassette (ABC) transporters and multidrug
CC resistance transporters. NHP polynucleotides are useful for the
CC therapeutic, diagnostic and pharmacogenomic applications. They are used
CC for detecting and treating mental disorders and cancers. They are also

CC used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and
CC disorders, and cosmetic or nutraceutical applications
XX
SQ Sequence 5262 BP; 1615 A; 888 C; 1012 G; 1743 T; 0 U; 4 Other;
|||
Alignment Scores:
Pred. No.: 0 Length: 5262
Score: 8395.00 Matches: 1637
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 5
Query Match: 99.63% Indels: 0
DB: 6 Gaps: 0
US-10-090-458-5 (1-1642) x AAD37620 (1-5262)
QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys 20
|||
Db 255 ATGTCCTGCTCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 314
|||
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
|||
Db 315 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGITCAGGAAATTTCTTTTCCACTA 374
|||
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
|||
Db 375 TTTTTTTTATTTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 434
|||
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
|||
Db 435 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTTACTTCTTAATCTAATCTTTGGA 494
|||
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
|||
Db 495 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 554
|||
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
|||
Db 555 CCTGATGTCATAAATTACTGAAGATATACAAATGAAAAGAAATGTTAAACATCCAGTCTC 614
|||
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
|||
Db 615 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTTCAAAGACTCCATGTCTTATGAACCTTCT 674
|||
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
|||
Db 675 TTTTTTCTGATATGATTCCAGTATCTTCTATTATATGGAATTCAGAGCTGGCTGTTCA 734
|||
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
|||
Db 735 AAATCATGTGAGGCTGCTCAGTACTGGTCTCCTCAGGTTTTCAGTTTACAAGCATCCATA 794
|||
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
|||
Db 795 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTTGAAGGAGCTGGAGTCAACT 854
|||
QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
|||
Db 855 AAAGCTGTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 914
|||
QY 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
|||
Db 915 ATTTTATATACCTAGTTATAGCAATTTTCACCTTTTGGATACTTTTGGCAATTCATATC 974
|||
QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
|||
Db 975 GTAGCAGAAAAAGAAAAAATAAAAGAAATTTTAAAGATAATGGGACTTCATGATACT 1034
|||
QY 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
|||
Db 1035 GCCTTTTGGCTTCTCTGGGTTCTTCTATAWACAAGTTTAAATTTTCTTATGTCCCTTCT 1094
|||
QY 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerIleValIlePhe 300
|||

Db 1095 ATGGCAGTCATTGCGACAGCTCTTTGTTATTTCTCAAGTAGCAGCAATTGTGATATTT 1154
Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 1155 CTGCTTTTTCCTTTATGGATATATCATCTGTATTTTGTCTTAAATGCTGACACCTCTT 1214
Qy 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 1215 TTTAAAAAATCAAAACATGTGGAAATAGTTGAATTTTGTACTGTGGCTTTTGGATTT 1274
Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 1275 ATTGGCCTTATGATAATCCTCATAGAAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 1334
Qy 361 ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 1335 CCTTCTGTCACTGTACTTTTGTGATTGGTATTGCACAGGTCATGCATTTAGAAAGATTTT 1394
Qy 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 1395 AATGAAGGTGCTTCAATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAAATATTACAAT 1454
Qy 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 1455 ATCATGTCTCACACTTAATAGTATATCTATGTCTCTGGCTGTCTATCTTGATCAAGTC 1514
Qy 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 1515 ATTCAGGGGAATTTGGCTTTACGGAGATCACTCTTTATATTTTCTGAAGCCTTCATATTGG 1574
Qy 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db 1575 TCAAAGAGCAAAAGAAATTTAGAGGAGTTATCAGAGGCAATGTTAATGGAATATTAGT 1634
Qy 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db 1635 TTTAGTGAAATTTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAACCCATAAGAATT 1694
Qy 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 1695 AGTGGTATTCAGAAGACATACAGAAAGAGGGTGAAATGTGGAGGCTTTTGAGAAATTTG 1754
Qy 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
Db 1755 TCATTTGACATATATGAGGGTCAGATTACTGCCCTTACTTGGCCACAGTGGAAACAGGAAG 1814
Qy 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 1815 AGTACATTGATGAATATTTCTTTGTGGACTCTGCCACCTCTGATGGGTTTGGCATCTATA 1874
Qy 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 1875 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCATT 1934
Qy 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
Db 1935 TGTCCACAGTTAGATATACACTTTGATGTTTTTGACAGTAGAAGAAAAATTTATCAATTTTG 1994
Qy 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 1995 GCTTCAATCAAAGGGATACCAGCCCAATATAATACAGAAAGTGCAGAGGTTTACTA 2054
Qy 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
Db 2055 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 2114
Qy 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
Db 2115 AGAAAGCTGTTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 2174
Qy 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660

Db 2175 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTTGTATGGAATCTTTTAAAAATACAGA 2234
Qy 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Db 2235 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGA 2294
Qy 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 2295 GATAGGAAAGCTGTGATATACAAAGGAATGCTGAAATGTGTGTTGTTCTTCAATGTTCTC 2354
Qy 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 2355 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 2414
Qy 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsn 740
Db 2415 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACACAGAAT 2474
Qy 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
Db 2475 GACCAACAACCTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCAGGTTTGT 2534
Qy 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 2535 TCTGCCCTAGACAGTCAATCAAATTTGGGTGGCATTTCTTATGGGTTTCCATGACGACT 2594
Qy 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 2595 TTGGAAGACGTTATTTTAAAGCTAGAGTTGAAGCAGAAATTTGACCAAGCAGATTATAGT 2654
Qy 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 2655 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAATGGAA 2714
Qy 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 2715 CAGAGCTTACTTATTTCTGAAACCAAGGCTKCTCTAGTGAGCACCATTGAGCCCTTGG 2774
Qy 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860
Db 2775 AAACACAGATGTATACATAGCAAAAGTTTCATTTCTTACCTTGAAACGTGAAAGTAAA 2834
Qy 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 2835 TCAGTCAGATCAGTGTTCCTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTT 2894
Qy 881 LeuValHisHisSerPheLysAsnAlaValProLysLeuValProAspLeuTyr 900
Db 2895 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCTCAAACTTGTTCACAGACTTATAT 2954
Qy 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
Db 2955 TTTCTAAAAACCTGGAGACAAACACACATAAAATACAAAACAAGTCTGCTTCTTCAAAATCT 3014
Qy 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
Db 3015 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGAACATATATGGTGACG 3074
Qy 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960
Db 3075 ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCACTAGTGGGCTTTAAATGTGRTG 3134
Qy 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
Db 3135 CATTCAGAAAAAGGACTATGTTTGTGAGCTGTTTTCACAGTACTATGTTTATTCTTTA 3194
Qy 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
Db 3195 CCTATATTAGTGAATATCATTTAGTAACACTACTATCTTTATCATTTAAATGTGACTGAAAC 3254
Qy 1001 IleGlnIleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLysIleGlu 1020
Db 3255 ATCCAGATCTGGAGTACCCCAATCTTCAAGAAATTTACTGATATAGTTTTTTAAAAATTGAG 3314

QY 1021 LeuTyrPheGlnAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040
Db 3315 CTGTATTTTCAAGCAGCTTTTGCTTGGAACTATTGTTACTGCAATGCCACCTTACTTTGCC 3374
QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
Db 3375 ATGGAAATGCAGAGAATCATAGAATCAAAAGCTTAYACTCAACTTAAACTTTTCAGGTCCT 3434
QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValAlaAspIleProLeuPhePheIleIle 1080
Db 3435 TTGCCATCTGCATATTGGATTGGACAAGCTGTGTTGATATCCCTTATTTTATCAT 3494
QY 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
Db 3495 CTTATTTTGATGCTAGGAAGCTTATTGGCACTTTCATTATGGATTATATTTTATACGTGA 3554
QY 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
Db 3555 AAGTTCCCTTGCTGTGGTTTTTTGCCCTTATTGGTTATGTTCCATCAGTTATCTGTTCACT 3614
QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
Db 3615 TATATTGCTTCTTTCACCTTTAAGAAATTTTAAATACCAAGAAATTTTGGTTCATTTATC 3674
QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
Db 3675 TATTCTGTGGCAGCGTTGGCTTGATTGCAATCACTGAAATAACTTCTTTATGGGATAC 3734
QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
Db 3735 ACAATTGCAACTATTCTTCATTATGCTTTTGTATCATCATTTCCATCTATCCACTTCTA 3794
QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
Db 3795 GGTGCTGCTGATTTCTTTCATAAAGATTTCTTGAAGAATGTACGAAATAATGTGGACACC 3854
QY 1201 TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220
Db 3855 TATAATCCATGGGATAGGCTTTTCAGTAGCTGTATATCGCCTTACCTGCAGTGTGTACTG 3914
QY 1221 TrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp 1240
Db 3915 TGGATTTTCTCTTACAACTACTATGAGAAAAAATAATGGAGGCAGATCAATAAGAAAAGAT 3974
QY 1241 ProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
Db 3975 CCCTTTTTCAGAAACCTTTCACACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACGAC 4034
QY 1261 AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280
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QY 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
Db 4095 TGCCAGTGTGTGAGGAGAAACCATCCATTATGCTCAGCAATTTGCTATAAAGAAATATGAT 4154
QY 1301 AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer 1320
Db 4155 GACAAGAAAGATTTTCTCTTTCAGAAAGTAAAGAAAGTGGCACTAAATAACATCTCTCT 4214
QY 1321 PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyValAlaGlyLysSer 1340
Db 4215 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGC 4274
QY 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360
Db 4275 ACAATTATTAATATTCTGTTGGTGTATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 4334
QY 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380
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QY 1401 ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
Db 4455 GTCAAAGGAATGAGTGAAGTGACATGAAGAAGTCAATAAGTCGAATAACACATGCACCT 4514
QY 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
Db 4515 GATTTAAAGAACAATCTTCAGAAGACTGTAAAGAAATACCTGCAGGAATCAAAACGAAAG 4574
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db 4575 TTGTGTTTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4634
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
Db 4635 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGCATTATA 4694
QY 1481 AsnArgLysArgAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
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QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
Db 4755 GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACACATCTA 4814
QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540
Db 4815 AAGAGTAAATTTGGAAAAAGGCTACTTTTTTGGAAATTAATTTGAAGGACTGGATAGAAAC 4874
QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
Db 4875 CTAGAAGTAGACCCGCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAG 4934
QY 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
Db 4935 GAAAGTTTTTCTTCTATTTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA 4994
QY 1581 GlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600
Db 4995 CAATCTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGGCCATTGAAGAAATATAGCTTT 5054
QY 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620
Db 5055 TCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAAGAACCAAGAGGAGGAAGAT 5114
QY 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
Db 5115 AATAGTTGTGGAACCTTAAACAGCACACTTTGGTGGGAACGAACACAAAGAAATAGAGTA 5174
QY 1641 ValPhe 1642
Db 5175 GTATTT 5180
RESULT 6
ABS57750
ID ABS57750 standard; cDNA; 4917 BP.
XX
AC ABS57750;
XX
DT 04-FEB-2003 (first entry)
XX
DE Coding sequence of human ATP binding cassette ABCA5 transporter #1.
XX
KW Human; ATP binding cassette; ABC; ABCA5; transporter;
KW neurotoxin transport; beta-amyloid peptide; chromosome mapping;
KW blood brain barrier transport; tissue typing; predictive medicine;
KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; Gene; ss.
XX
OS Homo sapiens.
XX

FH Key Location/Qualifiers
FT CDS 1. 4917
FT /tag= a
FT /product= "ABCA5"
FT /note= "ATP binding cassette (ABC) A5 transporter"
FT /transl_except= (pos:3160..3162, aa:Ser)
XX
XX US2002123107-A1.
XX
XX 05-SEP-2002.
XX
XX 01-MAR-2002; 2002US-00090458.
XX
XX 02-MAR-2001; 2001US-0272885P.
XX
XX (ACTI-) ACTIVE PASS PHARM INC.
XX
XX Chen H, Kilinski L, Le Bihan S;
XX WPI; 2003-066798/06.
XX P-PSDB; ABG72423.
XX
XX Novel isolated ATP binding cassette transporter family polypeptide,
XX ABCA5, useful for treating disorders associated with aberrant or unwanted
XX ABCA5 transporter expression or activity.
XX
XX Claim 2; Fig 1; 52pp; English.
XX
XX The invention describes an isolated ATP binding cassette (ABC)
XX transporter family polypeptide (I), designated ABCA5. (I) or the
XX polynucleotide encoding it (II) are useful as targets for developing
XX modulating agents to regulate a variety of cellular processes,
XX particularly the transport of neurotoxic molecules, e.g., beta-amyloid
XX peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
XX (BBB), as targets for developing modulating agents of multi-drug
XX resistance, as diagnostic and therapeutic tools, or to treat disorders
XX associated with aberrant or unwanted ABCA5 transporter expression or
XX activity. (I), (II) or a host cell (III) expressing (II) are useful in
XX screening assays, detection assays (e.g., chromosomal mapping, tissue
XX typing, forensic biology), predictive medicine (e.g., diagnostic assays,
XX prognostic assays, monitoring clinical trials and pharmacogenomics), and
XX in methods of treatment (e.g., therapeutic and prophylactic). (I) or
XX (III) are useful as reagents or targets in assays applicable to treatment
XX and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
XX screen for naturally occurring ABCA5 substrates; to screen for drugs or
XX compounds which modulate ABCA5 activity; as a bait protein in a yeast two
XX -hybrid or three-hybrid assay; and to identify other proteins which bind
XX to or interact with ABCA5. (II) is useful in: gene therapy; to detect
XX ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
XX activity; to locate gene regions associated with genetic disease or to
XX associate ABCA5 with the disease, to identify an individual from a minute
XX biological sample (tissue typing), and to aid in forensic identification
XX of the biological sample. This sequence encodes a novel human ATP binding
XX cassette (ABC) A5 transporter
XX
XX Sequence 4917 BP; 1540 A; 821 C; 955 G; 1599 T; 0 U; 2 Other;
XX
XX Alignment Scores:
XX Pred. No.: 0 Length: 4917
XX Score: 8309.00 Matches: 1629
XX Percent Similarity: 98.85% Conservative: 1
XX Best Local Similarity: 98.79% Mismatches: 2
XX Query Match: 98.61% Indels: 18
XX DB: 7 Gaps: 2
XX
XX US-10-090-458-5 (1-1642) x ABS57750 (1-4917)
XX
XX 1 MetSerThrAlaIleArgGluValGlyValTyrArgGlnThrArgThrLeuLeuLeuLys 20
XX
XX 1 ATGTCCACTGCAATTAGGAGGTAGAGTTGGAGACAGACCAGAACACTTCTACTGAAG 60
XX
XX 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
XX

Db 61 AATTACTTAATTAATGCAGAACCCAAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 120
Qy 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 121 TTTTCTTTTATTTTGGTTAATATTAATTAGCATGATGCATCCAAATAGAAATATGAAGAA 180
Qy 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuLeuGly 80
Db 181 GTGCCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGA 240
Qy 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 241 TATACTCCAGTGAATAATATTAAGCAGCATCATGCAGAAAGTGCTACTGATCATCTA 300
Qy 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 301 CCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAAGAAATGTTAATCATCCAGTCTC 360
Qy 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 361 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGCTCTATGAACCTTCGT 420
Qy 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 421 TTTTCTCTGATATGATTCAGTATCTTCTATTATATATGATTAAGATTCAGAGCTGGTGTTC 480
Qy 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 481 AAATCATGTGAGGCTGCTCAGTACTGGTCTCCTCAGGTTTTCACAGTTTTTACAAGCATCCATA 540
Qy 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
Db 541 GATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTTGAAGGAGCTGGAGTCAACT 600
Qy 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 601 AAAGCTGTTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 660
Qy 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db 661 ATTTAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACTTTTGGCAATTCATATC 720
Qy 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 721 GTACGAGAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTTCATGATACT 780
Qy 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 781 GCCTTTGGCTTTCTCTGGGTCTTCTATATACAGTTAATTTTCTTATGTGCTCTCTT 840
Qy 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
Db 841 ATGGCAGTCATTGCGACAGCTTCTTTGTTATTTCCCTCAAAGTAGCAGCATTTGATATTT 900
Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 901 CTGCTTTTTCCTTTTATGGATTATCATCTGTATTTTGTCTTTAATGCTGACACCTCTT 960
Qy 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 961 TTTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTGTTACTGTGGCTTTTGGATTT 1020
Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 1021 ATTGGCCTTATGATAATCCTCATAGAAAGTTTTCCTCAAATCGTTAGTGTGGCTTTTCAGT 1080
Qy 361 PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 1081 CCTTCTCTGTCACGTGATCTTTTGTGATTGGTATTTGCACAGGTCATGCAATTTAGAGATTTT 1140
Qy 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 1141 AATGAAGTGTCTTCATTTTCAAAATTTGACTGCAGGCCCATATCTCTTAATTATTACAAATT 1200

QY 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
 Db 1201 ATCATGCTCACACTTAATAGTATATCTATGTCCTCTTGGGTGTCTATCTTGATCAAGTC 1260
 QY 421 IleProGlyGluPheGlyLeuArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
 Db 1261 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTCTGAAGCCTTCATATTGG 1320
 QY 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
 Db 1321 TCAAAGAGCAAAAGAAATATAGAGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT 1380
 QY 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
 Db 1381 TTTAGTGAATATTATGAGCCAGTTTCTTCAGAAATTTGTAGAAAGAGCCATAAGAAATT 1440
 QY 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
 Db 1441 AGTGGTATTCAGAAAGACATACAGAAAGAGGGTGAAATGTGGAGGCTTTGAGAAATTTG 1500
 QY 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
 Db 1501 TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAAACAGGAAAG 1560
 QY 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
 Db 1561 AGTACATTGATGAATATTCTTTGTGACTCTGCCACCTCTGTGATGGGTTTGCATCTATA 1620
 QY 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
 Db 1621 TATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAATGATTGGCATT 1680
 QY 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
 Db 1681 TGTCCACAGTTAGATATACACTTTGATGTTTTCAGAGTAGAAGAAATTTATCAATTTTG 1740
 QY 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
 Db 1741 GCTTCAATCAAAGGGATACCAGCAACAAATATAATACAGAGTGCAGAGGTTTACTA 1800
 QY 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlnLys 620
 Db 1801 GATTTAGACATGCAGACTATCAAGATAACCAAGCTAAAAAATTAAGTGGTGCACAAA 1860
 QY 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
 Db 1861 AGAAAGCTGTCTATTAGGAATGCTGTTCTTGGGAACCCAAAGATACTGCTGTAGATGAA 1920
 QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLysTyrArg 660
 Db 1921 CCAACAGCTGGAATGGACCCCTGTCTCGACATATTGTATGGAATCTTTTAAATACAGA 1980
 QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
 Db 1981 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATCTTGCA 2040
 QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
 Db 2041 GATAGGAAGCTGTGATATCAAGAGAAATGCTGAAATGTGTTGTTCTTCAATGTTCCCTC 2100
 QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
 Db 2101 AAAAGTAAATGGGGATCGGCTACCGCCTGAGCATGTACATAGACAAATATTGTGCCACA 2160
 QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
 Db 2161 GAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACACAGAAAT 2220
 QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
 Db 2221 GACCAACAACCTTGTTATAGCTTGCCTTTCAGGAGCATGGACAAATTTTCAGGTTTGT 2280

QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
 Db 2281 TCTGCCCTAGACAGTCATTTCAAAATTTGGGTGTCAATTTCTTATGGTGTTCATGACGACT 2340
 QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
 Db 2341 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGT 2400
 QY 801 ValPheThrGlnGlnProLeuGluGluGluMetAspSerLysSerPheAspGluMetGlu 820
 Db 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTATGATGAAATGGAA 2460
 QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
 Db 2461 CAGAGCTTACTTATTTCTTCTGAACCAAGGCTGCTCTAGTGAGCACCATTGAGCCTTTGG 2520
 QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860
 Db 2521 AAACAACAGATGTATACAAATAGCAAAAGTTTCATTTCTTTACTTGAACCTGAAACGTGAAAGTAAA 2580
 QY 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
 Db 2581 TCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTTTCAGATTTCAGATTATTTATGTTT 2640
 QY 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
 Db 2641 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCTCATCAAACTTGTTCAGACTTATAT 2700
 QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSer 920
 Db 2701 TTTCTAAAAACCTGGAGACAAACCCACATAAATACAAACAAAGTCTGCTCTTCAAAATTC 2760
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 QY 955 AlaAlaLeuAsnValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSer 974
 Db 2881 GCGGCTTAAATGTATGTCATTACAGAAAAGGACTATGTTTTCAGAGCTGTTTTCACACAGT 2940
 QY 975 ThrMetValTyrSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHis 994
 Db 2941 ACTATGGTTTATCTTTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCAT 3000
 QY 995 LeuAsnValThrGluThrIleGlnIleTrpSerThrProPhePheGlnGluIleThrAsp 1014
 Db 3001 TTAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATCTCTTCAAGAAATTTACTGAT 3060
 QY 1015 IleValPheLysIleGluLeuTyrPheGlnAlaAlaLeuLeuGly-IleIleValThrAl 1034
 Db 3061 ATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCTTTGCTGGAAATCATTTGTAAGTGC 3120
 QY 1034 aMetProProTyrPheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGl 1054
 Db 3121 AATGCCACCTACTCTGCCATGGAATAATGCAGAGAAATCATAA----- 3162
 QY 1054 nLeuLysLeuSerGlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIle 1074
 Db 3163 -----GGTCTTTTGGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATAT 3209
 QY 1074 eProLeuPhePheIleIleLeuLeuMetLeuGlySerLeuLeuAlaPheHisTyrGl 1094
 Db 3210 CCCCATTATTTTATCATCTTATTTTGTAGTGTAGGAAGCTTATTTGGCATTTCATTATGG 3269
 QY 1094 yLeuTyrPheTyrThrValLysPheLeuAlaValPheCysLeuIleGlyTyrValPr 1114
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Db 3330 ATCAGTTATTCTGTTCACTTATATTGCTCTTTACCTTTAAGAAAAATTTTAAATACCAA 3389
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QY 1174 eProIleTyrProLeuLeuGlyCysIleuIleSerPheIleLysIleSerTrpLysAsnVa 1194
Db 3510 TCCAATCTATCCACTTCTAGGTTGCCGTGATTCTTTTCATAAAGATTTCTTTGGAAGAAATGT 3569
QY 1194 lArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerPr 1214
Db 3570 ACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCC 3629
QY 1214 oTyrLeuGlnCysValLeuTriPheLeuLeuGlnTyrTyrGluLysLysTyrGlyG 1234
Db 3630 TTACCTGCAGTGTGTACTGTGATTCTTCTTACAATACTATGAGAAAAAATATGGAGG 3689
QY 1234 yArgSerIleArgLysAspProPhePheArgAsnLeuSerThrLysSerLysAsnArgLy 1254
Db 3690 CAGATCAATAAGAAAGATCCCTTTTTCAGAAACCTTTTCAAGAAAGTCTAAAAATAGGAA 3749
QY 1254 sLeuProGluProProAspAsnGluAspGluAspValLysAlaGluArgLeuLy 1274
Db 3750 GCTTCCAGAACCCAGACACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAGACTAAA 3809
QY 1274 sVallysGluLeuMetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAs 1294
Db 3810 GGTCAAAGAGCTGATGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGTTGTCAGCAA 3869
QY 1294 nLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysLysVa 1314
Db 3870 TTTGCAATAAAGAATATGATGACAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGT 3929
QY 1314 lAlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyPr 1334
Db 3930 GGCAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCC 3989
QY 1334 oAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSe 1354
Db 3990 AAATGGTGCTGCCAAAAGCACAAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTC 4049
QY 1354 rGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLy 1374
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QY 1374 sCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHi 1394
Db 4110 GTGTATGGGTACTGTCTCTCAGATAAACCCCTTTGTGGCCAGATACTACATTGCGAGAAC 4169
QY 1394 sPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSe 1414
Db 4170 TTTTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAAGAAAGTCATAAG 4229
QY 1414 rArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPr 1434
Db 4230 TCGAATAACACATGCACCTTGATTTAAAAGAACATCTTCAGAAGACTGTAAAGAAACTACC 4289
QY 1434 oAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleTh 1454
Db 4290 TGCAGGAATCAACAGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTAC 4349
QY 1454 rLeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAl 1474
Db 4350 TTTGCTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGC 4409
QY 1474 aIleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGl 1494

Db 4410 AATTCGAACGTCATTTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACCTCACTATATGGA 4469
QY 1494 uGluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysI 1514
Db 4470 GGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGCAGTTAAGATGTAT 4529
QY 1514 eGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLe 1534
Db 4530 CGGAACAGTACAACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAAT 4589
QY 1534 uLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePh 1554
Db 4590 GAAGGACTGGATAGAAAACCTAGAAAGTAGACCCGCTTCAAAGAGAAATTCAGTATATTT 4649
QY 1554 eProAsnAlaSerArgGlnGlnSerPheSerSerIleLeuAlaTyrLysIleProLysGl 1574
Db 4650 CCCAATGCAAGCCGTCAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGA 4709
QY 1574 uAspValGlnSerLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPheAl 1594
Db 4710 AGATGTTCACTCCCTTTTCAACAATCTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGC 4769
QY 1594 aIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLy 1614
Db 4770 CATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAA 4829
QY 1614 sGluGlnGluGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluAr 1634
Db 4830 AGAACAAAGAGGAGGAAGATAATAGTTGTGGAACCTTTTAAACAGCACACTTTTGGTGGGAACG 4889
QY 1634 gThrGlnGluAspArgValValPhe 1642
Db 4890 AACACAAAGAGATAGAGTAGTATTT 4914
RESULT 7
ABS57749
ID ABS57749 standard; cDNA; 5463 BP.
XX
AC ABS57749;
XX 04-FEB-2003 (first entry)
DT
XX cDNA encoding novel human ATP binding cassette ABCA5 transporter #1.
DE Human; ATP binding cassette; ABC; ABCA5; transporter;
XX neurotoxin transport; beta-amyloid peptide; chromosome mapping;
KW blood brain barrier transport; tissue typing; predictive medicine;
KW ABCA5 mediated disorder; ABCA5 related disorder; gene therapy; gene; ss.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT CDS 114..5030
FT /*tag= a
FT /product= "ABCA5"
FT /note= "ATP binding cassette (ABC) A5 transporter"
FT /transl_except= (pos:3273..3275, aa:Ser)
XX
PN US2002123107-A1.
XX
PD 05-SEP-2002.
XX
PF 01-MAR-2002; 2002US-00090458.
XX
PR 02-MAR-2001; 2001US-0272885P.
XX (ACTI-) ACTIVE PASS PHARM INC.
XX Chen H, Kilinski L, Le Bihan S;
XX WPI; 2003-066798/06.
DR P-PSDB; ABG72423.
XX

PT Novel isolated ATP binding cassette transporter family polypeptide,
PT ABCA5, useful for treating disorders associated with aberrant or unwanted
PT ABCA5 transporter expression or activity.
XX

PS Claim 2; Fig 1; 52pp; English.

XX
CC The invention describes an isolated ATP binding cassette (ABC)
CC transporter family polypeptide (I), designated ABCA5. (I) or the
CC polynucleotide encoding it (II) are useful as targets for developing
CC modulating agents to regulate a variety of cellular processes,
CC particularly the transport of neurotoxic molecules, e.g., beta-amyloid
CC peptide (Abeta), across cell membranes or, e.g., the blood brain barrier
CC (BBB), as targets for developing modulating agents of multi-drug
CC resistance, as diagnostic and therapeutic tools, or to treat disorders
CC associated with aberrant or unwanted ABCA5 transporter expression or
CC activity. (I), (II) or a host cell (III) expressing (II) are useful in
CC screening assays, detection assays (e.g., chromosomal mapping, tissue
CC typing, forensic biology), predictive medicine (e.g., diagnostic assays,
CC prognostic assays, monitoring clinical trials and pharmacogenomics), and
CC in methods of treatment (e.g., therapeutic and prophylactic). (I) or
CC (III) are useful as reagents or targets in assays applicable to treatment
CC and diagnosis of ABCA5-mediated or related disorders. (I) is useful to
CC screen for naturally occurring ABCA5 substrates; to screen for drugs or
CC compounds which modulate ABCA5 activity; as a bait protein in a yeast two
CC -hybrid or three-hybrid assay; and to identify other proteins which bind
CC to or interact with ABCA5. (II) is useful in: gene therapy; to detect
CC ABCA5 mRNA or a genetic alteration in a ABCA5 gene; to modulate ABCA5
CC activity; to locate gene regions associated with genetic disease or to
CC associate ABCA5 with the disease, to identify an individual from a minute
CC biological sample (tissue typing), and to aid in forensic identification
CC of the biological sample. This sequence encodes a novel human ATP binding
CC cassette (ABC) A5 transporter
XX

SQ Sequence 5463 BP; 1699 A; 912 C; 1055 G; 1794 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.: 0 Length: 5463
Score: 8309.00 Matches: 1629
Percent Similarity: 98.85% Conservative: 1
Best Local Similarity: 98.79% Mismatches: 2
Query Match: 98.61% Indels: 18
DB: 7 Gaps: 2

US-10-090-458-5 (1-1642) x ABS57749 (1-5463)

Qy 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys 20
Db 114 ATGTCCACTGCAATTAGGAGGTAGGAGTTTGGACACAGACCAGAACTTCTACTGAAG 173
Qy 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 174 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 233
Qy 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 234 TTTTATTATTGGTTAATTAATTAGCATGATGCATCCAAATAGAAATATGAAGAA 293
Qy 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 294 GTGCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTTCTAATCTAATTTCTTGA 353
Qy 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 354 TATACTCCAGTGACTAATATTAACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 413
Qy 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 414 CCTGATGTCATAATTACTGAAGAATATACAATGAAAAAGAAATGTTAAACATCCAGTCTC 473
Qy 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 474 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCATGTCCTATGAACCTTCGT 533

Qy 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 534 TTTTTCCTGATATGATTCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTCA 593
Qy 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 594 AATCATGTGAGGCTGCTCAGTACTGGTCTCCTCAGGTTTCACAGTTTACAAAGCATCCATA 653
Qy 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
Db 654 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 713
Qy 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 714 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 773
Qy 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240
Db 774 ATTTTAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACTTTTGGCAATTATATC 833
Qy 241 ValAlaGluLysGluLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 834 GTAGCAAAAAAGAAAAATAAAGAAATTTTAAAGATAAATGGACTTTCATGATACT 893
Qy 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 894 GCCTTTGGCTTTCCCTGGGTCTTCTATATACAAAGTTAAATTTTCTTATGTCCTCTCTT 953
Qy 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
Db 954 ATGGCAGTCATTGCGACAGCTTCTTTGTTATTTCCTCAAAGTAGCAGCATTTGTGATATT 1013
Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 1014 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTGTGCTTTAATGCTGACACCTCTT 1073
Qy 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 1074 TTTAAAAAATCAAAACATGCGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTT 1133
Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 1134 ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAAATCGTTAGTGTGGCTTTTCAGT 1193
Qy 361 PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 1194 CCTTCTGTCACTGTACTTTTGTGATTGGTATTGCACAGGTCATGCATTTAGAAGATTTT 1253
Qy 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 1254 AATGAAGGTGCTTCATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAATATTACAAT 1313
Qy 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 1314 ATCATGCTCACACTTAATAGTATATTCTATGTCTCTTGGCTGTCTATCTTGATCAAGTC 1373
Qy 421 IleProGlyGluPheGlyLeuArgArgSerSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 1374 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCCTTCATATTGG 1433
Qy 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
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RESULT 8
AAD37619
ID AAD37619 standard; cDNA; 4785 BP.
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AC AAD37619;
DT 10-SEP-2002 (first entry)
XX
DE Human transporter protein cDNA #2.
XX
KW Human; novel human protein; NHP; transporter protein; mental disorder;
KW cancer; gene therapy; drug screening; nutraceutical application; gene;
KW cosmetic application; polymorphism; ss.
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FT misc_feature 2878
FT /*tag= d
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PN WO200231147-A2.
XX
PD 18-APR-2002.
XX
PF 04-OCT-2001; 2001WO-US031113.
XX
PR 10-OCT-2000; 2000US-0239629P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Hu Y, Nepomnichy B;
XX
DR WPI; 2002-454552/48.
DR P-PSDB; AAE23657.
XX
PT Novel nucleic acid molecule encoding novel human proteins, useful for
PT therapeutic, diagnostic and pharmacogenomic applications.
PS Claim 1; Page 39-41; 46pp; English.
XX
CC The present sequence is a cDNA coding for novel human protein (NHP),
CC human transporter protein. NHPs shares structural similarity with the
CC mammalian ATP-binding cassette (ABC) transporters and multidrug
CC resistance transporters. NHP polynucleotides are useful for the
CC therapeutic, diagnostic and pharmacogenomic applications. They are used

CC for detecting and treating mental disorders and cancers. They are also
CC used in gene therapy. NHP polypeptides are useful for diagnosis, drug
CC screening, clinical trial monitoring, treatment of diseases and
CC disorders, and cosmetic or nutraceutical applications
XX
SQ Sequence 4785 BP; 1489 A; 807 C; 917 G; 1568 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 0 Length: 4785
Score: 8112.00 Matches: 1583
Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 5
Query Match: 96.27% Indels: 0
DB: 6 Gaps: 0

US-10-090-458-5 (1-1642) x AAD37619 (1-4785)

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QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
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Db 2581 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2640
QY LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
Db 2641 TTGGTTTCATCACTCTTTTAAATATGCTGTGTTCCCATCAAACITGTTCCAGACTTATAT 2700
QY PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
Db 2701 TTTCTAAACCTGGAGACAAACCACATAAATACAAACAAGTCTGCTTCTTCAAAATTC 2760
QY AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
Db 2761 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAGCCAGAACATAATGGTGACG 2820
QY MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960
Db 2821 ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAGTGGGCTTTAAATGTGRTG 2880
QY HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
Db 2881 CATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTTATTCTTTA 2940
QY ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
Db 2941 CCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCATTTAAATGTGACTGAAACC 3000
QY IleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGlu 1020

Db 3001 ATCCAGATCTGGAGTACCCCATTTCTTTCAAGAAATTAATGATATAGTTTTTAAATTGAG 3060
QY LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040
Db 3061 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCAITGTGTACTGCAATGCCACCTTACTTTGCC 3120
QY MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
Db 3121 ATGGAAATGCAGAGAAATCATAAAGATCAAAGCTTAYACTCAACTTAAACTTTCAAGTCTT 3180
QY LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIle 1080
Db 3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTGTGTGATATCCCCCTTATTTTTTATCAT 3240
QY LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
Db 3241 CTTATTTTGATGCTAGGAAGCTTATTGGCATTTCATTATGGATTATATTTTATACTGTA 3300
QY LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
Db 3301 AAGTTCCTTGTCTGGTTTTTTTGGCTTATTGGTTATGTTCCATCAGTTATTCTGTTCACT 3360
QY TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
Db 3361 TATATTGCTTCTTTCACCTTTAAGAAAAATTTTAAATACCAAGAAATTTTGGTCATTATC 3420
QY TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
Db 3421 TATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATAC 3480
QY ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
Db 3481 ACAATTGCCAACTATTCTTCATTATGCCTTTTGTATCATCATTCCAATCTATCCACTTCTA 3540
QY GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
Db 3541 GGTGGCTGATTTCTTCATAAAGATTTCTTGGAAAGATGTACGAAAAAATGTGGACACC 3600
QY TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220
Db 3601 TATAATCCATGGGATAGGCTTTTCAGTAGCTGTATATCGCCTTACCTGCAGTGTGTACTG 3660
QY TrpIlePheLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp 1240
Db 3661 TGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGAT 3720
QY ProphePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
Db 3721 CCCTTTTTCAGAAACCTTTCAACGAAAGTCTAAAAAATAGGAAGCTTCCAGAACCCACGAC 3780
QY AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280
Db 3781 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGT 3840
QY CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
Db 3841 TGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAAATATGAT 3900
QY AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer 1320
Db 3901 GACAAAGAAAGATTTCTTCTTTTCAAGAAAAAGTAAAAAGAGTGGCACTTAAATACATCTCT 3960
QY PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340
Db 3961 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGGCAAAAGC 4020
QY ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360
Db 4021 ACAATTATTATCATTTCTGGTTGGTGTATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 4080
QY AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380
Db 4081 GATTATTCTTCAGACACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTACTGTCTCT 4140

QY 1381 GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400
Db 4141 CAGATAAACCCCTTTGTGGCCAGATACATTGCAGGAACATTTGAAATTTATGGAGCT 4200
QY 1401 ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
Db 4201 GTCAAAGGAATGAGTGCACATGAAAGAGTCATAAGTCGAATAACACATGCACATT 4260
QY 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
Db 4261 GATTTAAAGAACATCTTCAGAGAGCTGTAAAGAACTACCTGCAGGAATCAAACGAAAG 4320
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db 4321 TTGTGTTTTGCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACATCT 4380
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
Db 4381 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGCATTTAA 4440
QY 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
Db 4441 AACAGAAAGGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGCTGTCTGT 4500
QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
Db 4501 GATCGAGTAGCTATCATGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA 4560
QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTyrIleGluAsn 1540
Db 4561 AAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAAATTGAAGGACTGGATAGAAAAC 4620
QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
Db 4621 CTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAG 4680
QY 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
Db 4681 GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA 4740
QY 1581 GlnSerPhePheLysLeuGluGlu 1588
Db 4741 CAATCTTTTTTAAGCTGGAAGAA 4764

RESULT 9
ADA53416
ID ADA53416 standard; cDNA; 3268 BP.
XX
AC ADA53416;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human coding sequence, SEQ ID 984.
XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW Inflammatory disease; osteoporosis; neurological disease; gene; ss.
XX
OS Homo sapiens.
XX
PN EPI293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-395539/38.
DR P-PSDB; ADA55055.
XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 1; SEQ ID NO 984; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 3268 BP; 1022 A; 540 C; 622 G; 1084 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3268
Score: 4847.50 Matches: 941
Percent Similarity: 98.64% Conservative: 2
Best Local Similarity: 98.43% Mismatches: 2
Query Match: 57.53% Indels: 11
DB: 7 Gaps: 1

US-10-090-458-5 (1-1642) x ADA53416 (1-3268)
QY 698 MetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyr 717
Db 6 ATGTTCTCATAAAGTAAATGGGGATCGGCTACCGCTGACATGTACATAGACAAATAT 65
QY 718 CysAlaThrGluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeu 737
Db 66 TGTGCCACAGAAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTA 125
QY 738 GlnGlnAsnAspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSer 757
Db 126 CAACAGAAATGACCAACAACCTTGTTGTATAGCTTGCTTTCAAGGACATGGACAAATTTTCA 185
QY 758 Gly-----LeuPheSerAlaLeuAspSerHis 766
Db 186 GGAATTGCTGTATAGACAAAGGATGTTATTGATGTTTCTGCTTACAGATCAT 245
QY 767 SerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeu 786
Db 246 TCAAAATTTGGGTGTCATTTCTTATGTTGTTCCATGACGACTTTGGAAGACGTTATTTTA 305
QY 787 LysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThrGlnGlnPro 806
Db 306 AAGCTAGAAAGTTGAAGCAGAGAAATTCACCAAGCAGATTATAGTGTATTACTCAGCAGCCA 365
QY 807 LeuGluGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeuLeuIleLeu 826
Db 366 CTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAACAGAGCTTACTTATTTT 425
QY 827 SerGluThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGlnMetTyrThr 846
Db 426 TCTGAAACCAAGGCTTCTCTAGTCAGCACCATGAGCCCTTTGGAACCAACAGATGTATACA 485
QY 847 IleAlaLysPheHisPheThrValGlnIlePheMetPheLeuValHisSerPhe 866
Db 486 ATAGCAAAAGTTTCATTTCTTTTACCTTGAAACCGTGAAGTAAATCAGTGAGATCAGTGTG 545
QY 867 LeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHisSerPhe 886
Db 546 CTTCCTGCTTTTAAATTTTTTTCACAGTTCAGATTTTTTATGTTTTTGGTTCTCATCTCTTT 605
QY 887 LysAsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLysProGlyAsp 906

Db 606 AAAAAATGCTGTGGTTCCCAATCAAAACTTGTTCAGACTTATATTTCTAAAAACCTGGAGAC 665
Qy 907 LysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAspIleSer 926
Db 666 AAACCCACATAAATACAAAACAAGTCTGCTTCTTCAAAATTCGTGACTCAGATATCAGT 725
Qy 927 AspLeuIleSerPhePheThrSerGlnAsnIleMetValThrMetIleAsnAspSerAsp 946
Db 726 GATCTTATTAGCTTTTTCACAGCCAGAACATAAATGGTGACGATGATTAATGACAGTGAC 785
Qy 947 TyrValSerValAlaProHisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyr 966
Db 786 TATGTATCCGTGGCTCCCCATAGTGGGCTTTAAATGTGATGCATTCAGAAAAGGACTAT 845
Qy 967 ValPheAlaAlaValPheAsnSerThrMetValTyrSerLeuProIleLeuValAsnIle 986
Db 846 GTTTTTCAGCTGTTTTCACACGACTATATGGTTTATCTTTACCTATATTAGTGAATATC 905
Qy 987 IleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThrIleGlnIleTrpSerThr 1006
Db 906 ATTAGTAACACTACTATCTTTTATCATTTAAATGTGACTGAAACCATCCAGATCTGGAGTACC 965
Qy 1007 ProPhePheGlnGluIleThrAspIleValPheLysIleGluLeuTyrPheGlnAlaAla 1026
Db 966 CCATTCTTTCAAGAAATTACTGATATAGTTTTTAAATTGAGCTGTATTTTCAAGCAGCT 1025
Qy 1027 LeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsnAlaGluAsn 1046
Db 1026 TTGCTTGGAAATCATTTGTTACTGCAATGCCACCTTACTTTGCCATGGAAAATGCAGAGAAT 1085
Qy 1047 HisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAlaTyrTrp 1066
Db 1086 CATAAGATCAAAGCTTATACTCAACTTAAACTTTTCAGGTCCTTTTGCCATCTGCATATTGG 1145
Qy 1067 IleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeuIleLeuMetLeuGly 1086
Db 1146 ATGGCAAGCTGTTGTTGATATCCCTTATTTTTTATCATCTTATTTTGATGCTAGGA 1205
Qy 1087 SerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPheLeuAlaValVal 1106
Db 1206 AGCTTACTGGCATTTTCATTATGGATATATATTTTATACTGTAAAGTTCCCTGTGGTT 1265
Qy 1107 PheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSerPheThr 1126
Db 1266 TTTTGCCTTATGGTTATGTTCCATCAGTTATCTGTTCACTTATATTTGCTTCTTTTCAAC 1325
Qy 1127 PheLysLysIleLeuAsnThrLysGluPheTrpSerPheIleTyrSerValAlaAlaLeu 1146
Db 1326 TTTAAGAAAAATTTAAATACCAAGAATTTTGGTCAITTTATCTATTCTGTGGCAGCGTTG 1385
Qy 1147 AlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyrThrIleAlaThrIleLeu 1166
Db 1386 GCTTGATGTCAATCACCTGAATAAATTTCTTTATGGGATACACAATTGCAACTATTCTT 1445
Qy 1167 HisTyrAlaPheCysIleIleIleProIleTyrProLeuLeuGlyCysLeuIleSerPhe 1186
Db 1446 CATATAGCTTTTGTATCATCATCTCCAATCTATCCACTCTAGGTTGCCTGATTTCTTTC 1505
Qy 1187 IleLysIleSerTrpLysAsnValArgLysAsnValAspThrTyrAsnProTrpAspArg 1206
Db 1506 ATAAAGATTCTCTGGAGAATGTACGAAAAAATGTGGACACCTATAATCCATGGATAGG 1565
Qy 1207 LeuSerValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGln 1226
Db 1566 CTTTTCAGTAGCTGTTATATCGCCCTCACCTGCAGTGTGTACTGTGGATTTTCCCTTTACA 1625
Qy 1227 TyrTyrGluLysLysTyrGlyArgSerIleArgLysAspPropPhePheArgAsnLeu 1246
Db 1626 TACTATGAGAAAAAATATGGAGGAGATCAATAAGAAAAGATCCCTTTTTCAGAAAACCTT 1685
Qy 1247 SerThrLysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspGlu 1266
Db 1686 TCAACGAGTCTAAAAAATAGGAAGCTTCCAGAACCCACACAATGAGGATGAAGATGAA 1745

Qy 1267 AspValLysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGlu 1286
Db 1746 GATGTCAAAGCTGAAAGACTTAAAGGTCAAAGAGCTGATGGTTGCCAGTGTGTGAGGAG 1805
Qy 1287 LysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeu 1306
Db 1806 AAACCATCCATTATGGTCAGCAATTTGCATAAAGATATATGATGACAAGAAAGATTCTT 1865
Qy 1307 LeuSerArgLysValLysValAlaThrLysTyrIleSerPheCysValLysLysGly 1326
Db 1866 CTTTCAAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTTCTGTGTGAAAAAAGGA 1925
Qy 1327 GluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeu 1346
Db 1926 GAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGCACAAATTATTATATATTCTG 1985
Qy 1347 ValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThr 1366
Db 1986 GTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTTAGGAGATTATTTCTTCAGAGACA 2045
Qy 1367 SerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrp 1386
Db 2046 AGTGAAGATGATGGTTCACTGAAGTGTATGGTTACTGTCTCCTCAGATAAACCCCTTTTGG 2105
Qy 1387 ProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAla 1406
Db 2106 CCAGATACTACATTGCAGGAACATTTTGAATTTTATGGAGCTGTCAAAGGAATGAGTGCA 2165
Qy 1407 SerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeu 1426
Db 2166 AGTGACATGAAAGAGTCAATAAGTCGAATAACACATGGACTTGATTTTAAAGAACATCTT 2225
Qy 1427 GlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSer 1446
Db 2226 CAGAAAGACTGTAAAGAAACTACTGTCAGGAATCAAACGAAAGTTGTGTTTGTCTCTAAGT 2285
Qy 1447 MetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLys 1466
Db 2286 ATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCTACAGGTATGGATCCCAAA 2345
Qy 1467 AlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAla 1486
Db 2346 GCCAAACAGACACATGTGGCGAGCAATTCGAACCTGCAATTTAAAAACAGAAAGCGGCTGT 2405
Qy 1487 IleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMet 1506
Db 2406 ATTCGACCACCTCATATATGAGGAGGAGCAGAGGCTGTCTGTGATCGAGTAGCTATCATG 2465
Qy 1507 ValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLys 1526
Db 2466 GTGCTGGCAGTTAAGATGTATCGAACAGTACACATCTAAAGAGTAGATTTCGAAAAA 2525
Qy 1527 GlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeu 1546
Db 2526 GGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAAACCTAGAGTAGACCGCCTT 2585
Qy 1547 GlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGlnSerPheSerSerIle 1566
Db 2586 CAAAGAGAAAATTCAGTATATTTTCCAAATGCAAGCCCGTCAGGAAAGTTTTTCTCTATT 2645
Qy 1567 LeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeu 1586
Db 2646 TTGGCTTATAAAATTCCTAAGGAAGATGTTTCACTCCCTTTCACAACTCTTTTAAAGCTG 2705
Qy 1587 GluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGlu 1606
Db 2706 GAAGAAAGCTAAACATGCTTTTGGCATTTGAAGATATAGCTTTTCTCAGGCAACATTGGAA 2765
Qy 1607 GlnValPheValGluLeuThrLysGluGlnGluGluAspAsnSerCysGlyThrLeu 1626
Db 2766 CAGGTTTTTGTAGAACTCACTAAAGAACCAAGAGGAGGAAGATAATAGTTGTGGAACTTTA 2825

QY 1627 AsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgValValPhe 1642
|||||
Db 2826 AACAGCACACTTTGGTGGGAACGACGACAAAGATAGAGTAGTATTT 2873

RESULT 10
ADC51606
ID ADC51606 standard; DNA; 2723 BP.
XX
AC ADC51606;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human macroprotein-94.64 coding sequence, SEQ ID 1.
XX
KW Human; macroprotein-94.64; dementia; arrhythmia; asthma; diabetes; gene;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 12..2486
FT /*tag= a
FT /product= "Human macroprotein-94.64"

XX CN1382726-A.
XX
XX 04-DEC-2002.
XX
XX 26-APR-2001; 2001CN-00112765.
XX
XX 26-APR-2001; 2001CN-00112765.
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
XX WPI; 2003-269487/27.
DR P-PSDB; ADC51607.
XX
XX New human macroprotein-94.64, encoding polynucleotide, antagonist and
PT recombinant production, useful for treating dementia, arrhythmia, asthma
PT and diabetes.
XX
XX Claim 6; SEQ ID NO 1; 35pp; Chinese.
XX
XX The present invention relates to human macroprotein-94.64 (ADC51607) and
CC its coding sequence (ADC51606). The protein is useful for treating
CC dementia, arrhythmia, asthma and diabetes.
XX
XX Sequence 2723 BP; 855 A; 460 C; 518 G; 890 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 2723
Score: 4282.00 Matches: 827
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.82% Indels: 0
DB: 9 Gaps: 0

US-10-090-458-5 (1-1642) x ADC51606 (1-2723)

QY 816 PheAspGluMetGluGlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSer 835
Db 3 TTTGATGAATGGAACAGAGCTTACTTATCTTTCTGAACCAAGGCTTCTCTAGTGAGC 62
QY 836 ThrMetSerLeuTrpLysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeu 855
Db 63 ACCATGAGCCTTTGGAAACAACAGAGTATACATAGCAAGTTTCATTTCCTTACCTTG 122
QY 856 LysArgGluSerLysSerValArgSerValLeuLeuLeuLeuIlePhePheThrVal 875
Db 123 AAACGTGAAGTAATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTT 182

QY 876 GlnIlePheMetPheLeuValHisHisSerPheLysAsnAlaValValProIleLysLeu 895
|||||
Db 183 CAGATTTTATGTTTTTGGTTTCATCACTCTTTTAAAAATGCTGGTCCCATCAAACTT 242
QY 896 ValProAspLeuTyrPheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeu 915
|||||
Db 243 GTTCCAGACTTATATTTTCTAAACCTGGAGACAAACACATAAATACAAACAAAGTCTG 302
QY 916 LeuLeuGlnAsnSerAlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGln 935
|||||
Db 303 CTTCTTCAAAAATCTGCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAAGCCAG 362
QY 936 AsnIleMetValThrMetIleAsnAspSerAspTyrValSerValAlaProHisSerAla 955
|||||
Db 363 AACATAATGGTGACGATGATTAATGACAGTGACTATGATCCGTGGCTCCCATAGTCCG 422
QY 956 AlaLeuAsnValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThr 975
|||||
Db 423 GCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTCAGCTGTTTTCAACAGTACT 482
QY 976 MetValTyrSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeu 995
|||||
Db 483 ATGGTTTATCTTTACCTATATAGTAGAATATCATTAAGTAAGTACTATCTTTATCATTTA 542
QY 996 AsnValThrGluThrIleGlnIleTrpSerThrProphePheGlnGluIleThrAspIle 1015
|||||
Db 543 AATGTGACTGAAACCATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTTACTGATATA 602
QY 1016 ValPheLysIleGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMet 1035
|||||
Db 603 GTTTTTAAAATTGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTACTGCAATG 662
QY 1036 ProProTyrPheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeu 1055
|||||
Db 663 CCACCTTACTTTGCCATGGAATGCAGAGAAATCATAAGATCAAAGCTTATACTCAACTT 722
QY 1056 LysLeuSerGlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIlePro 1075
|||||
Db 723 AAACCTTTCAGGTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTGATATCCCC 782
QY 1076 LeuPhePheIleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeu 1095
|||||
Db 783 TTATTTTATCATCTTATTTTGTGATGCTAGGAAGCTTACTGGCATTTCATTATGGAATTA 842
QY 1096 TyrPheTyrThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSer 1115
|||||
Db 843 TATTTTATACTGTAAAGTTCTTGTCTGCTGGTTTTTTTGCCTTATTTGTTATGTTCCATCA 902
QY 1116 ValIleLeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGlu 1135
|||||
Db 903 GTTATTTCTGTTCACTTATATTTGTTCTTTCACCTTTTAAAGAAAATTTTAAATACCAAGAA 962
QY 1136 PheTrpSerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThr 1155
|||||
Db 963 TTTTGGTCACTTATCTATTTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACT 1022
QY 1156 PhePheMetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIlePro 1175
|||||
Db 1023 TTCTTTATGGGATACACAAATTGCAACTATTCTTTCATTATGCTTTTGTATCATCAITCCA 1082
QY 1176 IleTyrProLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArg 1195
|||||
Db 1083 ATCTATCCACTTCTAGGTTGCTGATTTCTTTTCATAAAGATTTCTTGAAGAATGTACGA 1142
QY 1196 LysAsnValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyr 1215
|||||
Db 1143 AAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTTAC 1202
QY 1216 LeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArg 1235
|||||
Db 1203 CTGCAGTGTGTACTGTGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAGGCGAGA 1262
QY 1236 SerIleArgLysAspProphePheArgAsnLeuSerThrLysSerLysAsnArgLysLeu 1255

||||| 1263 TCAATAAGAAAAGATCCCTTTTTCAGAAACCTTTTCAACGAAGCTCTAAAAATAGGAAGCTT 1322
QY 1256 ProGluProProAspAsnGluAspGluAspGluAspValysAlaGluArgLeuLysVal 1275
Db 1323 CCAGAACCCACAGACAAATGAGGATGAAGATGAAGATGTCAAGCTGAAAGACTAAAGGTC 1382
QY 1276 LysGluLeuMetGlyCysGlnCysGluGluLysProSerIleMetValSerAsnLeu 1295
Db 1383 AAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTG 1442
QY 1296 HisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysValAla 1315
Db 1443 CATAAAGATATGATGACAAAGAAATTTCTTCTTCAAGAAAAGTAAAGAAAGTGGCA 1502
QY 1316 ThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsn 1335
Db 1503 ACTAAATACATCTCTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAAT 1562
QY 1336 GlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGly 1355
Db 1563 GGTGCTGGCAAAAGCACAAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGC 1622
QY 1356 GlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLysCys 1375
Db 1623 CAGGTATTTTAGGAGATTATTTCTTCAGAGACAAAGTGAAGATGATGATTCACCTGAAGTGT 1682
QY 1376 MetGlyTyrCysProGlnIleAsnProLeuTyrProAspThrThrLeuGlnGluHisPhe 1395
Db 1683 ATGGGTTACTGTCTCAGATAAACCCCTTGTGGCCAGATACATTGCAGGAACATTTT 1742
QY 1396 GluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerArg 1415
Db 1743 GAAATTTATGGAGCTGTCAAAGGAATGAGTGCAGTGCATGAAAGAAAGTCATAAGTCGA 1802
QY 1416 IleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAla 1435
Db 1803 ATAACACATGCACCTTGATTTAAAGAAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCA 1862
QY 1436 GlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeu 1455
Db 1863 GGAATCAAACGAAAGTGTGTTTTGCTCTAAGTATGTAGGGAATCCTCAGATTACTTTG 1922
QY 1456 LeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIle 1475
Db 1923 CTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATT 1982
QY 1476 ArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGlu 1495
Db 1983 CGAACTGCATTTAAAAACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGAGGAG 2042
QY 1496 AlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGly 1515
Db 2043 GCAGAGGCTGTCTGTGATCGAGTAGCTATCATGTGTCTGGGCAATTAAGATGTATCGGA 2102
QY 1516 ThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLysLys 1535
Db 2103 ACAGTACAACATCTAAAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAATTTGAAG 2162
QY 1536 AspTrpIleGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePhePro 1555
Db 2163 GACTGGATAGAAAACCTAGAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCA 2222
QY 1556 AsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAsp 1575
Db 2223 AATGCAAGCCGTCAGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGAT 2282
QY 1576 ValGlnSerLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPheAlaIle 1595
Db 2283 GTTCAGTCCCTTTCACAAATCTTTTTTAAGTGGAGAGCTAAACATGCTTTTGCCATT 2342
QY 1596 GluGluTyrSerPheSerGlnAlaThrLeuGlnValPheValGluLeuThrLysGlu 1615
|||||

Db 2343 GAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCACTAAAGAA 2402
QY 1616 GlnGluGluGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTyrTrpGluArgThr 1635
Db 2403 CAAGAGGAGGAAGATAATAGTTGTGAACTTTTAAACAGCACACTTTGGTGGGAACGAACA 2462
QY 1636 GlnGluAspArgValValPhe 1642
Db 2463 CAAGAAGATAGAGTAGTATTT 2483
RESULT 11
ADA20300
ID ADA20300 standard; cDNA; 5797 BP.
XX
AC ADA20300;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human ATP-binding cassette transporter A8 (ABCA8) cDNA sequence.
XX
KW Human; ATP-binding cassette transporter A8 protein; ABCA8 protein;
KW active transporter protein; ion transport; amino acid transport;
KW peptide transport; sugar transport; vitamin transport;
KW steroid hormone transport; antilipaeimic; ophthalmological;
KW neuroprotective; cardiant; gene therapy; hypercholesterolaemia;
KW drug resistance; retinal degeneration transport; neurological disease;
KW elevated cholesterol level; neurological disease;
KW retinal degeneration transport; drug resistance; heart disease;
KW chemotherapy; ss; gene; chromosome 17q24.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 139..5004
FT /*tag= a
FT /product= "Human ABCA8 protein"
FT 1927..2046
FT /*tag= b
FT /note= "This sequence of this region was newly identified
FT in the specification and specifically claimed in claim 9"
XX
PN WO2003064591-A2.
XX
PD 07-AUG-2003.
XX
PF 18-OCT-2002; 2002WO-US033496.
XX
PR 19-OCT-2001; 2001US-0351004P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (AVET) AVENTIS PHARMA.
XX
PI Dean MC, Schriml L, Allikmets RL, Deneffe MP, Rosier-Montus M;
PI Arnould-Reguigne I, Prades C;
XX
DR WPI; 2003-618356/58.
DR P-PSDB; ADA20301.
XX
PT New ATP-binding cassette transporter A8 (ABCA8) proteins and nucleic acid
PT molecules, useful for diagnosing or treating diseases associated with
PT altered expression of ABCA8, e.g. hypercholesterolemia or neurological
PT disease.
XX
PS Claim 9; Fig 4; 114pp; English.
XX
CC This invention relates to a novel substantially purified (functional)
CC human ATP-binding cassette transporter A8 (ABCA8) protein. The protein,
CC encoded by a gene located on chromosome 17q24, is an active transporter
CC protein associated with transport of various substrates, for example
CC ions, amino acids, peptides, sugars, vitamins or steroid hormones.
CC Compounds which modulate the activity of the protein of the invention may
CC have antilipaeimic, ophthalmological, neuroprotective or cardiant
CC activities. The DNA sequence which encodes the protein of the invention

may be useful for gene therapy. The ATP-binding cassette transporter A8 (ABCA8) proteins and nucleic acid molecules may be useful for diagnosing, prognosticating, ameliorating, preventing or treating diseases and conditions associated with altered expression of ABCA8, for example hypercholesterolaemia, drug resistance, retinal degeneration or neurological disease. Detecting a biological condition of a subject associated with an altered expression of an ABCA8 nucleic acid (for example elevated cholesterol levels, neurological disease, retinal degeneration, drug resistance or an increased susceptibility to heart disease) is useful for detecting a cell that is resistant to chemotherapy, for detecting a predisposition to elevated cholesterol or heart disease, or for pre-symptomatic screening of an individual for hypercholesterolaemia or defects in extra- or intracellular transport of ions, amino acids, peptides, sugars, vitamins or steroid hormones. The present sequence is that of the cDNA which encodes the human ATP-binding cassette transporter A8 (ABCA8) protein of the invention.

XX
SQ Sequence 5797 BP; 1692 A; 1135 C; 1241 G; 1729 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.51e-254	5797
Score:	3259.00	693
Percent Similarity:	61.96%	330
Best Local Similarity:	41.97%	544
Query Match:	38.68%	84
DB:	8	24
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-10-090-458-5 (1-1642) x ADA20300 (1-5797)

QY	6	ArgGluValGlyValT	ArgGlnThrArgThrLeuLeuLeuLysAsnTyrLeuIleLys	25
		:::::	:::::	
Db	148	AGAAAGATCAGTG	TGTCAACAACTGGGCCTTATTATGCAAGAACTTTCCTTAATAAAA	207
QY	26	CysArgThrLysLysSerSerValGlnGluIleLeuPheProLeuPhePheLeuPheTrp	45	
		:::::	:::::	
Db	208	TGGAGATCGAAAAGAGAGTCCCTTAATGGAATGGCTGAATTCATTGCTCCTACTACTTTGT	267	
QY	46	LeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluValProAsnIleGlu	65	
		:::::	:::::	
Db	268	TTGTATATATATCCTCATAGTCATCAAGTAAATGATTTTTCTTCACTGCTTACCATGGAC	327	
QY	66	LeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProValThr	85	
		:::::	:::::	
Db	328	CTGGGACGGGTAGATACATTTAATGAATCCAGATTTCTGTGTATACACACCTGTCAAC	387	
QY	86	AsnIleThrSerSerIleMetGlnLysValSerThrAsp	98	
		:::::	:::::	
Db	388	AACACGACCCAACAGATAATGAATAAAGTAGCCTCTACTCCCTTCTGGCAGGTAAAGAG	447	
QY	99	-----HisLeuProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeu	116	
		:::::	:::::	
Db	448	GTC TTGGGACTGCCAGATGAGGAAAGTATTAAAGAATTACA	489	
QY	117	ThrSerSerLeuSerLysProSerAsnPheValGlyValValPheLysAspSerMetSer	136	
		:::::	:::::	
Db	490	-----GCAAATTATCCTGAAGAAATAGTAGAGTCACTTTACTAATATACTACTCA	540	
QY	137	TyrGluLeuArgPhe--PheProAspMetIleProValSerSerIleTyrMetAspSer	155	
		:::::	:::::	
Db	541	TATCATTTGAAGTTCTTGCTAGGACATGGAATGCCAGCAAGAGGAGCACACAGGACCAT	600	
QY	156	ArgAlaGlyCysSerLysSer-----CysGluAlaAlaGlnTyrTrpSer	170	
		:::::	:::::	
Db	601	ACAGCTCATTTGTTATGAACACAATGAAGATGTTTACTGTGGAAGTTTCAGTATTTTGGGAG	660	
QY	171	SerGlyPheThrValLeuGlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsn	190	
		:::::	:::::	
Db	661	GAAGGTTTGTGGCTCTTCAAGTGCCATTAAATGCTGCTATTATAGAAATCACAAACAAAT	720	
QY	191	ValSerLeuTrpLysGluLeuGluSerThrLysAlaValIleMet-----	205	
		:::::	:::::	
Db	721	CAC TCA GTG ATG GAG GAG CTG ATG TC AGT TACT GG AAAAAA AT GA AG ATGC ATTC CTT C	780	

QY 1295 LeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysVal 1314
DB 3991 CTACCAAGGAGTATGCAGGAGAGAGAAAGGCTGTTTCCAGAGGAAGATAAGATA 4050
QY 1315 AlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuGlyPro 1334
DB 4051 GCCACGAGAAATGCTCTCTCTGTTGTTAGAAAGGTAAGTTTATAGGATATAGGACAC 4110
QY 1335 AsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSer 1354
DB 4111 AATGGAGCTGGTAAAGACATCCATTAAAGGTGATACTGGAGACACAAACCAACTGCT 4170
QY 1355 GlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLys 1374
DB 4171 GGACAAAGTCTACTG-----AAAGGAGCGGTGGAGGGGATGCCCTGGAG 4215
QY 1375 CysMetGlyTyrCysProGlnIleAsnProLeuTyrProAspThrThrLeuGlnGluHis 1394
DB 4216 TTCTGGGGTACTGCCCTCAGGAGAACGCGCTGTGGCCCAACCTGACAGTGAGGCAGCAC 4275
QY 1395 PheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSer 1414
DB 4276 CTGGAGGTGTACGCCCGCTGTAAGGGCTGAGGAAGGGGATGCTGAGGTGCCATCACA 4335
QY 1415 ArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPro 1434
DB 4336 CGGTTAGTGGATCGCTCAAGCTGCAGGACCAGCTGAAGTCTCCGGTGAAGACCTTGTC 4395
QY 1435 AlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThr 1454
DB 4396 GAGGGAATAAAGAGAAAGCTGTGCTTGTCTGAGCATACTGGGGAACCCGCTCAGTGGTG 4455
QY 1455 LeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAla 1474
DB 4456 CTTCTGGATGAGCGCTCGACCGGATGGACCCCGAGGGGAGCAGCAAAATGTGGCAGGCC 4515
QY 1475 IleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGlu 1494
DB 4516 ATCCGGGGCCACCTTTAGAAACACCGAAAGGGGTGCCCTCTCTAACCACCCACTACATGGCA 4575
QY 1495 GluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIle 1514
DB 4576 GAGGCTGAGCGCGTGTGACCGAGTGGCCATCATGCTATCTGGAGGTTGAGATGTATC 4635
QY 1515 GlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeu 1534
DB 4636 GGTTCATCCACACCTGAAAGCAATTTGGCAAGATTACCTGCTGGAGATGAAGGTG 4695
QY 1535 LysAspTrpIleGluAsnLeu---GluValAspArgLeuGlnArgGluIleGlnTyrIle 1553
DB 4696 AAG-----AACCTGGCACAAGTGGAGCCCTCCATGCAGAGATCCTGAGGCTT 4743
QY 1554 PheProAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLys 1573
DB 4744 TTCCCCCAGGCTGCTCGGCAGGAAGGTACTCTCTCTGTGTTTATAAGTTGCCAGTG 4803
QY 1574 GluAspValGlnSerLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPhe 1593
DB 4804 GAAGATGTGCAACCTTTAGCCCAAGCTTCTTCAAAATTAGAGAAGGTTAAACAGAGCTTT 4863
QY 1594 AlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThr 1613
DB 4864 GACCTAGAGGAGTACAGCCTCTCACAGTCTACCCCTGGAGGAGGTTTCTCTGGAGCTCTCC 4923
QY 1614 LysGluGlnGlu-----GluGluAsp 1620
DB 4924 AAGGAGCAGGAGCTGGGTGATTTTTCAGGAGGAT 4956

RESULT 12

ABN89597

ID ABN89597 standard; cDNA; 6181 BP.

XX

AC ABN89597;
XX 18-SEP-2002 (first entry)
DT
XX Human ATP-binding cassette transporter ABCA10 cDNA SEQ ID NO:4.
DE
XX Human; ABCA5; ABCA6; ABCA9; ABCA10; ATP-binding cassette transporter;
KW chromosome 17; chromosome 17q; chromosome 17q24; antiarteriosclerotic;
KW gene therapy; cholesterol; lipophilic molecule; inflammation;
KW prostaglandin; prostacyclin; arteriosclerosis; transport; gene; ss.
XX
OS Homo sapiens.
XX WO200246458-A2.
PN 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-EP015401.
PF
XX 07-DEC-2000; 2000EP-00403440.
PR
PR 23-JAN-2001; 2001US-0263231P.
XX
PA (AVET) AVENTIS PHARMA SA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Deneffe P, Rosier-Montus M, Prades C, Arnould-Reguigne I;
PI Duverger N, Allikmets R, Dean M;
XX
XX WPI; 2002-557584/59.
DR P-PSDB; AB881577.
DR
XX
PT A novel nucleic acid corresponding to ATP-binding cassette transporter
PT genes and the encoded polypeptide, useful for preventing or treating a
PT dysfunction in reverse transport of cholesterol.
XX
PS Claim 1; Page 156-158; 216pp; English.
XX
CC The present invention describes human ATP-binding cassette transporters
CC (ABC). Specifically described are the human ABCA5, ABCA6, ABCA9 and
CC ABCA10 genes (see ABN89594 to ABN89597) which encode the proteins given
CC in AB881574 to AB881577). ABN89598 to ABN89715 represent ABCA5, ABCA6,
CC ABCA9 and ABCA10 nucleotide fragments; and ABN89716 to ABN89806 represent
CC primers for ABCA5, ABCA6, ABCA9 and ABCA10 genes which are used in the
CC exemplification of the present invention. The ABC sequences have
CC antiarteriosclerotic activities and can be used in gene therapy. ABC
CC sequences can be used in the manufacture of a medicament intended for the
CC prevention and/or treatment of a subject affected by a dysfunction in the
CC reverse transport of cholesterol. The ABC proteins are involved in the
CC reverse transport of cholesterol, in membrane transport of lipophilic
CC molecules, in particular inflammation mediating substance such as
CC prostaglandins and prostacyclins, or in any pathology whose candidate
CC chromosomal region is situated on chromosome 17. They are also useful for
CC the manufacture of a medicament intended for prevention of
CC arteriosclerosis in various forms. The ABCA5, ABCA6, ABCA9 and ABCA10
CC genes are located to chromosome 17, more specifically to the 17q24 locus
XX
SQ Sequence 6181 BP; 1956 A; 1067 C; 1220 G; 1937 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.:	1.79e-252	Length:	6181
Score:	3234.00	Matches:	714
Percent Similarity:	61.39%	Conservative:	313
Best Local Similarity:	42.68%	Mismatches:	561
Query Match:	38.38%	Indels:	86
DB:	6	Gaps:	30

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QY 6 ArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLysAsnTyrLeuIleLys 25

DB 624 AAAGAGATAAGCGTGGTCAACAAATTCAGGCTCTTCTGTACAGAATTTCTTAAAAA 683

QY 26 CysArgThrLysLysSerSerValGlnGluLeuPheProLeuPheLeuPheTrp 45

Db 684 TGGAGAAATAAAAGAG--AGTTTATTGGAATGGACAATAACATTGTTTCTAGGGCTATAT 741
QY 46 LeuIleLeuIleSerMetHisProAsnLysLysTyrGluGluValProAsnIleGlu 65
Db 742 TTGTGCATCTTTTCGGAACACCTTCAGAGCTACCCGTTTTCCTGAACAACCTCCTAAAGTC 801
QY 66 LeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProValThr 85
Db 802 CTGGGAAGCGTGGATCAGTTTAAATGACTCTGGCCTGGTAGTGGCATATACACCAGTCAGT 861
QY 86 AsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu-----ProAsp 102
Db 862 AACATAACACAAAGGATAATGAATAAGATGGCCTTGGCTTCCCTTATGAAAGGAACA 921
QY 103 ValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLys 122
Db 922 GTCATTGGGACACCAGAT-----GAAGAGACCATGGATATAGAACTTCCAAAAAAA 972
QY 123 ProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArgPhe-- 141
Db 973 TACCATGAATGGTGGGAGTTATATTAGTGATACTTTCTCATATCGCCTGAAGTTTAAT 1032
QY 142 PheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCys----- 159
Db 1033 TGGGGATATAGAATCCAGTTATAAAGGAGCACTCTGAATACACAGAACACTGTTGGGCC 1092
QY 160 -----SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeu 176
Db 1093 ATGCATGGTGAATTTTGTACTTGGCAAAAGTACTGGCTAAAGGGTTTGTAGCTTTT 1152
QY 177 GlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGlu 196
Db 1153 CAAGCTGCAATTAATGCTGCAATTATAGAAGTCACAACAATCATTTCTGTAATGGAGAG 1212
QY 197 LeuGluSerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPhe 216
Db 1213 TTGACATCAGTTATTGGAATAAATATG-----AAGATACCACCTTTC 1254
QY 217 ---ProArgGlyValIleLeu-----IleTyrLeuValIleAlaPheSer 230
Db 1255 ATTTCTAAGGAGAAATTATGAATGAATGGTTTCATTTTACTTGTCTTAGTTCTTCTCT 1314
QY 231 ProPheGlyTyrPheLeuAlaIleHisIleValAlaGluLysGluLysLysIleLysGlu 250
Db 1315 TCTTTTATATACTTTGCATCATTTAAAT--GTTGCAAGGGAAGAGGAAATTTAAGAAA 1371
QY 251 PheLeuLysIleMetGlyLeuHisAspThrAlaPheTrpLeuSerTrpValLeuLeuTyr 270
Db 1372 CTGATGACAGTAATGGTCTCCGAGAGTCAGCATTCCTGGCTCTCCTGGNGATTGACATAC 1431
QY 271 ThrSerLeuIlePheLeuMetSerIleLeuMetAlaValIleAlaThrAlaSerLeuLeu 290
Db 1432 ATTTGCTTCATCTTCATTATGTCCATTTTATGGCTCTGGTCTATAACATCAATCTCAATT 1491
QY 291 PheProGlnSerSerSerIleValIlePheLeuLeuPhePheLeuTyrGlyLeuSerSer 310
Db 1492 GTATTTCACTGGCTTTCATGGTGATATTACACTCTATAGCTTATATGGCCTTTCTTTG 1551
QY 311 ValPhePheAlaLeuMetLeuThrProLeuPheLysLysSerLysHisValGlyIleVal 330
Db 1552 ATAGCAATTGGCTTTCCTCATGAGTGTTTTAATAAGGAAACCTATGCTCGCTGGTTGGCT 1611
QY 331 GluPhePheValThrValAlaPheGlyPheIleGlyLeuMetIleIleLeuIleGluSer 350
Db 1612 GGATTCTCTTCACTGTATTTTGGGGATGTCTGGGA---TTCACGTGTGTATACAGACAA 1668
QY 351 PheProLysSerLeuValTrp-----LeuPheSerPropheCysHisCysThrPhe 367
Db 1669 CTTCCCTTATCTTTGGGATGGGTATTAAAGTCTTCTTAGCCCTTT-----GCCTTC 1719
QY 368 ValIleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSerPheSer 387

Db 1720 ACTGCTGGAATGCCCCAGGTTACACACCTCGATAATTACTTAAGTGGTGTATTATTTTCCT 1779
QY 388 AsnLeuThrAlaGlyProTyrProLeuIleIleThrIleIleMetLeuThrLeuAsnSer 407
Db 1780 GATCCCTCTGGGATTTCATACAAAATGATAGCCACTTTTTCATTTTGGCATTTGATACT 1839
QY 408 IlePheTyrValLeuLeuAlaValTyrLeuAspGlnValIleProGlyGluPheGlyLeu 427
Db 1840 CTTTTCATTTTGATATTTCACATTATATTGAGCGAGTTTACCTGATAAAGATGGCCAT 1899
QY 428 ArgArgSerSerLeuTyrPheLeuLysProSerTyrTrpSerLysSerLysArgAsnTyr 447
Db 1900 GGGGATTCTCCATTATTTTCTTAAGTCCTCATTTTGGTCCAAACATCAAAATACTCAT 1959
QY 448 GluGluLeuSerGluGlyAsnValAsnGlyAsnIleSerPheSerGluIleIleGluPro 467
Db 1960 CATGAAATCTTTGAGAAATGAAATAAATCCTGAGCATTCCTCTGATGATCTTTTGAACCG 2019
QY 468 ValSerSerGluPheValGlyLysGluAlaIleArgIleSerGlyIleGlnLysThrTyr 487
Db 2020 GTGTCTCCAGAAATTCATGGAAAAGAACCCATAAGAATCAGAAATGTTATATAAAGAATAT 2079
QY 488 ArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAspIleTyrGluGly 507
Db 2080 AATGGAAGACTGGAAAAGTAGAAGCATTCGAAGGCATATATTTTTCATATATATGAAGGA 2139
QY 508 GlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLysSerThrLeuMetAsnIleLeu 527
Db 2140 CAGATCACTGCAATACTTGGGCATATATGGAGCTGGTAAATCAACACTGCTAAACATTTCTT 2199
QY 528 CysGlyLeuCysProProSerAspGlyPheAlaSerIleTyrGlyHisArgValSerGlu 547
Db 2200 AGTGGATTGTCTGTTTCTACAGAAGGATCAGCCACTATTTATAAATACTCAACTCTCTGAA 2259
QY 548 IleAspGluMetPheGluAlaArgLysMetIleGlyIleCysProGlnLeuAspIleHis 567
Db 2260 ATAACGTACATGGAAGAAATTAGAAAGAATATTGGATTGTCACACAGTTCAATTTTCAA 2319
QY 568 PheAspValLeuThrValGluGluAsnLeuSerIleLeuAlaSerIleLysGlyIlePro 587
Db 2320 TTTGACTTCTCTCACTGTGAGAGAAAACCTCAGGGTATTTGCTAAAAATAAAGGGATTTCAG 2379
QY 588 AlaAsnAsnIleIleGlnGluValGlnLysValLeuLeuAspLeuAspMetGlnThrIle 607
Db 2380 CCAAAGGAAGTGAACAAGAGGTAAAAAGAATTATAATGGAATTAGACATGCAAAAGCAT 2439
QY 608 LysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIle 627
Db 2440 CAAGACATTATTGCTAAAAAATTAAAGTGGTGGGCAGAGAGAAAACTAACACTAGGGATT 2499
QY 628 AlaValLeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAlaGlyMetAspPro 647
Db 2500 GCCATCTTAGGAGATCCTCAGGTTTGTCTGTAGATGAACCAACTGCTGGATTGGATCCC 2559
QY 648 CysSerArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsnArgValThrVal 667
Db 2560 TTTTCAAGACACCCGAGTGTGGAGCCTCCTGAAGGAGCATAAAGTAGACCGACTTATCCTC 2619
QY 668 PheSerThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSer 687
Db 2620 TTCAGTACCCAATTTCATGGATGAGGCTGACATCTTGGCTGATAGGAAAGTATTTCTGTCT 2679
QY 688 GlnGlyMetLeuLysCysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGly 707
Db 2680 AATGGGAAGTTGAAATGTGCGAGGATCATCTTTGTTTCTGGAAGCGAAAGTGGGTATTGGA 2739
QY 708 TyrArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeuSerSerLeuVal 727
Db 2740 TATCATTTAAGTTTACACAGGAATGAAATGTGTGACACAGAAAAAATCACATCCCTTATT 2799
QY 728 LysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSer 747
Db 2800 AAGCAGCACATTCCTGTATGCCCAAGTTAAACAACAGAAAGTGAAGAAAAAAGTTGTATATAGT 2859

QY 748 LeuProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeuAspSerHisSer 767
 Db 2860 TTGCCTTTGGAAAAAAGCAAAATTCAGATCTTTACAGTGACCTTGATAAGTGTCT 2919
 QY 768 AsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLys 787
 Db 2920 GACCAGGGCATAAGGAATATATGCTGTTTCAGTGACATCTCTGAATGAAGTATTTCTGAAC 2979
 QY 788 LeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThrGlnGlnProLeu 807
 Db 2980 CTAGAAGGAAAAATCAGCAATTGATGAACCCAGATTTTGACATTTGGGAAACAGAGAAAAATA 3039
 QY 808 GluGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeuLeuIleLeuSer 827
 Db 3040 CATGTGACAAAGAAATACTGGAGATGAGTCTGAAATGGAACAGGTTCTTTGTTCTCTCTCT 3099
 QY 828 GluThrLysAlaSerLeuValSerThrMetSerLeuTyrLysGlnGlnMetTyrThrIle 847
 Db 3100 GAAACAAGAAAGGCT--GTCAGTAGTCAGCTCTCTGGAGACGACAAATCTATGCAGTG 3156
 QY 848 AlaLysPheHisPheThrLeuLysArgGluSerLysSerValArgSerValLeuLeu 867
 Db 3157 GCAACACTTCGTTCTTAAAGTTAAGCGCTGAAAGGAGAGCTCTTTTGTGTTGTTACTA 3216
 QY 868 LeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHisHisSerPheLys 887
 Db 3217 GTACTTGGAAATGCTTTT--ATCCCCATCATCTAGAGAAGATAATGTATAAGTAAC 3273
 QY 888 AsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLysProGlyAspLys 907
 Db 3274 CGTGAAACTCAATGTTGGGAGTTTTCACCCAGTAGTATTTCTTCTCTGGAACAAATC 3333
 QY 908 ProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAspIleSerAsp 927
 Db 3334 CCGAAGACGCCTCTTACCAGCCTGTTAATCGTTAATAATACAGGATCAATATTTGAAGAC 3393
 QY 928 LeuIleSerPhePheThrSerGlnAsnIleMetValThrMet-----Ile 942
 Db 3394 CTCGTGCATTTCAGTGAAGTGTGAGGATATAGTTTGGAAATAGATGACTTTAGAAACAGAC 3453
 QY 943 AsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMetHisSer 962
 Db 3454 AATGGCTCAGATGATCCCTCC-----TACAATGGAGCCATCATAGTGTCTGGTGAC 3504
 QY 963 GluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeuProIle 982
 Db 3505 CAGAAGGATTACAGATTTCTGTTGCGTGTAAATCAACAAAGAAATTTGAATGTTTCTCTGTT 3564
 QY 983 LeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThrIleGln 1002
 Db 3565 CTTATGGGAATTTAGCAATGCCCTTATGGGAATTTTAACTTTCACGGAGCTTATTCAA 3624
 QY 1003 IleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLysIleGluLeuTyr 1022
 Db 3625 ACGGAGACACTTCATTTTCTCGTGAT-----GACATAGTGTGGATCTTGGTTTATA 3678
 QY 1023 PheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGlu 1042
 Db 3679 GATGGTCCATATTTTGTGTTGTATGCACAAACTGCGTTTCTCCTTTTATCGGCATGAGC 3738
 QY 1043 AsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuPro 1062
 Db 3739 AGCATCAGCGATTATAAAAAAATGTTCAATCCAGATTATGATTTCAGGCCTCTGGCCT 3798
 QY 1063 SerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeuIle 1082
 Db 3799 TCAGCATACTGGTGTGGACAGGCTCTGGTGGACATTCATTATCTCTTGATT----- 3852
 QY 1083 LeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPhe 1102
 Db 3853 -----CTCTTTCAATACATTTAATTACTACTCTCATATTTCTGGGATTC 3897

QY 1103 -----LeuAlaValValPheCysLeuIleGlyTyrValProSer 1115
 Db 3898 CAGCTTTCATGGGAACATCATGTTTGTGTTGGTGTGATAAATGTTGTGTCAGTTTCT 3957
 QY 1116 ValIleLeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGlu 1135
 Db 3958 CTTATATTCTCATATATGCTGTTTCTCATCTTTTCGCAAGTGGAGAAAAAATAATGGC 4017
 QY 1136 PheTrpSerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThr 1155
 Db 4018 TTTTGGTCTTTTGGCTTTTATT--ATCTTAATATGIGTATCCACAATTATGGTATCA 4074
 QY 1156 PhePheMetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIle--Ile 1174
 Db 4075 -----ACTCAATATGAAAAAACAACCTCAACTTAATTTTGTGCATGATTTTCATA 4119
 QY 1175 ProIleTyrProLeuLeuGlyCysLeuIleSerPheIleLysIleSerTyrLysAsnVal 1194
 Db 4120 CCTTCCCTTCACTTTGCTGGGTATGTCATGTTATTGATCCAGCTCGACTTT----- 4170
 QY 1195 ArgLysAsnValAspThrTyrAsnProTyrAspArgLeuSer----- 1208
 Db 4171 ATGAGAAACTTGGACAGCTCTGGAC-----AATAGAATAAATGAAGTCAATAAACCAATT 4224
 QY 1209 ---ValAlaValIleSerProTyrLeuGlnCysValLeuTyrPheLeuLeuGlnTyr 1227
 Db 4225 CTTTAAACAACCTTAATACCATACCTTCAGAGTGTATTATTTTCTCTTTTGTGCATAAGGTGT 4284
 QY 1228 TyrGluLysLysTyrGlyArgSerIleArgLysAspProPhePheArgAsnLeuSer 1247
 Db 4285 CTGGAATATGAAGTATGGAATGAATAATGAATAAAGACCCAGTTTTCAGA--ATCTCT 4341
 QY 1248 ThrLysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAsp 1267
 Db 4342 CCACGGAGTAGAGAAACTCAT---CCCAATCCGGAAGAGCCCCGAAGAAGAAGATGAAGAT 4398
 QY 1268 ValLysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLys 1287
 Db 4399 GTTCAAGCTGAAAGAGTCCAAAGCAGCAAAATGCACCTCACTGCTCCAAACTTGGAGGAGGAA 4458
 QY 1288 ProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeu 1307
 Db 4459 CCAGTCATAACTGCAAGCTGTTTACACAAGGAATATTATGAGACAAAGAAAGTTGCTTT 4518
 QY 1308 SerArgLysValLysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGlu 1327
 Db 4519 TCAACAAGAAAGAAATAAGCCATCAGAGTGTGTTTCTCTTTTGTGTTAAAAAGGTGAA 4578
 QY 1328 IleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuVal 1347
 Db 4579 GTTTTGGGATTACTAGACACAAATGGAGCTGGTAAAGTACTTCCATTAAATGATAACT 4638
 QY 1348 GlyAspIleGluProThrSerGlyGlnValPheLeu--GlyAspTyrSerSerGluThr 1366
 Db 4639 GGGTGCACAAAGCCCAACTGCAGGAGTGTGTTGTTTACAAGGCAGCAGCATCAGTAAGG 4698
 QY 1367 SerGluAspAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrp 1386
 Db 4699 CAACAGCATGACACAGCCCTCAAGTTCTTGGGTACTGCCCTCAGGAGAACTCACTGTGG 4758
 QY 1387 ProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAla 1406
 Db 4759 CCCAAGCTTACAATGAAGAGACACTTGGAGTGTATGTCAGCTGTGAAGAGACTGGGCAAA 4818
 QY 1407 SerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeu 1426
 Db 4819 GAAGATGCTGCTCTCAGTATTTCCAGATTGCTGGAAGCTCTTAAGCTCCAGGAACAACTT 4878
 QY 1427 GlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSer 1446
 Db 4879 AAGGCTCCTGTGAAAACTCTATCAGAGGGGAATAAAGAGAAAGCTGTGCTTTGTGCTGAGC 4938
 QY 1447 MetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLys 1466

Db 4939 ATCCTGGGAACCCATCAGTGGTCTTCTAGATGAGCCGTTCCACCGGATGACCCCGAG 4998
QY 1467 AlalysGlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAla 1486
Db 4999 GGGCAGAGCAAAATGTGGCAGATACTTCAGGCTACCGTTAAAAACAAGGAGAGGGCACC 5058
QY 1487 IleLeuThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMet 1506
Db 5059 CTCTTGACCAACCCATTACATGTCAGAGGCTGAGGCTGTGTGACCGTATGGCCATGATG 5118
QY 1507 ValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLys 1526
Db 5119 GTGTCAGGAACGCTAAGGTGTATGGTTCCATTCAACATCTGAAAAACAAGTTGGTAGA 5178
QY 1527 GlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeu 1546
Db 5179 GATTATTACTAGAAATAAAATGAAA-----GAACCTACCCAGGTGGAAGCTCTC 5229
QY 1547 GlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerIle 1566
Db 5230 CACACAGAGATTTTGAAGCTTTTCCACAGGCTGCTTGGCAGGAAAGATATTCTCTTTA 5289
QY 1567 LeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeu 1586
Db 5290 ATGGCGTATAAGTTACCTGTGGAGGATGTCCACCCTCTATCTCGGCCCTTTTCAAGTTA 5349
QY 1587 GluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGlu 1606
Db 5350 GAGCGCATGAAACAGACCTTCAACCTGGAGGAATACAGCCTCTCTCAGGCTACCTGGAG 5409
QY 1607 GlnValPheValGluLeuThrLysGluGlnGluGluAspAsnSerCysGlyThrLeu 1626
Db 5410 CAGGTATTCTTAGAACTCTGTAAAGAGCAG--GAGCTGGGAAATGTTGATGATAAAATT 5466
QY 1627 AsnSerThrLeuTrpTrpGlu---ArgThrGlnGluAsp 1638
Db 5467 GATACACAGTTGAATGGAACTTCTCCACAGGAAGAC 5505

RESULT 13

ABZ22923
ID ABZ22923 standard; cDNA; 5722 BP.

XX AC ABZ22923;

DT 08-APR-2003 (first entry)

DE Human ABCA10 transporter encoding cDNA SEQ ID NO:3.

KW Human; ATP binding cassette transporter family; ABCA10 transporter;
KW chromosome 17; chromosome 17q24; gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 254..4885

FT /*tag= a

FT /product= "ABCA10 transporter"

XX WO2002103015-A2.

XX 27-DEC-2002.

XX 13-JUN-2002; 2002WO-CA000873.

XX 14-JUN-2001; 2001US-0298604P.

XX (ACTI-) ACTIVE PASS PHARM INC.

XX Le Bihan S, Chen H, Kilinski L;

XX WPI; 2003-167521/16.

DR P-PSDB; ABP56906.

XX

PT New ABCA10 transporter nucleic acid molecules and polypeptides, useful in
PT screening assays or in predictive medicine, e.g. diagnostic assays,
PT prognostic assays, monitoring clinical trials or pharmacogenetics.

XX Claim 1; Page 106-113; 117pp; English.

XX The present sequence encodes a human ATP binding cassette (ABC)

CC transporter, designated ABCA10 transporter (I). (I) is located on human
CC chromosome 17, more specifically to locus 17q24. (I) can be used in gene
CC therapy. The ABCA10 transporter nucleic acid molecules, proteins and
CC antibodies can be used in screening assays or in predictive medicine,
CC e.g. diagnostic assays, prognostic assays, monitoring clinical trials or
CC pharmacogenetics. The ABCA10 transporter nucleic acid molecules and
CC polypeptides are useful as targets for developing modulating agents that
CC regulate cellular processes, particularly the transport of neurotoxic
CC molecules across cell membranes. The nucleic acid molecules and
CC polypeptides are useful in treating a subject having a disorder
CC associated with aberrant or unwanted ABCA10 transporter protein or
CC nucleic acid expression or activity

XX Sequence 5722 BP; 1806 A; 987 C; 1153 G; 1776 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.1e-252 Length: 5722
Score: 3229.00 Matches: 713
Percent Similarity: 61.36% Conservative: 313
Best Local Similarity: 42.64% Mismatches: 561
Query Match: 38.32% Indels: 86
DB: 7 Gaps: 30

US-10-090-458-5 (1-1642) x ABZ22923 (1-5722)

QY 7 GluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLysAsnTyrLeuIleLysCys 26

Db 1 GAGATAAGCGTGGTCAACAATTCAGGCTCTTCTGTACAAGAATTTCTTAAATAATGG 60

QY 27 ArgThrLysLysSerSerValGlnGluIleLeuPheProLeuPhePheLeuPheTrpLeu 46

Db 61 AGAATAAAAGAG--AGTTTATTGGAATGGACAATAACATGTTTCTAGGGCTATATTG 118

QY 47 IleLeuIleSerMetMetHisProAsnLysLysTyrGluValProAsnIleGluLeu 66

Db 119 TGCATCTTTTCGGAACACTTCAGAGCTACCCGTTTCTCTGAACAACCTCTCTAAAGTCTG 178

QY 67 AsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProValThrAsn 86

Db 179 GGAAGCGTGGATCAGTTTAACTACTCTGGCTGGTAGTGGCATATACACCAGTCAGTAAC 238

QY 87 IleThrSerSerIleMetGlnLysValSerThrAspHisLeu-----ProAspVal 103

Db 239 ATAACACAAAGGATATGAATAAGATGGCCTTGGCTTCTTTATGAAAGGAAGAACAGTC 298

QY 104 IleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLysPro 123

Db 299 ATTGGGACACCAGAT-----GAAGAGACCATGGATATAGAACTTCCAAAAAATAC 349

QY 124 SerAsnPheValGlyValPheLysAspSerMetSerTyrGluLeuArgPhe---Phe 142

Db 350 CATGAAATGGTGGAGTTATATTAGTGATACTTTTCTCATATCGCCTGAAGTTTAAATGG 409

QY 143 ProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCys----- 159

Db 410 GGATATAGAATCCAGTTTATAAGGAGCAGCTCTGAATACACAGAACACTGTTGGGCCATG 469

QY 160 -----SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGln 177

Db 470 CATGGTGAATTTTGTGTTACTTGGCAAAGTACTGGCTAAAAGGGTTTGTAGCTTTTCAA 529

QY 178 AlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeu 197

Db 530 GCTGCAATTAATGCTGCAATTATAGAAGTCACAACAATCATCTCTGTAATGGAGAGTGTG 589

QY 198 GluSerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPhe--- 216
Db 590 ACCTCAGTATTGGAATAAATATG-----AAGATACCCTTTTCATT 631
QY 217 ProArgGlyValIleLeu-----IleTyrLeuValIleAlaPheSerPro 231
Db 632 TCTAAGGAGAAATTATGAATGAATGGTTTCATTTTACTTGCTTAGTTTCTTCTCT 691
QY 232 PheGlyTyrPheLeuAlaIleHisIleValAlaGluLysGluLysIleIysGluPhe 251
Db 692 TTTATATACTTTGCATCATTAAT---GTTGCAAGGGAAGAGGAAATTTAAGAACTG 748
QY 252 LeuLysIleMetGlyLeuHisAspThrAlaPheTyrLeuSerTrpValLeuLeuTyrThr 271
Db 749 ATGACAGTAATGGGTCTCCGAGAGTCAGCATTTCTGGCTCTCCTGGGATTGACATACATT 808
QY 272 SerLeuIlePheLeuMetSerLeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPhe 291
Db 809 TGCTTCATCTTCATTATGTCCATTTTATGGCTCTGTGCATAAACATCAATCTCAATTGTA 868
QY 292 ProGlnSerSerIleValIlePheLeuLeuPhePheLeuTyrGlyLeuSerSerVal 311
Db 869 TTTCATACTGGCTTCATGGTGATATTCACACTCTATAGCTTATATGGCTTTCTTTTGATA 928
QY 312 PhePheAlaLeuMetLeuThrProLeuPheLysLysSerLysHisValGlyIleValGlu 331
Db 929 GCATTGGCTTTCCTCATGAGTGTTTAATAAGGAACCTATGCTCGTGGTTGGCTGGA 988
QY 332 PhePheValThrValAlaPheGlyPheIleGlyLeuMetIleIleLeuIleGluSerPhe 351
Db 989 TTTCTCTTCACTGTATTTTGGGGATGCTGGGA---TTCACTGTGTATATACAGACAACCTT 1045
QY 352 ProLysSerLeuValTrp-----LeuPheSerProPheCysHisCysThrPheVal 368
Db 1046 CCTTTATCTTTGGGATGGGTATTAAGTCTTCTTAGCCCTTTT-----GCCTTCACT 1096
QY 369 IleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSerPheSerAsn 388
Db 1097 GCTGGAATGGCCAGATTACACACCTGGATAATTACTTAAGTGGTGTATTATTTTCTCTGAT 1156
QY 389 LeuThrAlaGlyProTyrProLeuIleIleThrIleIleMetLeuThrLeuAsnSerIle 408
Db 1157 CCTCTGGGATTCATACAAAATGATAGCCACTTTTTTTCATTTTGGCATTTGATACTCTT 1216
QY 409 PheTyrValLeuLeuAlaValTyrLeuAspGlnValIleProGlyGluPheGlyLeuArg 428
Db 1217 TTCTATTGATATTCACATTATATTTTGAGCGAGTTTTTACTGTATAAAGATGGCCATGGG 1276
QY 429 ArgSerSerLeuTyrPheLeuLysProSerTyrTrpSerLysSerLysArgAsnTyrGlu 448
Db 1277 GATTCTCCATTATTTTCTTAAGTCCTCATTTTGGTCCAAACATCAAAATACTCATCAT 1336
QY 449 GluLeuSerGluGlyAsnValAsnGlyAsnIleSerPheSerGluIleIleGluProVal 468
Db 1337 GAAATCTTTGAGAAATGAAATAAATCCTGAGCATTTCTCTCTGATGATTCTTTTGAACCGTG 1396
QY 469 SerSerGluPheValGlyLysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArg 488
Db 1397 TCTCCAGAAATCCATGGAAAAGAGCCATAAGAAATCAGAAATGTTATAAAAGATATAAT 1456
QY 489 LysLysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGln 508
Db 1457 GGAAGAGACTGGAAAAGTAGAAGCAATTCAGAGGCATATTTTGTGACATATATGAAGGACAG 1516
QY 509 IleThrAlaLeuLeuGlyHisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCys 528
Db 1517 ATCACTGCAATACTTGGGCATAATGGAGCTGGTAAATCAACACTGCTAAACATTCTTAGT 1576
QY 529 GlyLeuCysProProSerAspGlyPheAlaSerIleTyrGlyHisArgValSerGluIle 548
Db 1577 GGATTGTCTGTTTCTACAGAAGGATCAGCCACTATTTTATAATACTCAACTCTCTGAATA 1636
QY 549 AspGluMetPheGluAlaArgLysMetIleGlyIleCysProGlnLeuAspIleHisPhe 568

Db 1637 ACTGACATGGAAGAAATTAGAAAGAAATATTGGATTTGTCCACAGTTCATTTTCAATTT 1696
QY 569 AspValLeuThrValGluGluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAla 588
Db 1697 GACTTCTCACTGTGAGAGAAACCTCAGGGTATTTCGTAAATAAAAGGGATTGAGCCA 1756
QY 589 AsnAsnIleIleGlnGluValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLys 608
Db 1757 AAGAAAGTGGAAACAAGAGGTAAAGAAATATATAATGGAATTAGACATGCAAGCATTCAA 1816
QY 609 AspAsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAla 628
Db 1817 GACATTATTGCTAAAAAATAAAGTGGTGGGCAGAGAGAAAACTAACACTAGGGATTGCC 1876
QY 629 ValLeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAlaGlyMetAspProCys 648
Db 1877 ATCTTAGGAGATCCTCAGGTTTGTGCTAGATGAACCAACTGCTGGATTGGATCCCTTT 1936
QY 649 SerArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsnArgValThrValPhe 668
Db 1937 TCAAGACACCGAGTGTGGAGCCTCCTGAAGGAGCATAAAGTAGACCGACTTATCCTCTTC 1996
QY 669 SerThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGln 688
Db 1997 AGTACCCAAATTCATGGATGAGCTGACATCTTGGCTGATAGGAAAAGTATTTCTGTCTAAT 2056
QY 689 GlyMetLeuLysCysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyr 708
Db 2057 GGGAAAGTTGAAATGTGCAGGATCATCTTTGTTCTGAAGCGGAAAAGTGGGTATTGGATAT 2116
QY 709 ArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeuSerSerLeuValLys 728
Db 2117 CATTTAAGTTTACACACAGGAATGAAATGTGTGACACAGAAAAAATCACATCCCTTATTAAG 2176
QY 729 GlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeu 748
Db 2177 CAGCACATTCCTGATGCCAAGTTAAACAACAGAAAGTGAAGAAAAAATTTGTATATAGTTG 2236
QY 749 ProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeuAspSerHisSerAsn 768
Db 2237 CCTTTGGAAAAACGACAAATTTCCAGATCTTTACAGTACCTTGATAAGTGTCTTGAC 2296
QY 769 LeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLysLeu 788
Db 2297 CAGGGCATAAGGAATTTATGCTGTTTCAGTGACATCTCTGAATGAAGTATTTCTTGAACTA 2356
QY 789 GluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThrGlnGlnProLeuGlu 808
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QY 809 GluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeuLeuIleLeuSerGlu 828
Db 2417 GTGACAGAATAACTGGAGATGAGTCTGAAATGGAACAGGTCTCTTTGTTCTCTTCCTGAA 2476
QY 829 ThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGlnMetTyrThrIleAla 848
Db 2477 ACAAGAAAGGCT---GTCAGTAGTGCAGCTCTCTGGAGACGACAAATCTATGCAGTGGCA 2533
QY 849 LysPheHisPhePheThrLeuLysArgGluSerLysSerValArgSerValLeuLeuLeu 868
Db 2534 ACACCTCGCTTCTTAAAGTTAAGCGCTGAAAGGAGAGCTCTTTTGTGTTTGTACTAGTA 2593
QY 869 LeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHisHisSerPheLysAsn 888
Db 2594 CTTGGAATTGCTTTT---ATCCCATCATCTCTAGAGAAAGATAATGTATAAAGTAACCTCGT 2650
QY 889 AlaValProIleLysLeuValProAspLeuTyrPheLeuLysProGlyAspLysPro 908
Db 2651 GAAACTCATTTGTTGGAGTTTTCACCAGTATGATTTTCTCTCTCTGGAACAAATCCCG 2710
QY 909 HisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAspIleSerAspLeu 928

Db 2711 AAGACGCCTCTTACCAGCCTGTTAAATCGTTAAATAATACAGGATCAAAATATTGAGACCTC 2770
QY 929 IleSerPheThrSerGlnAsnIleMetValThrMet-----IleAsn 943
Db 2771 GTGCATTCACTGAAGTGTACGATATAGTTTGGAAATAGATGACTTTAGAAACAGAAAT 2830
QY 944 AspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMetHisSerGlu 963
Db 2831 GGCTCAGATGATCCCTCC-----TACAATGGAGCCCATCATAGTGTCTGGTGACCAG 2881
QY 964 LysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeuProIleLeu 983
Db 2882 AAGGATTACAGATTTTCTGTTGCGTGTAAATACCAAGAAATTGAATTGTTTTCCTGTTCTT 2941
QY 984 ValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThrIleGlnIle 1003
Db 2942 ATGGGAATGTTAGCAATGCCCTTATGGGAATTTTAACTTCACGGAGCTTATTCAAACG 3001
QY 1004 TrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGluLeuTyrPhe 1023
Db 3002 GAGAGCATTCATTTTCTCGTGAT-----GACATAGTGTGGATCTTGGTTTATAGAT 3055
QY 1024 GlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsn 1043
Db 3056 GGGTCCATATTTTGTGTTGATCACAACCTGCGTTTCTCTTATCGGCATGAGCAGC 3115
QY 1044 AlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSer 1063
Db 3116 ATCAGCGATTATAAAAAAANGTTCAATCCAGTTATGGATTCAGGCCTCTGGCCTTCA 3175
QY 1064 AlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeuLeu 1083
Db 3176 GCATACTGGTGGACAGGCTCTGGTGGACATTCATATATACTTCTTGATT----- 3226
QY 1084 MetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPhe--- 1102
Db 3227 -----CTCTTTTCAATACATTTAATTTACTACTCTCATATTTCTGGGATTCAG 3274
QY 1103 -----LeuAlaValValPheCysLeuIleGlyTyrValProSerVal 1116
Db 3275 CTTTTCATGGGAACCTCATGTTTGTGGTGTATGCATAAATGGTGTGTCAGTTTCTCTT 3334
QY 1117 IleLeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPhe 1136
Db 3335 ATATTCTCTCATATGTCCTTTCATTCATCTTTCGCAAGTGGAGAAAAATAATGSGCTTT 3394
QY 1137 TrpSerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhe 1156
Db 3395 TGGTCTTTTGGCTTTTATT--ATCTTAATATGTGTATCCACAATATATGGTATCA--- 3448
QY 1157 PheMetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIle---IlePro 1175
Db 3449 -----ACTCAATATGAARAACTCACTTAATTTTGTGCATGATTTTTCATACCT 3496
QY 1176 IleTyrProLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArg 1195
Db 3497 TCCTTCACITTCGCTGGGTATGTCATGTTATGATCCAGCTCGACTTT-----ATG 3547
QY 1196 LysAsnValAspThrTyrAsnProTrpAspArgLeuSer----- 1208
Db 3548 AGAAACTTGGACAGCTCTGGAC-----AATAGAATAAATGAAGTCAATAAAACCATTCCT 3601
QY 1209 ValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyr 1228
Db 3602 TTAACAACCTTAATACCATACCTTCAGAGTGTATTATTTCTCTTTTGTTCATAAGGTCTG 3661
QY 1229 GluLysLysTyrGlyArgSerIleArgLysAspProPhePheArgAsnLeuSerThr 1248
Db 3662 GAAATGAAGTATGGAAATGAATAATGAATAAAGACCCAGTTTTCAGA---ATCTCTCCA 3718
QY 1249 LysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspVal 1268
Db 3719 CGGAGTAGAGAAACTCAT---CCCAATCCGGAAGAGCCCGGAAGAAGATGAAGATGTT 3775

QY 1269 LysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysPro 1288
Db 3776 CAAGCTGAAGAGTCCAAGCAGCAAAATGCACCTACTGCTCCAAAATTTGGAGGAGGAACCA 3835
QY 1289 SerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSer 1308
Db 3836 GTCATACTGCAAGCTGTTTACACAAGGAATATTATGAGACAAAGAAAAGTTGCTTTTCA 3895
QY 1309 ArgLysValLysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluIle 1328
Db 3896 ACAAGAAAAGAAAATAGCCCATCAGAAAATGTTTCTCTTTGTGTAAAAAAGGTGAAGTT 3955
QY 1329 LeuGlyLeuLeuGlyProAsnGlyValAlaGlyLysSerThrIleIleAsnIleLeuValGly 1348
Db 3956 TTGGGATTACTAGGACACAATGGAGCTGGTAAAGTACTTCCATTAAAAATGATAACTGGG 4015
QY 1349 AspIleGluProThrSerGlyGlnValPheLeu---GlyAspTyrSerSerGluThrSer 1367
Db 4016 TGCACAAAGCCAACTGCAGGAGTGGTGGTGTATACAAGGCAGCAGAGCATCAGTAAGGCAA 4075
QY 1368 GluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrpPro 1387
Db 4076 CAGCATGACAACAGCCTCAAGTTCTTGGGGTACTGCCCTCAGGAGAACTCACTGTGGCCC 4135
QY 1388 AspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAlaSer 1407
Db 4136 AAGCTTACAATGAAGAGCACCTTGAGTGTATGCAGCTGTGAAAGGACTGGGCAAGAA 4195
QY 1408 AspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeuGln 1427
Db 4196 GATGCTGCTCTCAGTATTTCCAGATTGGTGAAGCTCTTAAGCTCCAGGAACAACCTTAAG 4255
QY 1428 LysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMet 1447
Db 4256 GCTCCTGTGAAAACTCTATCAGAGGGAATAAAGAGAAAGCTGTGCTTGTGTGAGCATC 4315
QY 1448 LeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLysAla 1467
Db 4316 CTGGGGAACCCATCAGTGGTGGCTCTAGATGAGCCGTTTCACCGGGATGGACCCCGAGGGG 4375
QY 1468 LysGlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaIle 1487
Db 4376 CAGCAGCAAAATGTGGCAGATACCTTCAGGCTACCGTTAAAAACAAGAGAGGGGCCCTC 4435
QY 1488 LeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMetVal 1507
Db 4436 TTGACCAACCCATTACATGTCAAGAGCTGAGGCTGTGTGTGACCGTATGGCCATGATGGTG 4495
QY 1508 SerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLysGly 1527
Db 4496 TCAGGAACGCTAAGGTGTATTGGTTCCATTCAACATCTGAAAAACAAGTTTGGTAGAGAT 4555
QY 1528 TyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeuGln 1547
Db 4556 TATTTACTAGAAAATAAAAAATGAAA-----GAACCTACCCAGGTGGAAAGCTCTCCAC 4606
QY 1548 ArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGlnSerPheSerSerIleLeu 1567
Db 4607 ACAGAGATTTTGAAGCTTTTCCACAGGCTGCTTGGCAGGAAAGATATTCTCTTTAATG 4666
QY 1568 AlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeuGlu 1587
Db 4667 GCGTATAAGTTACCTGTGGAGGATGTCCACCCCTCTATCTCGGGCTTTTCAAGTTAGAG 4726
QY 1588 GluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGln 1607
Db 4727 GCGATGAACAGACCTTCAACCTGGAGGAATACAGCCCTCTCTCAGGCTACCTTGGAGCAG 4786
QY 1608 ValPheValIleLeuThrLysGluGlnGluGluAspAsnSerCysGlyThrLeuAsn 1627
Db 4787 GTATTCTTAGAACTCTGTAAAGAGCAG--GAGCTGGGAAATGTTGATGATAAAATTTGAT 4843

847	DB	ACTTTAATGGCTCTTATTGTAAATACTGCACAAATTGTCGTCCTGACTGGTTTTTGTGATG	906
299	QY	IlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThr	318
907	DB	GTCTTCACCCCTCTTTCTCTCTATGGCCTGTCTTTGATAAACTTTAGCTTTCTCTGATGAGT	966
319	QY	ProLeuPheLysSerLysHisValGlyIleValGluPhePheValThrValAlaPhe	338
967	DB	GTGTTGATAAAGAAACCTTTCTCTTACGGGCTTGGTTGTGTTCTCTCTATTGTCTTTTGG	1026
339	QY	GlyPheIleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTyr--	357
1027	DB	GGGATCCTGGGATTCCCA--GCATTGTATACACGCTCTCTCTGTCATTTTGGAAATGGACT	1083
358	QY	-----LeuPheSerProPheCysHisCysThrPheValIleGlyIleAlaGlnValMet	375
1084	DB	TTGTGCTCTTTAGCCCTTT-----GCCCTTCACTGTTGGGATGGCCCGCAGCTTATA	1134
376	QY	HisLeuGlu--AspPheAsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyr	394
1135	DB	CATTTGGACTATGATGGAATCTAATGCCCACTTGGATTCT--TCACAAATCCATAC	1191
395	QY	ProLeuIleIleThrIleIleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAla	414
1192	DB	CTCATAAATAGCTACTCTTTTCATGTTGGTTTTTTGACACCCCTTCTGTATTGGTATTGACA	1251
415	QY	ValTyrLeuAspGlnValIleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPhe	434
1252	DB	TTATATTTGACAAAATTTTGCCCGCTGAATATGGACATCGATGTTCTCCCTTGTTTTC	1311
435	QY	LeuLysProSerTyrTrpSerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsn	454
1312	DB	CTGAAATCCTGTTTTTGGTTTCAACACGGAAGGGCTAATCATGTGTCCTTGAGAATGAA	1371
455	QY	ValAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPheValGly	474
1372	DB	ACAGATTCTGATCCTACCTTAATGACTGTTTTGAACCAAGTGTCTCCAGAAATCTGTGGG	1431
475	QY	LysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnVal	494
1432	DB	AAAGAAGCCATCAGAATCAAAAATCTTAAAAAGAAATATGCAGGGAAGTGTGAGAGATA	1491
495	QY	GluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGly	514
1492	DB	GAAGCTTTGAAAGGTGTGGTGTGTGACATATATGAAGGCCAGATCACTGCCCTCCTTGGT	1551
515	QY	HisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSer	534
1552	DB	CACAGTGGAGCTGAAAAAATCCCTGTGTTAAACATCTTAGTGGTGTGTCAAGTCCAAACA	1611
535	QY	AspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAla	554
1612	DB	TCAGGTTTCAGTCACTGTCTATAATCACACACTTTCAAGAATGGCTGATATAGAAAAATC	1671
555	QY	ArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGlu	574
1672	DB	AGCAAGTTCACCTGATTTTGTCCACAATCCCAATGTCGAATTTGGATTCTCTCACTGTGAAA	1731
575	QY	GluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGlu	594
1732	DB	GAAAACTCAGGCTGTTTGCTAAAATAAAGGGAATTTTGCCACATGAAGTGGAGAAAGAG	1791
595	QY	ValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLys	614
1792	DB	GTACAACGAGTTGTACAGGAATTAGAAATGGAAAATATTCAAGACATCCCTTGTCTCAAAAC	1851
615	QY	LeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLys	634
1852	DB	TTAAGTGGTGGACAAAATAGGAACTAACTTTTGGGATTGCCATTTTAGGAGATCCTCAA	1911
635	QY	IleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleValTyr	654
1912	DB	GTTTTTGCTATTGGATGAACCGACTGCTGGATTGGATCCTCTTTCAAGGCACCGAATATGG	1971

QY	655	AsnLeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPheMetAsp	674
DB	1972	AATCTCTGAAAGAGGGGAAATCAGACAGAGTAATCTCTTCAGCACCCAGTTTATAGAT	2031
QY	675	GluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLysCysVal	694
DB	2032	GAGGCTGACATCTGGCGGACAGGAAGGTGTTTCATATCCAATGGGAAGTGGAAGTGTGCA	2091
QY	695	GlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIle	714
DB	2092	GGCTCTCTCTGTTCTTAAGAAGAAATGGGCGCATAGGCTACCATTTAAAGTTTGCATCTG	2151
QY	715	AspLysTyrCysAlaThrGluSerLeuSerSerLeuValLysGlnHisIleProGlyAla	734
DB	2152	AATGAAAGGTGTGATCCAGAGAGTATAAACATCACTGGTTAAGCAGCACATCTCTGATGCC	2211
QY	735	ThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeuProPheLysAspMetAsp	754
DB	2212	AAATTGACAGCACAAAGTGAAGAAAACCTGTATATATTTTGCCTTTGGAAAGGACAAAC	2271
QY	755	LysPheSerGlyLeuPheSerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyr	774
DB	2272	AAATTCCAGAACTTTACAGGGATCTTGATAGATGTTCTTAACCAAGCATTGAGGATTAT	2331
QY	775	GlyValSerMetThrThrLeuGluAspValPheLeuLysLeuGluValGluAlaGluIle	794
DB	2332	GGTGTTCCTCATAACAACCTTTGAATGAGGTGTTTCTGAAATTAGAGGAAATCAACTATT	2391
QY	795	AspGlnAlaAspTyrSerValPheThrGlnGlnProLeuGluGluMetAspSerLys	814
DB	2392	GATGAATCAGATATTGGAATTTGGGACAAATTACAACTGATGGGCAAAAGATATAGGA	2451
QY	815	SerPheAspGluMetGluGlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuVal	834
DB	2452	AGCCTTGTTGAGCTGGAAACAAGTTTTGTCTCTCCACGAACAAGGAAACA--ATC	2508
QY	835	SerThrMetSerLeuTrpLysGlnGlnMetTyrThrIleAlaLysPheHisPheThr	854
DB	2509	AGTGGCGTGGCGCTCTGGAGCGCAGAGGTCTGTGCAATAGCAAAAGTTTCGCTTCTTAAAG	2568
QY	855	LeuLysArgGluSerLysSerValArgSerValLeuLeuLeuLeuIlePhePheThr	874
DB	2569	TTAAAGAAAGAAAGAAAGCCTGTGGACTATATTATTTGCTTTTGGTATTAGCTTTATC	2628
QY	875	ValGlnIlePheMetPheLeuValHisHisSerPheLysAsnAlaValProIleLys	894
DB	2629	CCTCAACTTTTGGAAACATCTATTCTACGAGTCATATCAGAAAAGT---TACCCGTTGGGAA	2685
QY	895	LeuValProAspLeuTyrPheLeuLysProGlyAspLysProHisLysTyrLysThrSer	914
DB	2686	CTGTCTCAAAATACATACTTCTCTCACCAGGACAAACCAACCAAGGATCCTCTGACCCAT	2745
QY	915	LeuLeuLeuGlnAsnSerAlaAspSerAspIleSerAspLeuIleSerPheThrSer	934
DB	2746	TTACTGTGCATCAATAAGACAGGGTCAACCATTTGATAACTTTTACATTCACTGAGGCGA	2805
QY	935	GlnAsnIleMetValThrMet-----IleAsnAspSerAspTyrValSer	949
DB	2806	CAGAACATAGCTATAGAAAGTGGATGCCTTTGGAACTAGAAATGGCACAGATGACCCATCT	2865
QY	950	ValAlaProHisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyrValPheAla	969
DB	2866	-----TACAAATGGTGTCTATCATTTGTGTTCAGGTGATGAAAAGGATCACAGATTTTCA	2916
QY	970	AlaValPheAsnSerThrMetValTyrSerLeuProIleLeuValAsnIleIleSerAsn	989
DB	2917	ATAGCATGTAATACAAAACGGCTGAATTGCTTTTCTGTCTCTCTGGATGTTCATTAGCAAT	2976
QY	990	TyrTyrLeuTyrHisLeuAsnValThrGluThrIleGlnIleTrpSerThrProphePhe	1009
DB	2977	GGACTACTTGGAAATTTTAAATTCGTGAGAACACATTCAGACTGACAGAAGCACATTTTTT	3036

QY 1010 GlnGluIleThrAspIleVal-----PheLysIleGluLeuTyrPheGlnAlaAlaLeu 1027
Db 3037 GAAGAGCATATGGATTATAGATATGGGTACCGAAGTAACACCTTCTTCTGGATACCGATG 3096
QY 1028 LeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsnAlaGluAsnHis 1047
Db 3097 -----GCAGCCTCTTTCACTCCATACATTCGCAATGAGCAGCATTTGGTGACTAC 3144
QY 1048 LysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAlaTyrTrpIle 1067
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QY 1068 GlyGlnAlaValAlaAspIleProLeuPhePheIleIleLeuIleLeuMetLeuGlySer 1087
Db 3205 GGCCAAAGCACTGGTGGATGTTTCCCTGTACTTTTGTGCTCCTCTGCTAATG-----CAA 3258
QY 1088 LeuLeuAlaPheHisTyrGly-----LeuTyrPheTyrThrValLysPheLeuAla 1104
Db 3259 ATAATGGATTATATTTTAGCCAGAGGAGATTATATTATATAATTCAAAACCTGTTAATT 3318
QY 1105 ValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSer 1124
Db 3319 CAAATCCTGTGTAGTATTGGCTATGTCTCATCTCTTGTCTTGTGACATATGTGATTCA 3378
QY 1125 PheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIleTyrSerValAla 1144
Db 3379 TTCAATTTTCGCAATGGGAGAAAAAATAGTGGCATTGTGGTCATTTTCTTCTTAATTGTG 3438
QY 1145 AlaLeuAlaCysIleAlaIleThrGluIleThr-----PhePheMetGlyTyrThrIle 1162
Db 3439 GTCATCTTCTCGATAGTTGCTACTGATCTAAATGAATATAGGATTCTAGGGCTATTTT 3498
QY 1163 AlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeuGlyCys 1182
Db 3499 GGCACCATGTTA-----ATACCTCCTTCACATTGATTGGCTCT 3537
QY 1183 LeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThrTyrAsn 1202
Db 3538 CTATTCAATTTTCTGAGATT----- 3558
QY 1203 ProTrpAspArgLeuSer-----ValAlaVal 1211
Db 3559 CCTCCTGATTCATGGATTTCCTTAGGAGCTTCAGAACTCTGAAATGTATACCTGGCACTG 3618
QY 1212 IleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLys 1231
Db 3619 CTGATCCCTTACCTTCATTTTCTCATTTTCTTTTCTTTCATCTTCCGATGCCTAGAAATGAAC 3678
QY 1232 TyrGlyGlyArgSerIleArgLysAspPropPhePheArgAsnLeuSerThrLysSerLys 1251
Db 3679 TGCAGGAAGAAACTAATGAGAAAGGATCCTGTGTTTCAGA---ATTCTCCAAGAGC--- 3732
QY 1252 AsnArgLysLeuProGluProProAspAsnGluAspGluAspGluAspValLysAlaGlu 1271
Db 3733 AACGCTATTTTCCAAACCCAGAGAGCCTGAAGAGAGGAGGAAGATATCCAGATGGAA 3792
QY 1272 ArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysProSerIleMet 1291
Db 3793 AGAATGAGAAACAGTGAATGCTATGGCTGTGCGAGACTTTGTATGAGACACCCGTCATCAT 3852
QY 1292 ValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysVal 1311
Db 3853 GCCAGCTGTCTACGGAAGGAATATGCGGCAAAAGAAAAAATTCCTTTTCTAAAGGAAG 3912
QY 1312 LysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeu 1331
Db 3913 AAAAAAATTGCCACAAGAAATGTCTCTTTTGTGTTAAAAAAGGTGAAGTTATAGGACTG 3972
QY 1332 LeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGlu 1351
Db 3973 TTAGGACACAATGGGGCTGGTAAAGTAAAGTAACTATTAAAGATGAATAACTGGAGACACAAA 4032
QY 1352 ProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAsp 1371

Db 4033 CCAACTGCAGGACAGGTGATTTTG-----AAAGGGAGCGGTGGAGGGGAA 4077
QY 1372 SerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeu 1391
Db 4078 CCCCTGGGCTTCTCTGGGTACTGCCCTCAGGAGAATGGCTGTGGCCCAACCTGACAGTG 4137
QY 1392 GlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGlu 1411
Db 4138 AGGCAGCACCTGGAGGTGTACGCTGCCGTGAAAGGTCTCAGGAAAGGGACGCAATGATC 4197
QY 1412 ValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLys 1431
Db 4198 GCCATCACACGGTTAGTGGATGCGCTCAAGCTGCAGGACACAGCTGAAGGCTCCCGTGAAG 4257
QY 1432 LysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnPro 1451
Db 4258 ACCTTGTACAGAGGAATAAAGCGAAAGCTGTGCTTTGTGTGAGCATCCTGGGGAACCG 4317
QY 1452 GlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMet 1471
Db 4318 TCAGTGGTCTTCTGGATGAGCGCTCGACCGGATGGACCGGAGGCGCAGCAGCAAAATG 4377
QY 1472 TrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThrThrHis 1491
Db 4378 TGGCAGGTGATTCGGGCCACCTTTAGAAACACGGAGAGGGCGGCCCTCCTGACCAACCCAC 4437
QY 1492 TyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeu 1511
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QY 1512 ArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGlu 1531
Db 4498 AGATGTATTGTTCCATCCAAACACTGAAAAGCAAAATTTGGCAAAAGACTACCTGCTGGAG 4557
QY 1532 IleLysLeuLysAspTrpIleGluAsnLeu---GluValAspArgLeuGlnArgGluIle 1550
Db 4558 ATGAAGCTGAAG-----AACCTGGCACAATGGAGCCCTCCATGCAGAGATC 4605
QY 1551 GlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLys 1570
Db 4606 CTGAGGCTTTTCCCCCAGGCTGTCTCAGCAGGAAAGGTTCTCTCCTCGATGGTCTATAAG 4665
QY 1571 IleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeuGluAlaLys 1590
Db 4666 TTGCCTGTGAGGATGTGCGACCTTATCAGAGGCTTTCTCAAATTAGAGATAGTTAAA 4725
QY 1591 HisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheVal 1610
Db 4726 CAGAGTTTCGACCTGGAGGAGTACAGCTCTCACAGTCTACCTGGAGCAGGTTTTCCTG 4785
QY 1611 GluLeuThrLysGluGlnGlu-----GluGluAsp 1620
Db 4786 GAGCTCTCCAAGGAGCAGGAGCTGGGTGATCTTTGAAGAGGAC 4827
RESULT 15
ABS57518
ID ABS57518 standard; cDNA; 5018 BP.
XX
AC ABS57518;
XX 04-FEB-2003 (first entry)
XX Human ABCA9 transporter cDNA.
DE
XX Human; gene; ABCA9 transporter; ATP binding cassette A9 transporter;
KW neuroprotective; nootropic; antiparkinsonian; anticonvulsant; cancer;
KW gene therapy; modulator; amyloid beta-protein export; prion disease;
KW neurotoxic molecule transport; beta-amyloid peptide; Alzheimer's disease;
KW multi-drug resistance; Huntington's disease; Parkinson's disease; ALS;
KW amyotrophic lateral sclerosis; spinocerebellar ataxia; immunogen;
KW frontotemporal dementia; cholesterol mis-regulation disease;
KW inflammatory disease; mood disorder; panic disorder; ss.

QY 376 HisLeuGlu--AspPheAsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyr 394
Db 1278 CATTTGGACTATGATGTGAATCTTAATGCCACTTGGATTCT--TCACAAAATCCATAC 1334
QY 395 ProLeuIleIleThrIleIleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAla 414
Db 1335 CTCATAATAGCTACTCTTTTCATGTTGGTTTTTGGACACCCCTCTGTATTTGGTATTGACA 1394
QY 415 ValTyrLeuAspGlnValIleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPhe 434
Db 1395 TTATATTTGACAAAATTTTGGCCGCTGAATATGGACATCGATGTTCTCCCTTGTTTTTC 1454
QY 435 LeuLysProSerTyrTrpSerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsn 454
Db 1455 CTGAAATCCTGTTTTTGGTTTCAACACGGGAGGGCTTAATCATGTGGTCCCTTGAGAAATGAA 1514
QY 455 ValAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPheValGly 474
Db 1515 ACAGATTCTGATCCTACACCTAATGACTGTTTTTGAACCAAGTGTCTCCAGAAATCTGTGGG 1574
QY 475 LysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnVal 494
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Job time : 1315 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 12, 2004, 21:08:44 ; Search time 176 Seconds
(without alignments)
5177.440 Million cell updates/sec

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Perfect score: 8426
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Scoring table: BLOSUM62
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Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553.5	18.4	6525	3	US-08-762-500-74
2	1521.5	18.1	5894	3	US-08-665-259-24
3	1521.5	18.1	5894	3	US-08-762-500-24
4	1479	17.6	7860	4	US-09-526-193A-2
5	1248	14.8	974	4	US-09-833-381-1085
6	900.5	10.7	1350	4	US-09-833-381-1082
7	647	7.7	3609	4	US-09-833-381-958
8	515	6.1	485	4	US-09-621-976-409
9	467	5.5	2075	4	US-09-833-381-962
10	461	5.5	1770	4	US-09-328-352-3466
11	426	5.1	1767	4	US-09-489-039A-6408
12	421.5	5.0	1824	4	US-09-252-991A-1780

13	413.5	4.9	15567	4	US-09-627-376-3	Sequence 3, Appli
14	407.5	4.8	4233	3	US-09-120-513-1	Sequence 1, Appli
15	407.5	4.8	4233	3	US-09-450-105-1	Sequence 1, Appli
16	404.5	4.8	4186	4	US-09-672-810-1	Sequence 1, Appli
17	404	4.8	1785	4	US-09-543-681A-1356	Sequence 1356, Ap
18	402	4.8	4195	4	US-09-672-810-3	Sequence 3, Appli
19	400.5	4.8	4646	1	US-08-181-471-2	Sequence 2, Appli
20	400.5	4.8	4646	4	US-09-023-655-1167	Sequence 1167, Ap
21	400.5	4.8	4669	6	5206352-3	Patent No. 5206352
22	398.5	4.7	4264	2	US-08-784-649A-1	Sequence 1, Appli
23	398.5	4.7	4264	2	US-08-784-649A-5	Sequence 5, Appli
24	396.5	4.7	6505	2	US-08-793-610-5	Sequence 5, Appli
25	396.5	4.7	8630	4	US-09-306-417-1	Sequence 1, Appli
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27	396.5	4.7	9318	2	US-08-793-610-6	Sequence 6, Appli
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31	395	4.7	3988	4	US-09-762-195-1	Sequence 1, Appli
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39	365	4.3	4443	4	US-09-425-453A-3	Sequence 3, Appli
40	365	4.3	4443	4	US-09-425-453A-9	Sequence 9, Appli
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42	365	4.3	4560	3	US-09-256-703-1	Sequence 1, Appli
43	365	4.3	6129	1	US-07-637-621-1	Sequence 1, Appli
44	365	4.3	6129	2	US-08-951-912-1	Sequence 1, Appli
45	365	4.3	6129	3	US-08-681-838A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-762-500-74
; Sequence 74, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996

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RESULT 2
US-08-665-259-24
; Sequence 24, Application US/08665259
; Patent No. 6028173
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,259
; FILING DATE: 17-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

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Search completed: April 13, 2004, 02:03:54
Job time : 6005 secs

REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2844)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
FEATURES
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ORIGIN
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Score: 1382.00 Conservative: 142
Percent Similarity: 59.02% Mismatches: 251
Best Local Similarity: 40.19% Indels: 58
Query Match: 16.40% Gaps: 14
DB: 11
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QY 1380 ProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGly 1399
Db |||||
5794 CCTCAGTTGATGCCATCACAGAGCTGTTGACTGGGAGAGAACACGTCGTGAGTTCTTGCC 5853
QY 1400 AlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAla 1419
Db |||||
5854 CTTTTGAGAGGAGTCCCAGAGAAAGAGTTGGCAAGTTGGTGGTGGCGGATTCGGAAA 5913
QY 1420 LeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArg 1439
Db |||||
5914 CTGGGCCTCGTGAAGTATGGAGAAAAATATGCTGTTAACTATAGTGGAGGCAACAACGC 5973
QY 1440 LysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluPro 1459
Db |||||
5974 AAGCTCTCTACAGCCATGGCTTTGATCGCGGGCCTCCTGGTGTCTTCTGGATGAACCC 6033
QY 1460 SerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPhe 1479
Db |||||
6034 ACCACAGCATGGATCCCAAAGCCCGCGGTTCTTGTGGAAATGTGCCCTAAGTGTGTGTC 6093
QY 1480 LysAsnArgLysArgAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaVal 1499
Db |||||
6094 AAG---GAGGGGAGATCAGTAGTGCTTACATCTCATAGTATGGAAGAATGTGAAGCTCTT 6150
QY 1500 CysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHis 1519
Db |||||
6151 TGCAC TAGGATGGCAATCATGGTCAATGGAAGTTTCAGGTGCTTGGCAGTGTCACGAT 6210

QY 1520 LeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGlu 1539
Db |||||
6211 CTAATAAATAGGTTTGAGATGGTTATACAAATAGTTGTACGAATAGCAGG-----TCC 6264
QY 1540 AsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArg 1559
Db |||||
6265 AACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGACTTGCATTTCTCTGGAAGTGTCTA 6324
QY 1560 GlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeu 1579
Db |||||
6325 AAAGAGAAAACACCGGAACATGCTACAATACCAGTCCA---TCTTCATTATCTTCTCTG 6381
QY 1580 SerGlnSerPhePheLysLeuGluAlaLysHisAlaPheAlaIleGluGluTyrSer 1599
Db |||||
6382 GCCAGGATATTACGATCCTCTCCAGAGCAAAAAGCGACTCCACATAGAAAGTACTCT 6441
QY 1600 PheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGlu 1619
Db |||||
6442 GTTCTCTCAGACAACACTTGACCAAGTATTGTGAAGTTCGCAAGGACCAAGTGTGATGAT 6501
QY 1620 AspAsn-----SerCysGlyThrLeu 1626
Db |||||
6502 GACCACTTAAAGGACCTCTCATTTACACAAAAACCAGACAGTAGTGGACGTTGCAGTTCTC 6561
QY 1627 AsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
Db |||||
6562 ACATCTTTTCTACAGGATGAGAAAAGTGAAAGAAAGCTATGTA 6603
RESULT 15
AK031843 2844 bp mRNA linear HTC 18-SEP-2003
LOCUS Mus musculus adult male medulla oblongata cDNA, RIKEN full-length
DEFINITION enriched library, clone:6330417A11 product:ATP-BINDING CASSETTE
PROTEIN homolog [Mus musculus], full insert sequence.
ACCESSION AK031843 GI:26327664
VERSION AK031843.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE Carninci, P. and Hayashizaki, Y.
AUTHORS Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
2
REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
AUTHORS Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
3
REFERENCE Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
AUTHORS Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
4
REFERENCE The RIKEN Genome Exploration Research Group Phase II Team and the
AUTHORS FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)

VERSION AY405472.1 GI:39761446
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 6606)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 6606)
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
1..6606
/organism="Pan troglodytes"
/mol_type="genomic DNA"
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<1..>6606
/gene="ABCA1"
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ORIGIN
Alignment Scores:
Pred. No.: 2.65e-140 Length: 6606
Score: 1396.00 Matches: 440
Percent Similarity: 41.58% Conservative: 281
Best Local Similarity: 25.37% Mismatches: 549
Query Match: 16.57% Indels: 464
DB: 29 Gaps: 51
US-10-090-458-5 (1-1642) x AY405472 (1-6606)
QY 240 IleValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAsp 259
Db 1795 ATCGTGTATGAGAGGAGGACGGCTGAAAGAGACCATGCGGATCATGGGCGCTGGACAAC 1854
QY 260 ThrAlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMet----- 277
Db 1855 AGCATCCTCTGGTTTAGTGGTTTCATT-----AGTAGCCTCATTCCTCTTCTGTGAGC 1908
QY 278 ---SerLeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSer 296
Db 1909 GCTGGCCTGCTGGTGTCTATCCTCAAGTTAGGAAACCTGCTG---CCCTACAGTGATCCC 1965
QY 297 IleValIlePheLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMet 316
Db 1966 AGCGTGTGTGTCTTCTCTGTCGGTGTGTGTTGCTGTGGTGACAATCCTGCAGTGTCTCCTG 2025
QY 317 LeuThrProLeuPheLysLysSerLysHisVal-----GlyIleValGluPhe 332
Db 2026 ATTAGCACACTCTTCTCCAGAGCCAACTGGCAGCAGCCTGTGTGGGGGATCATCTACTTC 2085
QY 333 PheValThrValAlaPhe-----GlyPheIleGlyLeuMetIle 345
Db 2086 ACGCTGTACTACCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTC 2145
QY 346 IleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSerProPheCysHisCys 365
Db 2146 AAGATCTTCGTAGC-----CTGCTGTCTCTCT-----GTG 2175

QY 366 ThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSer 385
Db 2176 GCTTTTGGGTTGGCTGTGAGTACTTTGCCCTTTTGGAGGAGAGGCGCATTTGGAGTGCAG 2235
QY 386 PheSerAsnLeuThrAlaGlyPro-----TyrProLeuIleIleThrIle 400
Db 2236 TGGGACAAACCTGTTGAGAGTCTCTGTGAGGAAAGATGGCTTCAATCTCACCACCTCGGTC 2295
QY 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 2296 TCCATGATGCTGTTTGACACCTTCTCTATGGGGTGATGACCTGGTACATTGAGGCTGTC 2355
QY 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 2356 TTTCAGGCCAGTACGGAATTCACAGGCCCTGGTATTTCTTCTTGACCAAGTCTACTGG 2415
QY 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db 2416 TTGGGT-----GAGGAAAGTGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2460
QY 461 -----PheSerGluIleIle-----GluProValSerSerGluPheValGlyLys 475
Db 2461 AAGAGAATGTCAGAAATCTGCATGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2508
QY 476 GluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGlu 495
Db 2509 CTGGGCGTGTCCATTGAGAACCTGGTAAAGTCTACCGA---GATGGGATGAAGGTG--- 2562
QY 496 AlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHis 515
Db 2563 GCTGNNATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACCTCCTCTCTCTGGGCCAC 2622
QY 516 SerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAsp 535
Db 2623 AATGAGCGGGGAGAGACGACANNNGTCAATCCTGACCGGGTGTTCCTCCCGACCTCG 2682
QY 536 GlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArg 555
Db 2683 GGCACCGCCTACATCCTGGGAAAGACATTTCG-----TCTGAGATGAGCACCATCCGG 2736
QY 556 LysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGluGlu 575
Db 2737 CAGAACCTGGGGTCTGTCTCCAGCATACGCTGCTGTGTTGACNNGTGTACTGTGGAAGAA 2796
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Db 2797 CACATCTGGTTCTATGCCCGCTTGAAAGGGCTCTCTGAGAAGCACCGTGAAGGCGGAGATG 2856
QY 596 GlnLysValLeuLeuAspLeuAspMetGlnThrIleLys---AspAsnGlnAlaLysLys 614
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QY 615 LeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLys 634
Db 2917 CTGTCAAGTGGAAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTTGTCGGGGGATCTAAG 2976
QY 635 IleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleValTrp 654
Db 2977 GTTGTCAATCTGGATGAACCCACAGCTGGTGTGGACCTTACTCTCCGAGGGGAAATATGG 3036
QY 655 Asn---LeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPheMet 673
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QY 674 AspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLysCys 693
Db 3094 GATGAAGCGGACATCCTGGGGAGAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGT 3153
QY 694 ValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMet--- 712
Db 3154 GTGGGCTCCTCCTGTTTCTGAAGAACCAGCTGGGAACAGGCTACTACTACCTGACCTGGTC 3213
QY 713 -----Tyr 713

Db 6286 CAGGATTTCTTGGACTTGCAATTTCTCGAAGTGTCTCTAAAGAGAAACACCGGAACATG 6345
Qy 1567 LeuAlaTyrlYsIleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeu 1586
Db 6346 CTACAATACCAGCTTCCA--TCTTCATTATCTTCTCTGGCCAGATATTCAGCATCTCTC 6402
Qy 1587 GluGluAlaLysHisAlaPheAlaIleGluGluTyrlYsSerPheSerGlnAlaThrLeuGlu 1606
Db 6403 TCCAGAGCAAAAGCGACTCCACATAGAGACTACTCTGTCTTCTCAGACAACACTTGAC 6462
Qy 1607 GlnValPheValGluLeuThrLysGluGlnGluGluGluAspAsn----- 1621
Db 6463 CAAGTATTTGGAAGTCTTGGCAAGGACCAAGTGAATGATGACCACTTAAAGACCTCTCA 6522
Qy 1622 -----SerCysGlyThrLeuAsnSerThrLeuTrpTrpGlu 1633
Db 6523 TTACACAAAACACAGACAGTAGTGGACGTTCCAGTCTCTCACATCTTTCTACAGGATGAG 6582
Qy 1634 ArgThrGlnGluAspArgVal 1640
Db 6583 AAAGTGAAGAAAGCTATGTA 6603

RESULT 13
CD250953 850 bp mRNA linear EST 22-MAY-2003
LOCUS AGENCOURT_14214041 NIH_MGC_179 Homo sapiens cDNA clone
DEFINITION IMAGE:30385589 5', mRNA sequence.

ACCESSION CD250953
VERSION CD250953.1 GI:31011419
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabps-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: NDAM452 row: o column: 06
High quality sequence stop: 719.
Location/Qualifiers

FEATURES
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30385589"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores: 3.53e-145 Length: 850
Pred. No.: 1427.00 Matches: 280
Score:

Percent Similarity: 98.94% Conservative: 0
Best Local Similarity: 98.94% Mismatches: 2
Query Match: 16.94% Indels: 1
DB: 14 Gaps: 0

US-10-090-458-5 (1-1642) x CD250953 (1-850)

Qy 1336 GlyAlaGlyLysSerThrIleIleAsn-IleLeuValGlyAspIleGluProThrSerGl 1355
Db 3 GGTGCTGGCAAAAGCACAATTAATAATNTCTGGTTGGTGATATTGAACCAACTTCAGG 62
Qy 1355 YGlnValPheLeuGlyAspTyrlYsSerSerGluThrSerGluAspAspSerLeuLysCy 1375
Db 63 CCAGGTATTTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGATCACTGAAGTG 122
Qy 1375 sMetGlyTyrlYsProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisph 1395
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Qy 1395 eGluIleTyrlYsAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerAr 1415
Db 183 TGAATTTATGGAGCTGTCAAAGGAATGAGTCAAGTGACATGAAAGAGTCATAAGTCG 242
Qy 1415 gIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLeuProAl 1435
Db 243 AATAACACATGCACCTGATTTAAAGAAACATCTTCAGAGACTGTAAAGAACTACCTGC 302
Qy 1435 aGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLe 1455
Db 303 AGGAATCAAACGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTT 362
Qy 1455 uLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaI 1475
Db 363 GCTAGATGAACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAAT 422
Qy 1475 eArgThrAlaPheLysAsnArgLysArgAlaIleLeuThrThrHisTyrlYsMetGluGl 1495
Db 423 TCGAACTGCATTTTAAACAGAAAGCGGGCTGCTATCTGACCCTCACTATATGGAGGA 482
Qy 1495 uAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGl 1515
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Qy 1515 yThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrlYsGlyTyrlYsLeuLysLeuLy 1535
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Qy 1555 oAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrlYsIleProLysGluAs 1575
Db 663 AAATGCAAGCCGTCAGGAAAGTTTTCTTCTATTATTGGCTTATAAAATTCCTAANGAAGA 722
Qy 1575 pValGlnSerLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPheAlaI 1595
Db 723 TGTTCAGTCCCTTTCAACAATCTTTTAAAGCTGGAAGAGCAAGCTAAACATGCTTTTGCCAT 782
Qy 1595 eGluGluTyrlYsSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGl 1615
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Qy 1615 uGlnGlu 1617
Db 843 ACAAGAG 849

RESULT 14
AY405472 6606 bp DNA linear GSS 16-DEC-2003
LOCUS AY405472
DEFINITION Pan troglodytes ABCA1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY405472

QY	925	IleSerAsp	-----LeuIleSerPhePheThrSerGlnAsn	936
DB	4333	ATTTCCGATTATCTGTTGAAGACGTATGTGCAGATCATAGCCAAAGCCTTAAAGAACAAG	4392	
QY	937	IleMetValThr	-----	940
DB	4393	ATCTGGTGAATGAGTTTAGGTATGGCGGCTTTTCCTGGGTGTCAGTAATACTCAAGCA	4452	
QY	941	-----MetIleAsnAspSer	-----AspTyrValSerVal	950
DB	4453	CTTCTCCGAGTCAAGAAAGTTAATGATGCCATCAAAACAATGAAGAAACACCTAAAGCTG	4512	
QY	951	AlaProHisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyrVal	967	
DB	4513	GCCAAAGGACAGTTCTGCAGATCGATTCTCAACAGCTTGGGAAGATTATGACAGGACTG	4572	
QY	968	-----PheAlaAlaValPheAsnSerThrMetValTyrSerLeuProIle	982	
DB	4573	GACACCAAAAATAATGTCAAGGTGTGGTTCAATAACAAGGCTGGCATGCAATCAGCTCT	4632	
QY	983	LeuValAsnIleIleSerAsnTyrTyrLeu	992	
DB	4633	TTCTGGAATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGAGAGAACCCT	4692	
QY	993	-----TyrHisLeuAsnValThrGluThrIleGlnIle	1003	
DB	4693	AGCCATTATGGAATTACTGCTTTCAATCATCCCTCGATCTCACCAAGCAG--CAGCTC	4749	
QY	1004	TrpSerThrProPheGlnGluIleThrAspIleValPheLysIleGluLeuTyrPhe	1023	
DB	4750	TCAGAGGTGGCTCTGATGACCACATCAGTGGATGTCTGTGTCCATCTGTGTCTCTTT	4809	
QY	1024	GlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsn	1043	
DB	4810	-----GCAATGTCCTTCGTCCAGCCAGCTTTGTGCTATTCCTG	4848	
QY	1044	AlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSer	1063	
DB	4849	ATCCAGGAGCGGTGACGAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTC	4908	
QY	1064	AlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeuIleLeu	1083	
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QY	1084	MetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPheLeu	1103	
DB	4969	GTCAATATCATCTTCATCTGCTTCCAGCAGAAAGTCCATGTGTCTCCACCAATCTGGCT	5028	
QY	1104	AlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAla	1123	
DB	5029	GTGCTAGCCCTTCTACTTTTGTGTATGGTGGTCAATCACAACCTCTCATGTACCCAGCC	5088	
QY	1124	SerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIleTyrSerVal	1143	
DB	5089	TCCTTTGTGTTCAAG-----ATC	5106	
QY	1144	AlaAlaLeuAlaCysIleAlaIleThrGluIleThrPheMetGlyTyr-----Thr	1161	
DB	5107	CCCAGCACAGCCTATGTGGTGCTCACCCAGCGTGAACCTCTTCATTGGCATTATGGCAGC	5166	
QY	1162	IleAlaThr-----Ile	1165	
DB	5167	GTGGCCACCTTTGTGCTGGAGCTGTTCACCGACAATAAGCTGAATAATCAATGATATC	5226	
QY	1166	LeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeuGlyCysLeuIleSer	1185	
DB	5227	CTGAAGTCCGTGTTCT--TTGATCTTCCACATTTTTCCTGGGACGAGGGCTCATCGAC	5283	
QY	1186	PheIleLys-----	1188	
DB	5284	ATGGTGAATAAACAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGAGAAATCGCTTTGTG	5343	

QY	1189	-----IleSerTrpLysAsnValArgLysAsnValAspThrTyrAsnProTrpAspArg	1200
DB	5344	TCACCAATTATCTGGGACTTGGTGGGACGAAACCTCTTCGCC	5385
QY	1207	LeuSerValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGln	1226
DB	5386	ATGGCCGTGGAAGGGTGGTGTCTCTCTCCTACTACTGTT	5433
QY	1227	TyrTyrGluLysLysTyrGlyArgSerIleArgLysAspProphePheArgAsnLeu	1246
DB	5434	TAC-----AGATTCTTC-----ATC	5448
QY	1247	SerThrLysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspGlu	1266
DB	5449	AGCCCCAGACCTCTAAATGCAAAGCTA-----TCTCCTCTGAAT--GATGAAGATGAA	5499
QY	1267	AspValLysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGlu	1286
DB	5500	GATGTGAGCGGGAAGACAGAGAATTCTTGATGGTGGAGGC-----CAG	5544
QY	1287	LysProSerIleMetValSerAsnLeuHisLysGluTyrAspLysLysAspPheLeu	1306
DB	5545	AATGACATCTAGAAATCAAGGAGTTGACGAAGATATAT-----	5583
QY	1307	LeuSerArgLysValLysValAlaThrLysTyrIleSerPheCysValLysLysGly	1326
DB	5584	-----AGAAGGAACGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCTCTGGT	5637
QY	1327	GluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeu	1346
DB	5638	GAGTGCTTTGGGCTCTCTGGGAGTTAATGGGCTGGAAATCATCAACTTTCAAGATGTTA	5697
QY	1347	ValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThr	1366
DB	5698	ACAGGAGATACCACTGTTACCAGAGGAGATGCTTTCCTT--AACAAANNNNNTATCTTA	5754
QY	1367	SerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrp	1386
DB	5755	TCAAACATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACA	5814
QY	1387	ProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAla	1406
DB	5815	GAGCTGTTGACTGGGAGAGAAACACGTGGAGTTCTTTTGCCCTTTTGAGAGGAGTCCCAGAG	5874
QY	1407	SerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeu	1426
DB	5875	AAAGAAGTTGGCAAGCTTGGTGAGTGGGCGAATCGGAAACTGGGCCTCGTGAAGATGGA	5934
QY	1427	GlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSer	1446
DB	5935	GAAAAATATGCTGGTAACCTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCT	5994
QY	1447	MetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLys	1466
DB	5995	TTGATCGCGGCGCTCTCTGTGGTGTCTTCTGGATGAACCCACACAGGCATGGATCCCAA	6054
QY	1467	AlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAla	1486
DB	6055	GCCCCGGGTTCTTGTGGAATTGTGCCCTAAGTGTGTCAAG--GAGGGGAGATCAGTA	6111
QY	1487	IleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMet	1506
DB	6112	GTGCTTACATCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATG	6171
QY	1507	ValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLys	1526
DB	6172	GTCAATGGAAGGTTCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGTTTGGAGAT	6231
QY	1527	GlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeu	1546
DB	6232	GGTTATACAATAGTTGTACGAATAGCAGGG-----TCCAAACCCGGACCTGAAGCCTGTC	6285
QY	1547	GlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerIle	1566

Db 2176 GCTTTGGGTTTGGCTGTGAGTACTTTTGGCCCTTTTGGAGGACGAGGCGCATTTGGAGTGCAG 2235
QY PheSerAsnLeuThrAlaGlyPro-----TyrProLeuIleIleThrIle 400
Db 2236 TGGGACAACTGTTTGAGAGTCTGTGTGGAGGAAGATGGCTTCAATCTCACCACTTCGGTTC 2295
QY IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 2296 TCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGGIACATTGAGGCTGTC 2355
QY IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 2356 TTTCCAGGCCAGTACGGAATTCCAGGCCCTCGTATTTTCTTGTGACCAAGTCCTACTGG 2415
QY 441 -----SerLysSerLysArgAsnTyrGluGluLeuSerGlu 452
Db 2416 TTTGGCGAGAAAGTATGAGAGAGCCACCTGGTTCCAAACGAGAGAGAATATCAGAA 2475
QY GlyAsnValAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPhe 472
Db 2476 -----ATCTGCATGGAGGAG-----GAACCCACCCACTTG----- 2505
QY ValGlyLysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGlu 492
Db 2506 -----AAGCTGGCGGTGCCATTTCAGAACCTGGTAAAGTCTACCGA---GATGGGATG 2556
QY AsnValGluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeu 512
Db 2557 AAGGTG---GCTGTGATGGCCTGGCACTGGAATTTTATGAGGGCCAGATCACCTCCTTC 2613
QY LeuGlyHisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysPro 532
Db 2614 CTGGGCCACAATGGAGCGGGGAAGACGACCAACCATGTCAATCCTGACCGGTTGTTCCCC 2673
QY ProSerAspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPhe 552
Db 2674 CCGACCTCGGGCACCGCTACATCCTGGGAAAAGACATTTCG-----TCTGAGATGAGC 2727
QY GluAlaArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThr 572
Db 2728 ACCATCCGGCAGAACCTGGGGTCTGTCCCCAGCATAAAGTGTCTGTTGACATGCTGACT 2787
QY ValGluGluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIle 592
Db 2788 GTCGAAGAACACATCTGGTTCTATGCCCGCTTGAAGGGCTCTCTGAGAAGCACGTTGAAG 2847
QY GlnGluValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLys---AspAsnGln 611
Db 2848 GCGGAGATGGAGCAGATGGCCCTGGATGTTGGTTGGCATCAAGCAAGCTGAAAGCAAA 2907
QY AlaLysLysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGly 631
Db 2908 ACAAGCCAGCTGTACGGTGAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTGTGCGGG 2967
QY AsnProLysIleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHis 651
Db 2968 GGATCTAAGTTGTTCATTCTGGATGAACCCACAGCTGGTGTGGACCTTACTCCCGCAGG 3027
QY IleValTrpAsn---LeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThr 670
Db 3028 GGAATATGGAGCTGCTGCTGAAATACCGACAA---GGCCGACCATTTACTTCTCTACA 3084
QY HisPheMetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMet 690
Db 3085 CACCACATGGATGAAGCGGACGTCCTGGGGACAGGATTGCCATCATCTCCCATGGGAAG 3144
QY LeuLysCysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeu 710
Db 3145 CTGTGCTGTGTGGGCTCTCCTGTTTCTGAAGAACCAAGCTGGGAACAGGCTACTACCTG 3204
QY 711 SerMet----- 712

Db 3205 ACCTTGGTCAAGAAAGATGTGGAATCCTCCTCAGTTCTCTGCAGAAACAGTAGTAGCACT 3264
QY 713 -----TyrIleAspLysTyrCysAla----- 719
Db 3265 GTGTCAATACCTGAAAAAGGAGGACAGTGTCTTCTCAGAGCAGTTCTGATGCTGGCCTGGGC 3324
QY 720 -----ThrGluSerLeuSerSerLeuValLys 728
Db 3325 AGCGACCATGAGAGTGACACGCTGACCATCGATGTCTGTCTATCTCCAACCTCATCAGG 3384
QY 729 GlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeu 748
Db 3385 AAGCATGTGTCTGAAGCCCGGCTGGTGGAGACATAGGGCATGAGCTGACCTATGTGCTG 3444
QY 749 ProPheLysAspMetAspLys-----PheSerGlyLeuPheSerAlaLeuAspSerHis 766
Db 3445 CCATATGAAGCTGCTAAGGAGGGAGCCCTTTGTGGAACCTCTTTCATGAGATTGATGACCGG 3504
QY 767 ---SerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPhe 785
Db 3505 CTCTCAGACCTGGGCATTTCTAGTTATGGCATCTCAGAGACGACCCCTGGAAGAAATATTC 3564
QY 786 LeuLysLeuGluValGluAlaGluIleAsp----- 795
Db 3565 CTCAAGGTGGCCGAGAGAGTGGGTGGATGTGTGAGACCTCAGATGGTACTTGCCAGCA 3624
QY 796 -----GlnAlaAspTyrSerValPheThrGln--- 804
Db 3625 AGACGAAACAGCGGGCCTTCGGGGACAAGCAGAGCTGTCTTCGCCCGTTCACTGAAGAT 3684
QY 805 -----GlnProLeuGluGluGluMetAspSerLysSerPheAspGluMetGluGln 821
Db 3685 GATGCTGTGATCCAAATGATTCTGACATAGACCCAGATCC-----AGAGAGACA 3735
QY 822 SerLeuLeuIleLeuSerGluThrLysAlaSerLeu---ValSerThrMetSerLeuTrp 840
Db 3736 GACTTGCTCAGTGGGATGGATGGCAAAGGGTCTTACCAGGTGAAAGGCTGGAACTTACA 3795
QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860
Db 3796 CAGCAACAGTTTGTGGCCCTTTTGTGGAAAGACACTGCTAATTGCCAGACGGAGTCGGAAA 3855
QY 861 SerValArgSerValLeuLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 3856 GGATTTTGTCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGTCATTTGCCCTTGTGTTTCAGC 3915
QY 881 LeuVal----- 882
Db 3916 CTGATCGTGCCACCTTTGGCAAGTACCCACGCTGGAACCTTCAGCCCTGGATGTACAAC 3975
QY 882 ----- 882
Db 3976 GAACAGTACACATTTGTCAAGCAATGATGTCTCTGAGGACACGGGAACCTTGAACCTCTTA 4035
QY 882 ----- 882
Db 4036 AACGCCCTCACCAAGACCCCTGGCTTCGGGACCCCGCTGTATGGAAGGAACCAATCCCA 4095
QY 883 -----HisHisSerPheLysAsnAlaValValProIleLysLeu 895
Db 4096 GACAGCCCTGCCAGGCGGGGAGGAGAGTGGACCACTGCCCCAGTTCCC---CAGACC 4152
QY 896 ValProAspLeuTyr----- 900
Db 4153 ATCATGGACCTCTTCCAGAATGGGAACCTGGACAATGCAGAACCCCTTCACCTGCATGCCAG 4212
QY 901 -----PheLeuLysProGly----- 905
Db 4213 TGTAGCAGCGACAAATCAAGAAGATGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4272
QY 906 ---AspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAsp 924
Db 4273 CCTCTCCACAAAGAAAACAAACACTGCAGATATCTTTCAGGACCTTCAGAGGAAAGAAC 4332

Db 5632 CCGGAGAGTGCTTTGGACTCCTGGGAGTTAACGGAGCTGGGAAGTCAACAACCTTTCAAG 5691

Qy 1345 IleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSer 1364

Db 5692 ATGCTGACTGGAGACACCCCTGTGACCAGAGGGGATCGGTTCTCTTAACAACATCTTATCA 5751

Qy 1365 GluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnPro 1384

Db 5752 AATATCCATGAAGTACACCAAGAC-----ATGGCTACTGCCCTCATTGACGCC 5802

Qy 1385 LeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMet 1404

Db 5803 ATCACAGAGCTGCTGACGGGAAGAGAGCATGTGGAGTTCTTTGCCCTCCTGAGGGAGTC 5862

Qy 1405 SerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGlu 1424

Db 5863 CCAGAAAAGGAAGTTGGCAAGTTGGTGAATGGGCAATTGCAAACTGGGCTGGTAAAG 5922

Qy 1425 HisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAla 1444

Db 5923 TATGGAGAAAATATGCCAGTAACACTACAGTGGCGGCAACAACGAAAGCTCTCCACAGCC 5982

Qy 1445 LeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAsp 1464

Db 5983 ATGGCTTTGATTGGCGGACCTCCTGTGGTGTCTCTGGATGAACCAACCAAGCATGGAC 6042

Qy 1465 ProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArg 1484

Db 6043 CCTAAAGCCCGGAGATTCTTGTGGAATTGTGCCCTAACCATTTGTCAAG---GAGGGGAGA 6099

Qy 1485 AlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAla 1504

Db 6100 TCTGTAGTCCTTACATCTCATAGTATGGAAGAAATGTGAAGCTCTTTGTACAGGATGGCC 6159

Qy 1505 IleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPhe 1524

Db 6160 ATAATGGTCAATGGAAGTTTCAGTGCCTTGGCAGTGTCCTCAACATCTGAAACACAGGTTT 6219

Qy 1525 GlyLysGlyTyrPheLeuGluIleLysLysLeuLysAspTrpIleGluAsnLeuGluValAsp 1544

Db 6220 GGAGATGGTTATACAATAGTTGTACGAATAGCAGGC-----TCCAACCCCTGACCTGAAG 6273

Qy 1545 ArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSer 1564

Db 6274 CCGTCCAGAGATTCTTTGGACTTCGGTTTCCGGGAAGTGCCTAAAGAGAGAAACATCGA 6333

Qy 1565 SerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePhe 1584

Db 6334 AACATGCTTCAGTACCAGCTTCCA---TCCTCCTTGTCACTCTCTAGCAGGATATTCAGC 6390

Qy 1585 LysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThr 1604

Db 6391 ATCCCTCTCCAGAGCAAAAAGCGACTCCACATAGAAGACTACTCTGTCTCTCAGACAACA 6450

Qy 1605 LeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAspAsn----- 1621

Db 6451 CTTGACCAAGTATTGTGAACCTTTGCCAAGGACCAAGATGATGATGACCACTTAAAGGAC 6510

Qy 1622 -----SerCysGlyThrLeuAsnSerThrLeuTrp 1631

Db 6511 CTGTCACTGCACAAAACCAGACAGTTGTGGATGTGGCCGTTCTCACATCCTTTTTCAG 6570

Qy 1632 TrpGluArgThrGlnGluAspArgVal 1640

Db 6571 GATGAGAAAGTGAAAGAAAGTTATGTA 6597

RESULT 12

AY405471 6606 bp DNA linear GSS 16-DEC-2003

LOCUS

DEFINITION Homo sapiens ABCA1 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION AY405471

VERSION AY405471.1 GI:39761445

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 6606)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene tricos

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 6606)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1..6606

organism="Homo sapiens"

mol_type="genomic DNA"

db_xref="taxon:9606"

gene<1..>6606

gene="ABCA1"

locus_tag="HCM2235"

ORIGIN

Alignment Scores:

Pred. No.: 1.42e-145 Length: 6606

Score: 1444.00 Matches: 450

Percent Similarity: 43.41% Conservative: 291

Best Local Similarity: 26.36% Mismatches: 556

Query Match: 17.14% Indels: 410

DB: 29 Gaps: 55

US-10-090-458-5 (1-1642) x AY405471 (1-6606)

Qy 240 IleValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAsp 259

Db 1795 ATCGTGTATGAGAAGGAGGCGGCTGAAAGAGACCATCGGATCATGGGCTGGACAAC 1854

Qy 260 ThrAlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMet----- 277

Db 1855 AGCATCCTCTGGTTTAGTGGTTCATT-----AGTAGCTCATTCCTCTTCTTGTGAGC 1908

Qy 278 ---SerLeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSer 296

Db 1909 GCTGGCCTGCTAGTGGTCACTCCTGAAGTTAGGAAACCTGCTG---CCCTACAGTGATCCC 1965

Qy 297 IleValIlePheLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMet 316

Db 1966 AGCGTGGTGTGTCTTCTCCTGTCCGTGTTTGTGTGTGTGACAAATCCTGCAGTGTCTCTG 2025

Qy 317 LeuThrProLeuPheLysLysSerLysHisVal-----GlyIleValGluPhe 332

Db 2026 ATTAGCACACTCTTCTCCAGAGCCAACTGGCAGCAGCCTGTGTGGGGCATCATCTACTTC 2085

Qy 333 PheValThrValAlaPhe-----GlyPheIleGlyLeuMetIle 345

Db 2086 ACGCTGTACCTGCCCTACGTCCTGTGTGTGGCATGGCAGACTACGTGGGCTTCACACTC 2145

Qy 346 IleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSerProPheCysHisCys 365

Db 2146 AAGATCTTCGTAGC-----CTGCTGTCTCCT-----GTG 2175

Qy 366 ThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSer 385

QY 805 -----GlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 3682 GATGATGCTGTGATCCCAATGACTCTGACATAGACCAGAAATCC-----AGGGAG 3732
QY 821 GlnSerLeuLeuLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 3733 ACCGACCTGCTCAGTGGGATGGACGGCAAGGCTCCTAC-----CAGCTGAAGGGCTGG 3786
QY 841 Lys-----GlnGlnMetTyrThrIleAlaLysPheHisPheThrLeuLysArgGlu 858
Db 3787 AAACCTCACCAGCAACAGATTGTGGCCCTTTTGTGGAGAGGCTGCTGATTGCCAGACGG 3846
QY 859 SerLysSer-----ValArgSerValLeuLeuLeuLeuLeuLeu 871
Db 3847 AGCGGAAGGGTTTCTTTTGTCTCAGATTGTCTCTGCCAGCTGCTTTTGTGTCATTGCCCTG 3906
QY 872 PhePheThr-----ValGlnIlePhe 878
Db 3907 GTCTTCAGCCTGATTGTGCCACCCCTTTTGGCAAGTACCCAGCCTGGAACTTCAGCCCTGG 3966
QY 879 MetPheLeuValHisHisSerPheLysAsnAlaValValProIleLysLeu----- 895
Db 3967 ATGTATAATGAGCAGTATACATTGTTCAGTAATGATGCTCCCGAGGACATGGGCACCCAG 4026
QY 895 ----- 895
Db 4027 GAACTCCTGAATGCTCTGACCAAGATCCAGGCTTTGGACCCGCTGTGTATGGAAGAAAC 4086
QY 896 ---ValProAsp----- 898
Db 4087 CCAATCCCAGATACCCCTTGCTTGGCTGGGGAGGAGGACTGGACCATCAGCCCGCTCCCC 4146
QY 898 ----- 898
Db 4147 CAGAGCATCGTGGACCTTTCAGAAATGGAACCTGGACCATGAAGAACCCCTCACCTGCG 4206
QY 899 -----LeuTyrPheLeuLysProGly----- 905
Db 4207 TGCAGTGTAGCAGTGACAAAATCAAGAAGATGCTGCTGTGTGTCCTCCCGAGGGCAGGG 4266
QY 906 -----AspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAsp 922
Db 4267 GGGGTGCCACCTCCTCAGAGAAAACAGAAAACCGCAGACATCCTTCAGAAATCGACAGGA 4326
QY 923 SerAspIleSerAsp-----LeuIleSerPhePheThrSer 934
Db 4327 AGAAATATTTCAGATTACCTGCTGAAGACGTACGTCGACATCATAGCAAGAGCTTAAAG 4386
QY 935 GlnAsnIleMetValThrMetIleAsnAspSerAspTyrValSerValAlaProHisSer 954
Db 4387 AATAAGATCTGGGTGAACGAGTTTCGGTATGGCGGGTTTCCCTGGGTGTCAGTAATTCT 4446
QY 955 AlaAlaLeuAsnValMetHisSerGluLysAspTyrVal----- 967
Db 4447 CAAGCACTTCCTCCGAGCCATGAAGTTAATGATGCTATCAAGCAAAATGAAGAAACTCCTG 4506
QY 968 -----PheAlaAla 970
Db 4507 AAGCTGACCAAGGACAGCTCCGAGATCGCTTCTCAGCAGCCTGGGAAGGTTTCATGGCA 4566
QY 971 -----ValPheAsnSerThrMetValTyrSerLeu 980
Db 4567 GGGCTGGATACGAAAACAATGTCAAGGTGTGGTTCAATAACAAGGGCTGTCATCTATC 4626
QY 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeu----- 992
Db 4627 AGTTCGTTCTGTAATGTTCATCAACAATGCCATTCTCCGGGCCAACCTGCAGAGGGAGAG 4686
QY 993 -----TyrHisLeuAsnValThrGluThrIle 1001
Db 4687 AACCAGCCAGTATGGAATCACTGCTTTTCAACCAACCCCTTGAACCTCACTAAACAG--- 4743
QY 1002 GlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGluLeu 1021

Db 4744 CAGCTCTCAGAGGTGGCTCTGATGACCACCTCTGTGCGACGTCTCTGTGTCTATCTGTGTC 4803
QY 1022 TyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMet 1041
Db 4804 ATCTTT-----GCGATGTCCTTTGTCCCTGCCAGCTTTGTGTGTG 4842
QY 1042 GluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeu 1061
Db 4843 TTCCTGATCCAGGAGCGGTGAGCAAAAGCCAAGCATCTTCAGTTTCATCAGCGCGTGAAG 4902
QY 1062 ProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleLeu 1081
Db 4903 CCTGTCTACTGCTGCTGCCAATTTGTCTGGGATATGTGCAATTATGTGGTCCCTGCT 4962
QY 1082 IleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLys 1101
Db 4963 ACACGTGTCATTATCATCTTCATCTGCTTCCAGCAGAGTCCTATGTGTCTCTACCAAC 5022
QY 1102 PheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyr 1121
Db 5023 CTGCCGCTTAGCCCTTCTGCTCTTGTGTATGGGTGTCGATCACTCCTCTCATGTAT 5082
QY 1122 IleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIleTyr 1141
Db 5083 CCAGCATCCTTTGTGTTCAAG----- 5103
QY 1142 SerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr--- 1160
Db 5104 ---ATCCCCAGCACCGCCTATGTGTTCTCACCCAGTGTGAACCTCTTCATCGGCATCAAT 5160
QY 1161 ---ThrIleAlaThr----- 1164
Db 5161 GGCAGTGTGGCCACTTTTCGTACTGGAGCTGTTTACAAACAATAAGCTCAATGACATCAAT 5220
QY 1165 ---IleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeuGlyCysLeu 1183
Db 5221 GACATCCTGAAGTCTGTGTT---CTTATCTTCCCACATTTTTCCTGGGGCGAGGCTC 5277
QY 1184 IleSerPheIleLys----- 1188
Db 5278 ATCGACATGGTGAAGAACCCAGGCCATGGCCGATGGCCCTGGAGAGGTTTGGGGAGAACCGC 5337
QY 1189 -----IleSerTrpLysAsnValArgLysAsnValAspThrTyrAsnProTrp 1204
Db 5338 TTCGTCTCTCGCTCTCTTGGGACTTGGTAGGACGGAACCTT----- 5379
QY 1205 AspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeu 1224
Db 5380 -----TTTGCCATGGCCGTG-----GAAGGGGTGGTGTCTCTCCTCAT 5418
QY 1225 LeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAspProPhePheArg 1244
Db 5419 ACTGTTCTGATCCAGTACAGATTT-----TTCATCAGG 5451
QY 1245 AsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGlu 1264
Db 5452 CCCAGACCTGTAAAGGCGAAG-----CTTCCTCTCTTTGAAT---GACGAG 5493
QY 1265 AspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCys 1284
Db 5494 GATGAGGATGTGAGCGGGGAGACAGAGGATTCTGGACGGTGGCGGA----- 5541
QY 1285 GluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAsp 1304
Db 5542 ---CAGAATGACATCCTAGAGATCAAGGAACCTGACCAAGATCTAT----- 5583
QY 1305 PheLeuLeuSerArgLysValLysValAlaThrLysTyrIleSerPheCysValLys 1324
Db 5584 -----AGGAGGAACGGAAGCCTGCAGTCGACAGGATCTGCATCGGCATCCCT 5631
QY 1325 LysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsn 1344

Alignment Scores:

Pred. No.: 1.54e-148 Length: 6600
Score: 1471.00 Matches: 458
Percent Similarity: 43.26% Conservative: 290
Best Local Similarity: 26.49% Mismatches: 559
Query Match: 17.46% Indels: 422
DB: 29 Gaps: 57

US-10-090-458-5 (1-1642) x AY405473 (1-6600)

QY	223	IleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIle-----His	239
Db	1744	CTCTTCATGACTTAGCCTGGATC-----TACTCTGTCGCTGTGATCATCAAGAGC	1794
QY	240	IleValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAsp	259
Db	1795	ATTGTGTATGAGAGAGGCTCGGCTGAAGGAGACCATCGGATCATGGGTCTGGACAAT	1854
QY	260	ThrAlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMet-----	277
Db	1855	GGCATCCTCTGGTTTAGCTGGTTTGT-----AGCAGCCTCATCCCTCTGCTGTGAGC	1908
QY	278	---SerLeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSer	296
Db	1909	GCTGGCTGTGGTGTCACTCTGAAGTTAGGAACCTGCTG---CCCTATAGTGACCCC	1965
QY	297	IleValIlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMet	316
Db	1966	AGCGTGGTGTTCGTTCTCTCTGCTGTGTTTGCCATGCTGACCATCCTACAGTGTTCCTC	2025
QY	317	LeuThrProLeuPheLysLysSerLysHisVal-----GlyIleValGluPhe	332
Db	2026	ATTAGACAGCTCTTCTCCCGTGCCAACTGGCAGCAGCCTGTGGGGCATCATCTACTTC	2085
QY	333	PheValThrValAlaPhe-----GlyPheIleGlyLeuMetIle	345
Db	2086	ACGCTGTACCTGCCCTATGTGCTGTGCTGCTAGCCTGGCAGGACTATGTGGGCTTCTCCATC	2145
QY	346	IleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSerProPheCysHisCys	365
Db	2146	AAGATCTTTGCTAGC-----CTGCTGTCTCCT-----GTG	2175
QY	366	ThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSer	385
Db	2176	GCCTTTGGATTGGCTGTGAGTATTTCGCCCTTTTCGAGGAGCAAGGTATCGGGGTCCAA	2235
QY	386	PheSerAsnLeuThrAlaGlyPro-----TyrProLeuIleIleThrIle	400
Db	2236	TGGGACAATCTCTTTGAGAGCCCGGTGGAGGAGGACGGTTCATCTCACCACTGCAGTG	2295
QY	401	IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal	420
Db	2296	TCCATGATGCTCTTTGACACCTTTCTCTATGGCTGTGATGACATGGTACATCGAAGCCGTC	2355
QY	421	IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp	440
Db	2356	TTTCCAGGACAGTATGGAATTCACAGGCCCTGGTATTTCCTTGTACCAAGTCACTAGG	2415
QY	441	SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIle---	459
Db	2416	TTTGGT-----GAGGAAATTGATGAGAGAGCCACCCTGGTTCCAGCCAG	2460
QY	460	---SerPheSerGluIleIle-----GluProValSerSerGluPheValGlyLys	475
Db	2461	AAGGGAGTGTCAAGAAATCTGCATGGAAGAGGAACCCACTCATCTGAGGCTG-----	2511
QY	476	GluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGlu	495
Db	2512	---GGGGTGTCCATTCAAGAACCTGGTGAAGTTTACCGA---GATGGCATGAAGTT---	2562
QY	496	AlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHis	515
Db	2563	GCTGTGGATGGCTTGGCGCTCAACTTTTACGAAGGCCAGATTACTCTCTTCTCTGGGCCAC	2622

QY	516	SerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAsp	535
Db	2623	AATGGAGCAGGGAAGACACCATGTCTAATACTAGCTGGCTGTTTCCCCCACTTCT	2682
QY	536	GlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArg	555
Db	2683	GGCAGGCTTACATCTCGGGAAGGACATTCCG-----TCGGAGATGAGCTCCATCCG	2736
QY	556	LysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGluGlu	575
Db	2737	CAGAACCTGGGAGTCTGTCCCCAGCATAATGTGCTGTTTGACATGCTGACTGTGGAAG	2796
QY	576	AsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluVal	595
Db	2797	CACATCTGGTTCTATGCCGCCCTAAAGGGGCTCTCAGAGAAGCACCTGAAACAGAGATG	2856
QY	596	GlnLysValLeuLeuAspLeuAspMetGlnThrIleLys---AspAsnGlnAlaLysLys	614
Db	2857	GAGCAGATGGCCCTGGATGTTGGCTTACCCCGCAGCAAGCTGAAAGCAACAGAGTCAG	2916
QY	615	LeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLys	634
Db	2917	CTCTCAGTGGGATGCAGAGAAAGCTGTCTGTGGCTTGGCCTTCGTGGTGGATCCAAAG	2976
QY	635	IleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleValTrp	654
Db	2977	GTTCTCATTTCTGGACGAGCCACAGCCGGGTGGACCCCTACTCTCGCAGGGGAATATGG	3036
QY	655	Asn---LeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPheMet	673
Db	3037	GAACCTCTGTAAATACCGCAA---GGCCGCAACCATATTATTTGTCTACACACCATG	3093
QY	674	AspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLysCys	693
Db	3094	GACGAAGCTGACATCCTTGGGACAGAAATGCCCATCATTTCCCATGGGAAGCTGTGTGT	3153
QY	694	ValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyr	713
Db	3154	GTGGCTCCTCCTCTGTTTGAAGAACCAAGTTGGGAACGGGTACTATCTGACCCCTGGT	3213
QY	713	-----	713
Db	3214	AAGAAAGATGTGAATCGTCCCTCAGTTCTCTGCAGAAACAGTAGCAGCCCTGTCTGT	3273
QY	713	-----	713
Db	3274	CTGAAAAAGGAGGACAGTGTCTCTCAGAGCAGTTCTGATGCTGGCCTGGGCAGCGACCAT	3333
QY	714	-----IleAspLysTyrCysAlaThrGluSerLeuSerSerLeuVal	727
Db	3334	GAAAGTGACACGCTGACCATCGAT-----GTCTCTGCTATCTCCACCTCATC	3381
QY	728	LysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSer	747
Db	3382	AGGAAGCAGTGTCTGAAGCCCGCTGGTGGAGGACATTGGGCACGAGCTGACCTATGTG	3441
QY	748	LeuProPheLysAspMetAspLys-----PheSerGlyLeuPheSerAlaLeuAspSer	765
Db	3442	CTGCCGTACGAAGCCGAGAGGAGGGAGCCCTTTGTGGAACCTCTCCATGAGATTGATGAC	3501
QY	766	His---SerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspVal	784
Db	3502	CGGCTCTCAGACCTGGGCATCTCCAGTTATGGCATCTCGGAGACCCCTTGGAGAAATA	3561
QY	785	PheLeuLysLeuGluValGluAlaGluIleAsp-----	795
Db	3562	TTCCCTCAAAGTGGCTGAAGAGAGCGGGGTGGATGCTGAGACCTCAGATGGTACTTTGCCA	3621
QY	796	-----GlnAlaAspTyrSerValPheThrGln	804
Db	3622	GCAAGACGAAACAGACGGGCTTCCGGGACAAGCAGAGCTGTCTGCACCCATTACGGAA	3681

PUBMED 8894702
REFERENCE 2 (bases 1 to 1346)
AUTHORS Alikmets,R., Gerrard,B. and Dean,M.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-1996) Human Genetics Section, National Cancer Institute, NCI-FCRDC, Frederick, MD 21702, USA
FEATURES
Location/Qualifiers
source
1..1346
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="EST90625"
/note="similar to ATP-binding cassette transporter"

ORIGIN

Alignment Scores:
Pred. No.: 2.66e-172 Length: 1346
Score: 1677.00 Matches: 358
Percent Similarity: 93.80% Conservative: 5
Best Local Similarity: 92.51% Mismatches: 17
Query Match: 19.90% Indels: 12
DB: 11 Gaps: 1

US-10-090-458-5 (1-1642) x U66672 (1-1346)

QY 1260 AspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMet 1279
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QY 1280 GlyCysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyr 1299
Db 63 GGTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAATAT 122

QY 1300 AspAspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIle 1319
Db 123 GATGACAAAGAAAGATTTTCTCTTTCAAGAAAGTAAAGAGAGTGGCACTAAATACATC 182

QY 1320 SerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLys 1339
Db 183 TCCTTCTGTGTGAAAAAGAGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAA 242

QY 1340 SerThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeu 1359
Db 243 AGCACAATTATTATATTCTGGTTAGTGTATTTGAACACAGCTTCAGGCCAGGTATTTTA 302

QY 1360 GlyAspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCys 1379
Db 303 GGAGATTATTCTTCAGACACAAGTGAAGATGATGATTCACCTGAAGTGTATGGTTACTGT 362

QY 1380 ProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGly 1399
Db 363 CCTCAGATAAACCCCTTTGTGGCCAGATACTACATTGCAGGAACATTTTGAAATTTATGA 422

QY 1400 AlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAla 1419
Db 423 GCTGTCAAAGGAATGAGTGCAGGTGACATGAAAGAAGTCATAAGTCGAATAACACATGCA 482

QY 1420 LeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArg 1439
Db 483 CTTGATTATAAAGAACATCTTCAGAAGACTGTAAAGAACTACCTGCNAGGAATCAAACG 542

QY 1440 LysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluPro 1459
Db 543 AAAGTGTGTTTGTCTTAAGTATGCTAGGGATCCTCAGATTACTTTGCTAGATGAACCA 602

QY 1460 SerThrGlyMetAspProLys-AlaLys-GlnHisMetTrpArgAlaIleArgThrAlap 1479
Db 603 TCTACAGGTCTGGATCCCAATGCCAAACATGCACATGTGGCATGCAATTCGAACCTGCA- 661

QY 1479 heLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluAlaGluAlav 1499
Db 662 -----TNNAGCGGGCTGCTATTCTGACCACCTCACTATATATGAGGAGGCAGAGGCTG 713

QY 1499 alCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnH 1519
Db 714 TCTGTGATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAAC 773

QY 1519 isLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLys-AspTrpIle 1538
Db 774 ATCTAAAGAGTAAATTTGGAAAAG--NACTTTTTTGGAAATTAATTAACCGGACTGGATA 831

QY 1539 GluAsnLeuGlu-ValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSe 1558
Db 832 GAAAACCTAGAAGCTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAATGCAAG 891

QY 1558 rArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSe 1578
Db 892 CCGTCA-GAAAAGTTTTTCTTCTATTTTGGCTTCTAAAATTAATAAGGAAGATGTTCAAGTC 950

QY 1578 rLeuSerGlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTy 1598
Db 951 CCTTCCCAATCTTTTTTAAGCTGGAAGAGCTAAACATGCT-TTTGCCATTGAAGAATA 1009

QY 1598 rSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluG1 1618
Db 1010 TAGCTTTCT-CAAGCAACATTTGAACAGGTTTTTTGAGAACTCACTAAAGAACAGAGGA 1068

QY 1618 uGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAs 1638
Db 1069 GGAAGATAATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGAA-CGAACACAGAAGA 1127

QY 1638 parqValValPhe 1642
Db 1128 TAGAGTAGTATTT 1140

RESULT 11
AY405473
LOCUS Mus musculus ABCA1 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY405473
VERSION AY405473.1 GI:39761447
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 6600)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
source
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ORIGIN

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QY	449	uLeuSerGluGlyAsnValAsnGlyAsnIleSerPheSerGluIleIleGluProValse	469
DB	1513	GGTCCTTGAGAAATGAATAGATTTCGGATCCCTCGCTGAATGACTCACTGGAACCAAGTGTC	1572
QY	469	rSerGluPheValGlyLysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLy	489
DB	1573	TCCAGAAATTCAGGGGAAAGAAGCCATCAGGATCAAAAAATCTTAAAAAAGACATATCTTGG	1632
QY	489	sLysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnI1	509
DB	1633	AAAGCATGGGAAAGTAGAACCTTGAGAGGTCCTGGGTTTGACATATATGAAGGCCAGAT	1692
QY	509	eThrAlaLeuLysHisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysG1	529
DB	1693	CACGTGCCCTCCTTGGTCAAGTGGAGCTGGGAAACACCCCTGATAAATACACTCAGTGG	1752
QY	529	yLeuCysProProSerAspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAs	549
DB	1753	ACTGTCACCCCTACTACAGGTTCCGTCAACCAATTTAATACACAGACAGTTTCAGAGATGA	1812
QY	549	pGluMetPheGluAlaArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAs	569
DB	1813	CGACTCTGACGCCCTCCTCAGCATCACGGAGTTTGTCCACAGTCCCACGTACAGTTGG	1872
QY	569	pValLeuThrValGluGluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAs	589
DB	1873	CTTTCTCACCCCTCGAGAAAACCTCAGGCTTTTGGCCAAAGATAAAGGAATTTTGGCACA	1932
QY	589	nAsnIleIleGlnGluValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLysAs	609
DB	1933	TGAAGTGGAACAAGAGGTACAACAAGTTCTACAGGACTTAGAAATGGAAAATATTCAAGA	1992
QY	609	pAsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaVa	629
DB	1993	CATTCTTGCTCAGAAATTTAAGTGGCGGACCAAAAAGGAAGTTGACTCTTGGGATGCCAT	2052
QY	629	lLeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSe	649
DB	2053	TTTAGGAGACCCCCAGGTTTGTCTCTGGATGAACCAACTGCTGGGTGGATCCACTCTC	2112
QY	649	rArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsnArgValThrValPheSe	669
DB	2113	GAGGCATCGCATATGGAAACCTACTGAAAGAGAGGAGGAGCAGGAGTATTTGTCTTCAG	2172
QY	669	rThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnG1	689
DB	2173	TACTCAGTTTCATGGATGAGGCTGATATCATGGCCGACAGGAAGGTGTTTATATCCAAATGG	2232
QY	689	yMetLeuLysCysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrAr	709
DB	2233	GAGACTGAAGTGTGCGGCTCTTCTCTGTCTCTGAAGAAGAAATGGGTCATTTGGTATCA	2292
QY	709	gLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeuSerSerLeuValLysG1	729
DB	2293	TCTAAGTTTGCATTTGAATGAAGCGTGTGTATCCAGAGGGTATTAACGTCACCTGGTCAAAA	2352
QY	729	nHisIle-ProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeuP	749
DB	2353	GCACATCTCCGACGCCCGCTGACCAACGCAAGCGAAGAACCGCTTGTCTATATCTTGC	2412
QY	749	roPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeuAspSerHisSerAsnL	769
DB	2413	CCCTGGAAGGACAAACAGTTTCCAGACCTTTACCGGATCTTGTATAGATGTTCTTAACC	2472
QY	769	eGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLysLeuG	789
DB	2473	AAGGCATTGAGGATTATGGCGTTTCCATGACAACCCCTGAATGAGGTGTTCTGAGATTAG	2532

QY	789	luValGluAlaGluIleAspGlnAlaAspTyrSerValPheThrGlnGlnProLeuGluG	809
DB	2533	AAGGGAAGTCGATGGCTGATGAATCAGATGTTGGAATTTGTGGCGCTTACAAAGCGATG	2592
QY	809	luGluMetAspSerLysSerPheAspGluMetGluGlnSerLeuLeuLeuLeuSerGluT	829
DB	2593	GGGCAAGAGACATGGAAGCCTCGTTGAGCTGGAGCAAGTGTGTCTTTA-----GATT	2646
QY	829	hrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGln---MetTyrThrIleA	848
DB	2647	CGTCAGGAAGTCAGTGAGTGGCATGGCGCTGTGGAGGCAGCAGCCTCTGCGCAGCCC-G	2705
QY	848	laLysPheHisPhePheThrLeuLysArgGluSerLysSerValArgSerValLeuLeuL	868
DB	2706	CGAAGGTTTCGCTCTTCAAGCTCAAGATGAACGGAAGAGTCTGTATGACTGTGTTATTGC	2765
QY	868	euLeuLeuIlePhePheThrValGlnIlePheMetPheLeuVal-----HisH	884
DB	2766	TTTTGGGCATTAGCTTTGTCCCCCACTTTTGGAAACATCTCGTCTACAAGGTATACCACA	2825
QY	884	isSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLysP	904
DB	2826	AAAGTTATTTCATGGGG-----CTATCTCCAAGTATGATGTTCTTTTCAC	2870
QY	904	roGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSerAlaAspSerA	924
DB	2871	CAGGACAGCCACCACAGGATCCTCTGACCCACTTACTGGTTCATCAATAGAACAGGTTCAA	2930
QY	924	spIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThrMet-----I	942
DB	2931	GCATCGATAACTTTGTACACGCACCTAAGACAGAGGGCATAGCATAGACCTGGATGCC	2990
QY	942	leAsnAspSerAspTyr-ValSerValAlaProHisSerAlaAlaLeuAsnValMetHis	961
DB	2991	TGGGGAGCCAGAAATGGCACAGAAAGAGCGCGCTGTACAATGGTGTCTATCCCGTGTCTGGGT	3050
QY	962	SerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeuPro	981
DB	3051	GAAGAAAAGGCTCTCAGATTTTCCGTAGCGGTGTAATGCCAAAAGACTAAACTGCTTCCCA	3110
QY	982	IleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThrIle	1001
DB	3111	GTCCTCATGGATATTATTAGCAATGGGCTGCTTGGAAATATTTAACTCTCTGAACGCATC	3170
QY	1002	GlnIleTrpSerThrProPhePheGlnGlu-----IleThrAspIleValPheLysIle	1019
DB	3171	CAGACCCACAGAAAGCACAGTCTTTTGAAAGAACACATGCTTTATGATACGGATTTCATGAGC	3230
QY	1020	GluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPhe	1039
DB	3231	AACGCATTTTTTTCGGATACCA-----GTGGCTGCCAGCCTTCACCCCTTACATT	3278
QY	1040	AlaMet	1041
DB	3279	GCGATG	3284

RESULT 10

U66672	U66672	1346 bp	linear	HTC 23-JUL-2001
LOCUS	Homo sapiens clone EST90625 mRNA sequence.			
DEFINITION	U66672			
ACCESSION	U66672.1	GI:1906557		
VERSION	HTC.			
KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 1346)			
AUTHORS	Allikmets, R., Gerrard, B., Hutchinson, A. and Dean, M.			
TITLE	Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed sequence tags database			
JOURNAL	Hum. Mol. Genet. 5 (10), 1649-1655 (1996)			
MEDLINE	97049974			

Db 1325 GAGTTATATCTGTGATGGAGCCCTGTTGATTTCAGATCCCATGTAGTATGGCTATGCA 1384

QY 1114 ProSerValIleLeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThr 1133

Db 1385 TCATCTCTCATATTTCATGACTATGTGATTTCATTTCATTTTCGTAATGGCAGAAAAAT 1444

QY 1134 LysGluPheTrpSerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGlu 1153

Db 1445 AGTGGCATCTGGTCATTTTCTCTCCTAATTGTCACCATCTTCTTTATCATTTGCTACTGAC 1504

QY 1154 IleThr-----PhePheMetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCys 1171

Db 1505 ATAAATGAATACGGCTTTCTAGAGCTGCTAATCTGCACCTTTTTA----- 1549

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Db 1550 -----GTCCCTCCTTTTCACACTGATTTGGCTCACTATTGATTTTTCCTGAGTTTCTCTAT 1603

QY 1192 LysAsnValArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSer----- 1208

Db 1604 GACTCTGTG-----GATTACTTGGGAACGTCAGAA 1633

QY 1209 -----ValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePhe 1223

Db 1634 TCTCAACTCGTATTTCCTGGCATGTGATACCTTACCTTCACTTCTCTCTTTTCTTTTC 1693

QY 1224 LeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAspProphePhe 1243

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QY 1264 GluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCys 1283

Db 1808 GAGGATGAAGATGTTTCAGATGGAAGAGTGAAGAACACACGGCGCCATGGCTACCCCTACAG 1867

QY 1284 CysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLys 1303

Db 1868 ACTGATGAGAAACCGATCATCTATTCGAAGCTGTCTCGGAAGGAATATATAGGCAGAACG 1927

QY 1304 AspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSerPheCysVal 1323

Db 1928 AAAAGTGCTTTTCCAAATGAAGAAAGATCGCCACGAGGAACATCTCTCTGTGT 1987

QY 1324 LysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIle 1343

Db 1988 AAAAAAGGTGAAGTCTTAGGCTCTTAGGACACATGGAGCTGGCAAAAGTACAACAATT 2047

QY 1344 AsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSer 1363

Db 2048 AGCATGATAACAGGAGACACATACCAACCGCAGGTGAGTGTGTTT----- 2095

QY 1364 SerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsn 1383

Db 2096 ---AAAGGGAGCGGTGGGGGTGCTGCCCTCGGATTCTTGGGTACTGCCCTCAGGAGAAC 2152

QY 1384 ProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGly 1403

Db 2153 GTGCTGTGGCCCCAACCTGACACTGAAGGAACACCTGGAGTTGTATGCTGCTGTGAAGGG 2212

QY 1404 MetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLys 1423

Db 2213 CTGAAGAAAAAGGATGCTGTGGTCACTACACACCGGTGGTGAATGCCCTTAAACTGCAG 2272

QY 1424 GluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPhe 1443

Db 2273 GACCACCTTGAAGGCTCTTGTTCAGGACCTTGTTCAGAGGAGTGAAGAGAAAGCTGTGTTT 2332

QY 1444 AlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMet 1463

Db 2333 GTGCTGAGCATCCTGGGGAACCTCCTGTGTGTTACTTCTGGATGAGCCATCGACTGGGATG 2392

QY 1464 AspProLysAlaLysGlnHisMetTyrArgAlaIleArgThrAlaPheLysAsnArgLys 1483

Db 2393 GACCCCGAAGGGCAGCAGCAAAATGTGGCAGGCGATCCGAGCCACTTTCACAAAACACAGAG 2452

QY 1484 ArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgVal 1503

Db 2453 CGGGCGCCCTCCTGACCACTTACATGGCAGAGCAGAGGCTGTGTGTGACCGTGTG 2512

QY 1504 AlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLys 1523

Db 2513 GCCATCATGGTGTCTGGAGGCTGAGGTGCATGGTTCTATCCAACATCTGAAGAGCAA 2572

QY 1524 PheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluVal 1543

Db 2573 TTGGCAAGATTACCTCTGAGATGAAGGTGAAG-----ACCCCTCACAGGTG 2623

QY 1544 AspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGlnSerPhe 1563

Db 2624 GAACCCCTGAACACGAGATCATGAGACTGTTCCTCCAGGCTGCTCGGCAGAAAGGTAC 2683

QY 1564 SerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhe 1583

Db 2684 TCCTCTCTGATGGTCTATAAGTTGCCTGTTGAGACGTACGACCTTTATCCGAGGCTTTC 2743

QY 1584 PheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAla 1603

Db 2744 TTCAAAATTGGAGAGATTGAAGAGAATTTTGACCTGGAAGATACAGCCTCTCACAGTCT 2803

QY 1604 ThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAspAsnSerCys 1623

Db 2804 ACTCTGGAGCAGGTCTCTCTGGAGCTCTCCAAGAGCAGGAGCTGGACGACTTTGGCGAA 2863

QY 1624 GlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAsp 1638

Db 2864 GAAGCCAAATTCCTCAGTGAATGAAGACTCCTCCACACAGGAAGAG 2908

RESULT 8

BC037309 3357 bp mRNA linear HTC 04-MAR-2003

LOCUS Homo sapiens, clone IMAGE:5262251, mRNA.

DEFINITION BC037309

ACCESSION BC037309.1 GI:233336952

VERSION HTC.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 3357)

Strausberg,R.

Direct Submission

Submitted (03-SEP-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

AUTHORS

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK

COMMENT

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 73 Row: f Column: 14

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 6005700

Db 601 GAAGCCATCCAGACCTGGAGTACCCCGTTTCATTCAAGAAATTACTGACATTGTTTTTAAA 660

Qy 1019 ILeGluLeuTyrPheGlnAlaLeuLeuGlyIleIleValThrAlaMetProProTyr 1038

Db 661 ATTGAGCTATATTTTCAAGCAGCTTTGCTTGGAAATCATCTGTACTGCAATGCCACCTTAC 720

Qy 1039 PheAlaMetGluAsnAlaGluAsnHisLysIleLeuAlaTyrThrGlnLeuLysLeuSer 1058

Db 721 TTTGCCATGGAAATGCAGAGAAATCATAGATCAAGCTTATACCTCAACTTAAACTTCG 780

Qy 1059 GlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePhe 1078

Db 781 GGTCTTTTGCCATCAGCCTATTGGTTGGACAAGCTGTGTGGATATTCCTTGTGTTTT 840

Qy 1079 IleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyr 1098

Db 841 GTTGTTCTGATTTTGATGCTGGGAAGTTTATTTGCAATTCATCAGGACTGTATTTTAT 900

Qy 1099 ThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeu 1118

Db 901 CCTGCAAAATTTCTTGCTGTGTGTTTTCCTCATTCCTTATGTGCCCTCCGTCATTCTG 960

Qy 1119 PheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSer 1138

Db 961 TTCAGCTACATAGCTTCGTTCACTTTCAAGAAAATTTAAATACCAAGGAATTTGGTCA 1020

Qy 1139 PheIleTyrSerValAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMet 1158

Db 1021 TTTATCTATTCTGTGACCGCATGGCTTGTGTGGCAATCACGGAACAACCTTTCTTCTG 1080

Qy 1159 GlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrPro 1178

Db 1081 CAATATGCAGTTACGGCTGTCTTTTCATTACACCTTCTGCATAGCCATTCCAATCTACCT 1140

Qy 1179 LeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnVal 1198

Db 1141 CTCCTGGGTTGTCTGATTCTTTTCATAAAGGGTTCTTGAAGAATATGCCAAAAAATGAG 1200

Qy 1199 AspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCys 1218

Db 1201 AATACCTACAATCCCTGGGATAGACTTTTAGTTGCTGTAATCATGCCCTACCTGCAGTGT 1260

Qy 1219 ValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGlyArgSerIleArg 1238

Db 1261 ATACTGTGGATTTTCCTCTTACAACACTATGAGAAAATACATGGAGGCAGATCTATAAGA 1320

Qy 1239 LysAspPropPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluPro 1258

Db 1321 AAGGATCCATTTTTCAGGSCCTTTTCACAAAAGSCCAAAATAAGAAGTTTCCAGAACCA 1380

Qy 1259 ProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeu 1278

Db 1381 CCCATCAATGAGGATGAGATGAGATGTCAAGCTGAAAGACTGAAGCTTAAAGAGCTG 1440

Qy 1279 MetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGlu 1298

Db 1441 ATGGGTTGCCAGTGTGTGAGGAGAAGCCAGCCATTATGGTATGCAATTTGCATAAAGAG 1500

Qy 1299 TyrAspAspLysLysAspPheLeu 1306

Db 1501 TATGATGACAAGAAAGATTTTCTT 1524

RESULT 7

AK029256

LOCUS

DEFINITION

AK029256 4119 bp mRNA linear HTC 18-SEP-2003
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4831444G21 product:similar to CDNA FLJ32506 FIS, CLONE SMINT100042, WEAKLY SIMILAR TO ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 3 (FRAGMENT) [Homo sapiens], full insert sequence.

ACCESSION

AK029256

VERSION

AK029256.1

KEYWORDS

HTC; CAP trapper.

SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS

TITLE
JOURNAL
MEDLINE
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REFERENCE
AUTHORS

Mus musculus (house mouse)
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

99279253
10349636

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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20499374
11042159

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

20530913
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 4119)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

Location/Qualifiers
1. 4119

FEATURES

Source


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QY 1469 nHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaIleLeuTh 1489
Db 4090 GCAAATGTGGCAGGCTATCCAGGCCACCTTTTCAAACACAGAACGGGGCCCTCTGAC 4149

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QY 1509 yGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPh 1529
Db 4210 GAGGCTGAGGTGTATTGGATCCATCCACATCTCAAAAGCAAATTTGGCAAAGATTACCT 4269

QY 1529 eLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArgGl 1549
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QY 1549 uIleGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTy 1569
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QY 1589 aLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPh 1609
Db 4441 TAAACAGAGCTTTGACCTGGAGAGTACAGCCTTTTCAGTCCACCTCGGAGAGGTCTT 4500

QY 1609 eValGluLeuThrLysGluGlnGlu-----GluGluAspAsnSerCysGlyTh 1625
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QY 1625 rLeuAsnSerThrLeuTrpTrpGlu 1633
Db 4547 -CTTGATCCCTCAGTCAAGTGAAG 4570

RESULT 5
LOCUS AY414283 4620 bp DNA linear GSS 17-DEC-2003
DEFINITION Pan troglodytes ABCA9 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY414283
VERSION AY414283.1 GI:39770245
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 4620)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 4620)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source
location/Qualifiers
1..4620
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>4620
gene
```

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ORIGIN
/gene="ABCA9"
/locus_tag="HCM5172"

Alignment Scores: 6.52e-242 Length: 4620
Pred. No.: 2319.00 Matches: 566
Score: 2319.00
Percent Similarity: 49.79% Conservative: 251
Best Local Similarity: 34.49% Mismatches: 678
Query Match: 27.52% Indels: 146
DB: 29 Gaps: 28

US-10-090-458-5 (1-1642) x AY414283 (1-4620)
QY 6 ArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLysAsnTyrIleuIleLys 25
Db 10 AGATGCATGAGCGTGGGTGAGCAACGCTGGGCTCTTCTCTGCAAGAACTGTCTCAAAAA 69
QY 26 CysArgThrLysLysSerSerValGlnGluIleLeuPhePro---LeuPhePheLeuPhe 44
Db 70 TGGAGCAATGAAAAGANNNNNNNNNGAATGGCTCTTTTCATTTCTCTGGTACTGTTT 129
QY 45 TrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGluValProAsnIle 64
Db 130 CTGTACCTATTTTCTCCAAATTTACATCAAGTTTCATGACACTCCTCAAATGCTTCAATG 189
QY 65 GluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProVal 84
Db 190 GATCTGGGACGTGTAGATAGTTTAAATGATATACTAATATGTTATTGCAATTTGCACCTGAA 249
QY 85 ThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeuProAspValIle 104
Db 250 TCCAAAACTACCCAGAGATAATGAACAAAGTGGCTTCAGCCCCATTCCTTAAAGGAAGA 309
QY 105 IleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLysProSer 124
Db 310 ACAATCATGGGTGGCTGTGATGAAAAAAGCATGGATGCAATTTGGATTGAACTATTCAATA 369
QY 125 AsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArgPhe---PhePro 143
Db 370 GACGAGTGAGAGTCACTTTACTGATACCTTCTCCTACCATTGGAAGTTTTCTTGGGGA 429
QY 144 AspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCys----- 159
Db 430 CATAGAATCCCATGATGAAAGAGACACAGAGACCATTCACTCACTGTCAGAGTGAAT 489
QY 160 ---SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAla 178
Db 490 GAAAAAATGAAGTGTGAAGGTTCAAGATTCTGGGAGAAAGGCTTTGTAGCTTTTCAAGCT 549
QY 179 SerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGlu 198
Db 550 GCCATTAATGCTGCTATCAFAAGANNNNCAACAATCATTCAGTCACTGATGGAACAGCTGATG 609
QY 199 SerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArg 218
Db 610 TCAGTTACTGGGTACATATGAAGATATTACCTTTTGTGCCCCAAGGAGGAGTTGCAACT 669
QY 219 GlyValIleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIle 238
Db 670 GATTTTTCATTTCTTTTGGCATTTATTTCTTTTCTACATTTATATACATATGATATCAGTC 729
QY 239 HisIleValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHis 258
Db 730 AATGTTACACAAGAAAGACAA--TACATTACGTCATGATGACAAATGATGGGACTCCGA 786
QY 259 AspThrAlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSer 278
Db 787 GAGTCAGCATTTCTGGCTTCTCCGGGTTTGATGTATGGTGGCTTCATCCTTATCATGGCC 846
QY 279 LeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleVal 298
Db 847 ACTTTAATGGCTCTTATTGTAAATACTGCACAAATTCGTCCTGCTGCTGCTGCTGCTGCTG 906
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Db 2158 GGCCTTTCCATGACAAACCTGAATGAGGTGTTCTCTGAAGTTAGAAG----- 2203
QY 794 eAspGlnAlaAspTyrSerValPheThrGlnGlnProLeuGluGluMetAspSerLy 814
Db 2204 -----GATGTTGGAATTTGTGGCGCTTACAAAGCGATGGGGCAAGACATGGA 2253
QY 814 sSerPheAspGluMetGluGlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuVa 834
Db 2254 AAGCCTCGTTGAGCTGGAGCAAGTGTGTCTTWA-----GATTCGTACGAAAGCTCAGT 2307
QY 834 lSerThrMetSerLeuTrpLysGlnGlnMetTyrThrIleAlaLysPheHisPhePheTh 854
Db 2308 GAGTGGCATGGCGCTGTGGAGGCAGCAGCTCTGCGCAGTCGCGAAGGTTCTTCAA 2367
QY 854 rLeuLysArgGluSerLysSerValArgSerValLeuLeuLeuLeuLeuLeuPhePheTh 874
Db 2368 GCTCAAGAATGAACGGAAAGTCTGATGACTGTGTATTGCTTTTGGCATTAGCTTTGT 2427
QY 874 rValGlnIlePheMetPheLeuVal-----HisHisSerPheLysAsnAlaVa 890
Db 2428 CCCCCAACTTTTGGAAACATCTCGTCTACAAAGGTATACACAAAGTTATTTCATGGGGG-- 2485
QY 890 lValProIleLysLeuValProAspLeuTyrPheLeuLysProGlyAspLysProHisLy 910
Db 2486 -----CTATCTCCAAGTATGTTATTTCTTCCACGAGACACCCACACAGGA 2532
QY 910 sTyrLysThrSerLeuLeuGlnAsnSerAlaAspSerAspIleSerAspLeuIleSe 930
Db 2533 TCCTCTGACCCACTTACTGTCATCAATAGAACAGGAGCAAAATCGATGACTTTATACA 2592
QY 930 rPhePheThrSerGlnAsnIleMetValThrMet-----I-I 942
Db 2593 TTCACTGGAAACAACAGACATAGCTTTGGAAAGTTGATGCCCTTTGGGACTAGAAATGGCAC 2652
QY 942 eAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMetHisSe 962
Db 2653 CGAGGACAGTCAGTAT-----AATGGAGCTATCATCTCTATCAGGTGA 2694
QY 962 rGluLys----- 964
Db 2695 CGAGAAAGNN 2754
QY 965 -----AspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLe 980
Db 2755 NNN 2814
QY 980 uProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluTh 1000
Db 2815 NNN 2874
QY 1000 rIleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGl 1020
Db 2875 CGCATTTTCTGGATACCA----- 2893
QY 1020 uLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProproTyrPheAl 1040
Db 2894 -----GTGGCTGCCAGCCTCACCCCTTACATTGC 2922
QY 1040 aMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLe 1060
Db 2923 GATGGGCAGCATCAGTGACCACCAAAAAAAGTTCTTTCCAGCTGTGGACTTCAGGCCT 2982
QY 1060 uLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIl 1080
Db 2983 TTACCCGTCTGCTTACTGGTGTGGACAGGCTCTGGTGACATTCCCATATACTTCTCTCAT 3042
QY 1080 eLeuIleLeuMet-----LeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTy 1098
Db 3043 TCTCTTTCTCATGCAATAATGGACAGTGTT-----TTTAG 3078
QY 1098 rThrValLysPheLeuAlaVal-----ValPheCysLeuIleGl 1111
Db 3079 TTCTGAGGAGTTTATATCTGTGATGGAGAGCCTGTTGATTTCAGATCCCATGTTAGTTGG 3138

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DEFINITION genomic survey sequence.
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VERSION AY414284.1 GI:39770246
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 4594)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 4594)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4620)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 4620)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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Percent Similarity: 56.36% Conservative: 289
Best Local Similarity: 38.77% Mismatches: 567
Query Match: 33.78% Indels: 150
DB: 29 Gaps: 30
US-10-090-458-5 (1-1642) x AY414282 (1-4620)
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Db 10 AGACGCATGAGCGTGGTGAGCAACATGGGCTCTTCTGCAAGAACTGCTCAAAAAA 69
QY 26 CysArgThrLysLysSerSerValGlnGluIleLeuPhePro---LeuPhePheLeuPhe 44
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Qy 1100 lLysPheLeuAlaValPheCysLeuIleGlyTyrValProSerValIleLeuPheTh 1120

Db 3547 AAAATTTCTGTGTGGTGTGCTTTCCTCATTTGCTTATGTGCCCTCCGTCATCTGTTTCCAC 3606

Qy 1120 rTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIl 1140

Db 3607 GTACATAGCTTCGTTTCACITTCAGAAATTTTAAATACCAAGGAATTTTGGTCATTTAT 3666

Qy 1140 eTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTy 1160

Db 3667 CTATTTCTGTGACCGCATTTGGCTTGTGTGGCAATCATCGGAAACAACCTTTCTTCTGCAATA 3726

Qy 1160 rThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLe 1180

Db 3727 TGCAGTTACGGCTGTCTTTCATTACACCTTCTGCTAGCCATTCCAATCTACCTCTCCT 3786

Qy 1180 uGlyCysLeuIleSerPheIleLysIleSerTyrLysAsnVal 1194

Db 3787 GGGTTGCTGATTTTCTTTTCAAAAGGGTTCTTTGGAAGAATATG 3829

RESULT 3
AY414282
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

AY414282 4620 bp DNA linear GSS 17-DEC-2003
Homo sapiens ABCA9 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY414282
AY414282.1 GI:39770244
GSS.

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1..3831
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="B230352G14"
/sex="male"
/tissue type="corpora quadrigemina"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"

misc_feature 1..3831
/note="ATP-BINDING CASSETTE PROTEIN homolog [Homo sapiens] (SPTR|CAB93535, evidence: FASTY, 89.4%ID, 76.5%length, match=3750)"

ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 3831
Score: 5571.00 Matches: 1076
Percent Similarity: 94.90% Conservative: 58
Best Local Similarity: 90.04% Mismatches: 60
Query Match: 66.12% Indels: 1
DB: 11 Gaps: 0

US-10-090-458-5 (1-1642) x AK046203 (1-3831)

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Qy 21 AsnTyrLeuIleLysCysArgThrLysLysSerValGlnGluIleLeuPheProLeu 40
Db 307 AATTACCTAATTAAATGCAGGACTAAAAAAGTAGTGTTCAGGAAATCTTTTCTCTCTA 366

Qy 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 367 TTTTCTTATTTTGGCTGATATTAGTTAGCATGATGCATCCAAATAAGAAATATGAAGAG 426

Qy 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 427 GTATCTGATATAGAGCTCAGCCCTATGGACAAATTCAGCCTTTCCAAACGTTATTCTTGA 486

Qy 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 487 TACACTCCCGTGACTAACATTACAAGCAGCATTATGCAGAGGGTTTCTACCGATCATCTT 546

Qy 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
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Qy 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 607 TCTAAGTCCAGCAACTTCGTAGGTGTGGTTTTCAAAGACACCATTGTCCTGAACCTCGT 666

Qy 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160

Db 667 TTTTTCCTGAAATGATTCCAGTGTCTTCTATTATATGAATTCAGAGAGGCTGTTC 726

Qy 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 727 AAGACATGTGATGCTGCTCAGTACTGTCTTTGGGGTTTACAGTTCTGCAGGCATCGATA 786

Qy 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
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Qy 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
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Qy 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db 907 ATCCTCATCTACCTCGTCATAGCCTTCTCGCCCTTCGGCTACTTTCCTGGCAATCCACATC 966

Qy 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 967 GTGGCAGAAAAAGAAAGAAAGTTAAAGGAATTTTAAAGATAATGGGACTTCATGACACT 1026

Qy 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
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Qy 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
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Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
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Qy 441 Ser-LysSerLysArgAsnTyrGluGluLeuSerGlyAsnValAsnGlyAsnIleSe 460
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Qy 480 eSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLe 500
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Qy 500 userPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520

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QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 621 TTTTTCCTGAAATGATCCAGTGTCTTCTATTATATGAATTCAAAGAGAGGCTGTTCA 680
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 681 AAGACATGTGATGCTGCTCAGTACTGGTCTTTGGGGTTTACAGTTCTCGAGGCATCGATA 740
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
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QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 801 AAAGCTGTGATCATGGAGAGCGCGCTGTTGTGGAGATTGACACCTTCCCGCGAGGGGTC 860
QY 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
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QY 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 1161 TTTAAAAAATCAAAACACGTGGGAGTCGTGAGTTTTTGTACCCGTGGTGTGGATTT 1220
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QY 361 PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
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QY 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 1341 AATGAGGGTCCCTTATTCTAATTTGACTGAAGTCCCTATCCTCTAATATTACTATT 1400
QY 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
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QY 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
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QY 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 1761 AGCACACTGATGAATATTTCTGTGTGGACTGTGTCACCCCTCTGTATGGGTTTGTCTTATA 1820
QY 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
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Db 1881 TGTCCGCACTCAGATATAAACTTTGATGTTCTGACAGTAGAAGAAAAATTTATCAATTTT 1940
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QY 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
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QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660
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QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
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QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
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QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
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QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
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QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
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Db 2721 AAGCAGCAAGTGTCTACGATTGCAAGATTTTCATTTCTCTCATTTGAACCGAGAAAGCAAA 2780

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 12, 2004, 21:03:35 ; Search time 5792 Seconds
(without alignments)
8465.763 Million cell updates/sec

Title: US-10-090-458-5
Perfect score: 8426
Sequence: 1 MSTAIREVGWVRQTRTLK.....CGTLNSTLWERTQEDRVVF 1642
Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Command line parameters:
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-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOCPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10090458 @CGN 1 1 3643 @runat_08042004_121553_25490 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_estfun:*

15: em_estom:*

16: em_gss_hum:*

17: em_gss_inv:*

18: em_gss_pln:*

19: em_gss_vrt:*

20: em_gss_fun:*

21: em_gss_mam:*

22: em_gss_mus:*

23: em_gss_pro:*

24: em_gss_rod:*

25: em_gss_phg:*

26: em_gss_vrl:*

27: gb_gss1:*

28:

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	5815	69.0	3950	11	AK047188	AK047188 Mus muscu
2	5571	66.1	3831	11	AK046203	AK046203 Mus muscu
3	2846	33.8	4620	29	AY414282	AY414282 Homo sapi
4	2785	33.1	4594	29	AY414284	AY414284 Mus muscu
5	2319	27.5	4620	29	AY414283	AY414283 Pan trogl
6	2313	27.5	1529	11	AK034961	AK034961 Mus muscu
7	2024.5	24.0	4119	11	AK029256	AK029256 Mus muscu
8	1837	21.8	3357	11	BC037309	BC037309 Homo sapi
9	1688.5	20.0	3300	11	AK085555	AK085555 Mus muscu
10	1677	19.9	1346	11	U66672	U66672 Homo sapien
11	1471	17.5	6600	29	AY405473	AY405473 Mus muscu
12	1444	17.1	6606	29	AY405471	AY405471 Homo sapi
13	1427	16.9	850	14	CD250953	CD250953 AGENCOURT
14	1396	16.6	6606	29	AY405472	AY405472 Pan trogl
15	1382	16.4	2844	11	AK031843	AK031843 Mus muscu
16	1351.5	16.0	872	13	BQ722933	BQ722933 AGENCOURT
17	1270	15.1	771	12	BG564439	BG564439 602584385
18	1251	14.8	809	11	BC029426	BC029426 Homo sapi
19	1216.5	14.4	926	13	BU146839	BU146839 AGENCOURT
20	1208	14.3	800	13	BU750944	BU750944 CH3#036_H
21	1167	13.8	3890	11	BC053340	BC053340 Mus muscu
22	1152	13.7	769	14	CD349566	CD349566 UI-M-FY0-
23	1147	13.6	756	12	BG435656	BG435656 602506942
24	1107	13.1	724	14	CB962917	CB962917 AGENCOURT
25	1100	13.1	633	14	CA773136	CA773136 im60b03.Y
26	1078	12.8	670	12	BG570726	BG570726 602591840
27	1069	12.7	768	13	BU853701	BU853701 AGENCOURT
28	1066	12.7	961	14	CD242938	CD242938 AGENCOURT
29	1063	12.6	713	14	CF745072	CF745072 UI-M-GV0-
30	1058	12.6	623	14	CA773849	CA773849 im58a04.Y
31	1057	12.5	642	14	CA773183	CA773183 im60g04.Y
32	1055	12.5	773	13	BQ441353	BQ441353 AGENCOURT
33	1053	12.5	664	14	CB044826	CB044826 NISC_gc06
34	1051	12.5	4585	11	AK089794	AK089794 Mus muscu
35	1049	12.4	627	14	CD767029	CD767029 AGENCOURT
36	1048.5	12.4	772	12	BG173854	BG173854 602333913
37	1036	12.3	614	14	CA771132	CA771132 io71b12.X
38	1024	12.2	687	10	BB341620	BB341620 BB341620
39	1009.5	12.0	3199	11	BC047342	BC047342 Homo sapi
40	993	11.8	658	14	CD351000	CD351000 UI-M-GI0-
41	992	11.8	627	10	BB192788	BB192788 BB192788
42	991	11.8	702	10	BB099251	BB099251 BB099251
43	981.5	11.6	650	10	BB190957	BB190957 BB190957
44	964	11.4	581	14	CA941420	CA941420 ir34h12.X
45	961	11.4	578	13	BU069128	BU069128 im58a04.X

ALIGNMENTS

RESULT 1
AK047188
LOCUS
DEFINITION
AK047188 3950 bp mRNA linear HTC 20-SEP-2003
Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:B930033A02 product:ATP-BINDING CASSETTE
PROTEIN homolog [Homo sapiens], full insert sequence.
ACCESSION
AK047188
VERSION
AK047188.1 GI:26338625
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Qy	1524	PheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeu-----	1541
Db	6367	TTTGAGATGGCTATATCGTCACAATGAAGATCAAAATCCCCGAAGGACGACCTGCTTCCT	6426
Qy	1542	GluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGlu	1561
Db	6427	GACCTGAACCTGTGGAGCAGTTCTTCCAGGGGAACCTCCAGGCAGTGTGCAGAGGGAG	6486
Qy	1562	SerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGln	1581
Db	6487	AGGCACTACAACATGCTCCAGTCTCCAGGTCTCCTCC-----TCCTCCCTGGCGAGG	6537
Qy	1582	SerPhePheLysLeuGluGlnAlaLysHisAlaPheAlaIleGluGluTyrSerPheSer	1601
Db	6538	ATCTTCAGCTCCTCTCTCCACAAGGACAGCCTGCTCATCGAGGAGTACTCAGTCACA	6597
Qy	1602	GlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGlu	1618
Db	6598	CAGACCACACTGGACCAGGTGTTTGTAAATTTTGCTAAACAGCAGACTGAA	6648

Search completed: April 13, 2004, 04:19:02
Job time : 781 secs

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QY 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
Db 4462 ACGGACAGGAACATCTCCGACTTCTTGTA----- 4491
QY 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960
Db 4492 -----AAAACGTATCCTGCTCTTATAAGAAGCAGCTTAAAGACGAAATTTCTGG 4539
QY 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
Db 4540 GTCAATGAACAGAGGTATGGAGAAATTTCCATTGGAGGAAAGCTCCCAAGTC-----GTC 4593
QY 981 ProIle-----LeuValAsnIleIleSerAsnTyr----- 990
Db 4594 CCCATCAGGGGGAAGCACTTGTGGGTTTTTAAGCGACCTTGGCCCGATCATGAATGTG 4653
QY 991 -----TyrLeuTyrHisLeu 995
Db 4654 AGCGGGGGCCCTATCACTAGAGAGGCCCTCTAAAGAAATACCTGATTTCTTAAACATCTA 4713
QY 996 AsnValThrGluThrIleGlnIleTrp----- 1004
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QY 1031 IleVal-----ThrAlaMetProProTyrPheAlaMetGluAsnAlaGluAsn 1046
Db 4939 TCGGTGATTTTCTCCATGTCCTTCGTCGCCAGCAGCTTGTCCCTTTATTTGATCCAGGAG 4998
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QY 1087 SerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPheLeuAlaValVal 1106
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QY 1147 AlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyrThrIleAla----- 1163
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QY 1164 -----ThrIleLeuHisTyr----- 1168
Db 5317 TTCATCTTGGAAATTATTGAGAAATAACCGGACGCTGCTCAGGTTTCAACGCCGCTGCTGAGG 5376
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QY 1202 -----AsnPro-----TrpAspArgLeuSerValAlaValIleSerProTyrLeuGln 1217
Db 5482 TCTGCAAATCCGTTCCACTGGGACCTGATTGGGAAGAACCTGTTTGGCATGGTGGTGGAA 5541
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RESULT 15
US-09-032-438C-5
; Sequence 5, Application US/09032438C
; GENERAL INFORMATION:
; APPLICANT: Rattner, Amir
; APPLICANT: Sun, Hui
; APPLICANT: Lupski, James R.
; APPLICANT: Nathans, Jeremy
; APPLICANT: Anderson, Kent L.
; APPLICANT: Leppert, Mark
; APPLICANT: Dean, Michael
; APPLICANT: Singh, Nanda
; APPLICANT: Shroyer, Noah F.
; APPLICANT: Smallwood, Philip M.
; APPLICANT: Allikmets, Rando
; APPLICANT: Lewis, Richard A.
; APPLICANT: Li, Yixin
; TITLE OF INVENTION: Nucleic Acid And Amino Acid Sequences For ATP-Binding Cassette
; TITLE OF INVENTION: Transporter And Methods Of Screening For Agents That Modify
; TITLE OF INVENTION: ATP-Binding Cassette Transporter
; FILE REFERENCE: BYLR-0065
; CURRENT APPLICATION NUMBER: US/09/032,438C
; CURRENT FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: US 60/039,388
; PRIOR FILING DATE: 1997-02-27
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; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 6705
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-032-438C-5

Alignment Scores:
Pred. No.: 5,53e-123 Length: 6705
Score: 1363.00 Matches: 458
Percent Similarity: 42.62% Conservative: 325
Best Local Similarity: 24.93% Mismatches: 630
Query Match: 16.18% Indels: 424
DB: 5 Gaps: 59

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Db 2795 ATGCTGTTTRACACCTTCCTCTATGGGTGATGACCTGGTACATTGAGGCTGTCTTTCCA 2854
QY 423 GlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp----- 440
Db 2855 GGCAGTAGCGGAATTCCAGGCCCTGGTATTTTCTCTGACCAAGTCTCTACTGGTTTGGC 2914
QY 441 -----SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsn 454
Db 2915 RAGGAAAGTGATGAGAGAGCCACCCTGGTTCCAAACAGAGAGAAATTCAGAA----- 2968
QY 455 ValAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPheValGly 474
Db 2969 -----ATCTGCATGGAGGAG-----GAACCCACCCTTG----- 2998
QY 475 LysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnVal 494
Db 2999 AAGCTGGCGTGTCCATTTCAGAACCTGGTAAAGTCTAC---YGAGATGGGATGAAGGTG 3055
QY 495 GluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGly 514
Db 3056 ---GCTGTCGATGGCCTGGCCTGCAATTTTATGAGGGCCAGATCAVCTCCTTCTCTGGGC 3112
QY 515 HisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSer 534
Db 3113 CACAATGGAGYGGGRAAGACGACCACCATGTCTCAATCCTGACCGGTTGTTCCTCCCGACC 3172
QY 535 AspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAla 554
Db 3173 TCGGCACYGCCTACATCCTGGGAAAGACATTCGC-----TCTGAGATGAGCACCATC 3226
QY 555 ArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGlu 574
Db 3227 CGGCAGAACCTGGGGTCTGTCTCCCGACATAACGTGCTGTTTGACATGCTGACTGTCGAA 3286
QY 575 GluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGlu 594
Db 3287 GAACACATCTGGTTCTATGCCCGCTTGAAAGGGCTCTCTRAGAAGCAGCTGAAGCGGAG 3346
QY 595 ValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLys---AspAsnGlnAlaLys 613

Db 3347 ATGGAGCAGATGGCCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAGCAAAACAAGC 3406
QY 614 LysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnPro 633
Db 3407 CAGCTGTAGGTGAATCGAGAGAAAGCTATCTGTGGCCTTGGCCTTTGTGGGGGATCT 3466
QY 634 LysIleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleVal 653
Db 3467 AAGTKGTCAATTCTGGATGAACCCACACAGCTGGTGTGGACCCCTTACTCCCGCAGGGGAATA 3526
QY 654 TrpAsn---LeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPhe 672
Db 3527 TGGAGCTGCTGTGAAATACCGACAA--GGCCGACACCATATTATTCTCTACACACCAC 3583
QY 673 MetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLys 692
Db 3584 ATGGATGAAGCGGACGTCCTGGGGKACAGGATTGCCATCATCTCCATGGGAAGCTGTGC 3643
QY 693 CysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMet 712
Db 3644 TGTGTGGCTCCTCCCTGTTTCTGAAGAACCAGTGGGAACAGGCTACTACCTGACCTTG 3703
QY 712 ----- 712
Db 3704 GTCAAGAAAGATGTGGAATCCTCCTCAGTTCCTGCAGAAACAGTAGTAGCACTGTGTCA 3763
QY 713 TyrIleAspLysTyrCysAla----- 719
Db 3764 TACCTGAAAAGAGGAGGACAGTGTTTCTCAGAGCAGTTTCTGATGCTGGCCTGGGACGGAC 3823
QY 720 -----ThrGluSerLeuSerSerLeuValLysGlnHis 730
Db 3824 CATGASAGTGACACGCTGACCATCGATGTCTCTGTATCTCCAACCTCATCAGGAAGCAT 3883
QY 731 IleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeuProPhe 750
Db 3884 GTGTCTGAAGCCCGGCTGTGGAAAGACATAGGGCATGAGCTGACCTATGTGTGCCATAT 3943
QY 751 LysAspMetAspLys-----PheSerGlyLeuPheSerAlaLeuAspSerHis---Ser 767
Db 3944 GARGCTGCTAAGGAGGGAGCCCTTTGTGGAACCTTTTCATGAGATTGATGACCGRCTCTCA 4003
QY 768 AsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLys 787
Db 4004 GACCTGGGCATTTCTAGTTATGGCATCTCAGAGACGACCCCTGGAAGAAATATTCCTCAAG 4063
QY 788 LeuGluValGluAlaGluIleAsp----- 795
Db 4064 GTGCCCGAAGAGAGATGGGGTGGATGCTGAGACCTCAGATGGTACCTTGGCCAGCAAGACGA 4123
QY 796 -----GlnAlaAspTyrSerValPheThrGln----- 804
Db 4124 AACAGCGGGCCCTTCGGGGACAAGCAGAGAGCTGTCTTCGCCCTTCACTGAAGATGATGCT 4183
QY 805 ---GlnProLeuGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeu 823
Db 4184 GCTGATCCAAATGATTCTGACATAGACCCAGAAATCC-----AGAGAGACAGACTTG 4234
QY 824 LeuIleLeuSerGluThrLysAlaSerLeu---ValSerThrMetSerLeuTrpLysGln 842
Db 4235 CTCAGTGGGATGGATGGCAAAGGRTCCCTACCAGGTGAAAGGCTGGAAACTTACACAGCAA 4294
QY 843 GlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLysSerVal 862
Db 4295 CAGTTTGTGGCCCTTTTGTGGAAAGAGACTGCTAATTCAGACGGAGTCGGAAGGATTT 4354
QY 863 ArgSerValLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuVal 882
Db 4355 TTTGCTCAGATTGTCTTGCAGCTGTGTTTGTCTGTCATTCGCCCTTGTGTTCAGCCTGATC 4414
QY 883 HisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeu----- 899

Db 5823 GATGAAGATGAAGATGTAGCGCGGAAAGACAGAGAATTCCTTGATGGTGAGGC----- 5876

Qy 1283 CysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLys 1302

Db 5877 -----CAGAATGACATCTTAGAAATCAAGGAGTGTGACGAAGATATAY----- 5918

Qy 1303 LysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSerPheCys 1322

Db 5919 -----AGAGGAAGCGGAAGCCTGTGTTGACAGGATTTGCGTGGGC 5960

Qy 1323 ValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIle 1342

Db 5961 ATTCTCTCGTGTGAGTCTTGGCTCCTGGGAGTTAATGGGCTGGAATAATCATCAACT 6020

Qy 1343 IleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyr 1362

Db 6021 TTCAAGATGTTAACAGGAGATACCACCTGTTACCAGAGAGATGCTTTCCTT--AACAAA 6077

Qy 1363 SerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIle 1382

Db 6078 AATAGTATCTTATCAACATCCATGAAGTACATCAGAACATGGCTACTGCCCTCAGTTT 6137

Qy 1383 AsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLys 1402

Db 6138 GATGCCATCACAGAGCTGTTGACTGGGAGAGAACACCTGGAGTYCTTTGCCCTTTTGAGA 6197

Qy 1403 GlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeu 1422

Db 6198 GGAGTCCCAGAGAAAGAGTGGCAAGTTGGTGAGTGGCGGATTCGGAAACTGGCCCTC 6257

Qy 1423 LysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCys 1442

Db 6258 GTGAAGTATGGAGAAAATATGCTGGTAATACTAGTGAGGCAACAACCGAAGCTCTCT 6317

Qy 1443 PheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGly 1462

Db 6318 ACAGCCATGGCTTTGATCGGCGGCTCCTGTGGTGTCTTGATGAACCCACACAGGC 6377

Qy 1463 MetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArg 1482

Db 6378 ATGGATCCCAAGCCCGCGGTCTTGTGGAATTGTCCTTAAGTGTGTCAAG---GAG 6434

Qy 1483 LysArgAlaAlaIleLeuThrThrHisTyrMetGluAlaGluAlaValCysAspArg 1502

Db 6435 GGGAGATCAGTAGTGCTTACATCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGG 6494

Qy 1503 ValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSer 1522

Db 6495 ATGGCAATCATGGTCAATGGAAGGTTTCAGGTGCTTGGCAGTGTCCAGCATCTAAAAAAT 6554

Qy 1523 LysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGlu 1542

Db 6555 AGGTTTGGAGATGGTTATACAAATAGTTGTACGAATAGCAGGG-----TCCAACCCYRGAC 6608

Qy 1543 ValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGluSer 1562

Db 6609 CTGAAGCCTGCTCCAGGATTTCTTTGGACTTGCAATTTCTGGAAGTGTCTTAAAAAGAGAAA 6668

Qy 1563 PheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSer 1582

Db 6669 CACCGAAACATGCTACAAATACCAGCTTCCA---TCTTCATTATCTTCTCTGGCCAGGATA 6725

Qy 1583 PhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGln 1602

Db 6726 TTCAGCATCCTCTCCAGAGCAAAAGCGACTCCACATAGAAGACTACTCTGTTCTCTCAG 6785

Qy 1603 AlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAspAsn--- 1621

Db 6786 ACAACACTTGACCAAGTATTGTGAACCTTTGCCAAGACCAAAAGTGAATGATGATGACCACTTA 6845

Qy 1622 -----SerCysGlyThrLeuAsnSerThr 1629

Db 6846 AAAGACCTCTCATTACACAAAAACACAGACAGTAGTGGAMGTTGCAGTTCTCTCATCTTTT 6905

Qy 1630 LeuTrpTrpGluArgThrGlnGluAsp-----ArgValValPhe 1642

Db 6906 CTACAGGATGAGAAAGTGAAGAAGCTATGTATGAAGATCCTGTTC 6953

RESULT 14

US-10-796-307-77

; Sequence 77, Application US/10796307

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001509

; CURRENT APPLICATION NUMBER: US/10/796,307

; CURRENT FILING DATE: 2004-03-10

; NUMBER OF SEQ ID NOS: 44201

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 77

; LENGTH: 10405

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-796-307-77

Alignment Scores:

Pred. No.: 3.67e-130 Length: 10405

Score: 1439.00 Matches: 485

Percent Similarity: 41.88% Conservative: 309

Best Local Similarity: 25.58% Mismatches: 632

Query Match: 17.08% Indels: 470

DB: 6 Gaps: 64

US-10-090-458-5 (1-1642) x US-10-796-307-77 (1-10405)

Qy 89 SerSerIleMetGlnLysValSerThrAspHisLeuProAspValIleIleThrGluGlu 108

Db 1808 TCTCGCTTCATGGAGTGTCTCAACCTGAACAAGCTR---GAACCCATAGCAACAGATC 1864

Qy 109 TyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLysProSerAsnPheValGly 128

Db 1865 TGGCTCATCAACAAGTCCATG-----GAGCTGCTGGATGAGAGGAAGTTCTGGCTGGT 1918

Qy 129 ValValPhe-----LysAspSerMetSerTyrGlu 138

Db 1919 ATTGTGTTCACTGGAATTACTCCAGGCAGYATTGAGCTGCCCATCATGTCAAGTACAAG 1978

Qy 139 LeuArgPheProAspMetIle-----ProValSerSerIleTyrMetAsp 154

Db 1979 ATCCGAATGGACATTGACAATGTGGAGAGGACAAATAAATAAATCAAGGATGGTACTGGGAC 2038

Qy 155 -----SerArgAlaGlyCysSerLysSerCysGluAlaAlaGlnTyrTrpSerSerGly 172

Db 2039 CCTGTCTCTCGAGCT-----GACCCCTTTGAGGACATCGGTACGTTCTSGGGGGC 2089

Qy 173 PheThrValLeuGlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSer 192

Db 2090 TTCGCCTACTTGCRCGATGTGGTGGAGCAGGCAATCATCAGGTGTGTGACGGCACC--- 2146

Qy 193 LeuTrpLysGluLeuGluSerThrLysAlaValIleMetGlyGluThrAlaValGlu 212

Db 2147 -----GAGAAGAAAACCTGGTGTCTATATGCAACAGATG----- 2179

Qy 213 IleAspThrPheProArgGlyValIleLeuIleTyrLeuValIleAlaPheSerProphe 232

Db 2180 -----CCCTATCCCTGTTASGTTGATGACATCTTCTGCGGTGATGAGCGCGTCAATG 2233

Qy 233 GlyTyrPheLeuAlaIle-----HisIleVal 241

Db 2234 CCCCTCTTCATGACGCTGGCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATYGTG 2293

Qy 242 AlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThrAla 261

Db 2294 TATGAGAAGGAGGCGCTGAAAGAGACCATGCGGATCATGGCCTGGCAACACAGCATM 2353

Db 1761 ATTGTGTTCACTGGAAATTACTCCAGGCGAGYATTGAGCTGCCCCATCATGTCAAGTACAAG 1820
QY 139 LeuArgPhePheProAspMetIle-----ProValSerSerIleTyrMetAsp 154
Db 1821 ATCCGAATGGACATTGACAATGTGGAGAGGACAAATAAATCAAGGATGGGTACTGGGAC 1880
QY 155 -----SerArgAlaGlyCysSerLysSerCysGluAlaAlaGlnTyrTrpSerSerGly 172
Db 1881 CCTGGTCTCGAGCT-----GACCCCTTTGAGGACATGCGGTACTCTSGGGGGC 1931
QY 173 PheThrValLeuGlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSer 192
Db 1932 TTCGCCTACTTGCRCGATGTGGTGAGGACGAGCAATCATCAGGGTGCTGACGGGCACC--- 1988
QY 193 LeuTrpLysGluLeuGluSerThrLysAlaValIleMetGlyGluThrAlaValValGlu 212
Db 1989 -----GAGAAGAAAACCTGGTGCTATATGCAACAGATG----- 2021
QY 213 IleAspThrPheProArgGlyValIleLeuIleTyrLeuValIleAlaPheSerProphe 232
Db 2022 -----CCCTATCCCTGTTASGTTGATGACATCTTTCTGCGGTGATGAGCCGGTCAATG 2075
QY 233 GlyTyrPheLeuAlaIle-----HisIleVal 241
Db 2076 CCCCTCTTCATGACGCTGGCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATYGTG 2135
QY 242 AlaGluLysGluLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThrAla 261
Db 2136 TATGAGAAAGGAGGRCGCTGAAAGAGACCATCGCGATCATGGCCTGGACAAACAGCATM 2195
QY 262 PheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMet-----Ser 278
Db 2196 CTCTGGTTTAGCTGGTTCAATT-----AGTAGCCTCATTCCTCTTCTGTGAGCGCTGGC 2249
QY 279 LeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleVal 298
Db 2250 CTGCTAGTGGTCATCCTGAAGTTAGGAAACCTGCTG---CCCTACAGTGATCCCAGCGTG 2306
QY 299 IlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThr 318
Db 2307 GTGTTGTCTTCCTGTCCGTGTTTGTGTGGTGACAATCCTGCAGTGCTTCCTGTATTAGC 2366
QY 319 ProLeuPheLysLysSerLysHisVal-----GlyIleValGluPhePheVal 334
Db 2367 ACACCTCTTCCAGAGCCAAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCAACGCTG 2426
QY 335 ThrValAlaPhe-----GlyPheIleGlyLeuMetIleIleLeu 347
Db 2427 TACCTGCCCTACGTCCTGTGTGTGGCATGGCAGACTACRTGGCTTCMCACCTCAAGATC 2486
QY 348 IleGluSerPheProLysSerLeuValTrpLeuPheSerPropheCysHisCysThrPhe 367
Db 2487 TTCGCTAGC-----CTGCTGTCTCCT-----GTGGCTTTT 2516
QY 368 ValIleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSerPheSer 387
Db 2517 GGGTTTGGCTGTGAGTACTTTGCCCCTTTTGGAGAGCAGGGCATTTGGAGTGCAGTGGGAC 2576
QY 388 AsnLeuThrAlaGlyPro-----TyrProLeuIleIleThrIleIleMet 402
Db 2577 AACCTGTTTGAGAGTCTCTGTGGAGGAAGATGGCTTCAATCTCACCACCTTCGRTCTCCATG 2636
QY 403 LeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnValIlePro 422
Db 2637 ATGCTGTTTRACACCTTCCTCTATGGGTGATGACCTGGTACATTGAGCGTGTCTTTCCA 2696
QY 423 GlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp----- 440
Db 2697 GGCAGTACGGAATTCACAGGCCCTCGGTATTTTCCTTGCACCAAGTCTCTACTGTTTGGC 2756
QY 441 -----SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsn 454
Db 2757 RAGGAAGTGATGAGAGAGCCACCCTGGTTTCCAAACCAGAGAGATRTCAGAA----- 2810

QY 455 ValAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPheValGly 474
Db 2811 -----ATCTGCATGGAGGAG-----GAACCCACCCACTTG----- 2840
QY 475 LysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnVal 494
Db 2841 AAGCTGGCGTGTCCATTTCAGAACCTGGTAAAGTCTAC---YGAGATGGGATGAAGGTG 2897
QY 495 GluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGly 514
Db 2898 ---GCTGTTCGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACTCCTTCTCTGGGC 2954
QY 515 HisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSer 534
Db 2955 CACAATGGAGYGGGAAAGACGACCAACCATGTCAATCCTGACCGGTTGTTCCTCCCGGACC 3014
QY 535 AspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAla 554
Db 3015 TCGGCACYGCCTACATCCTGGGAAAAGACATTGCG-----TCTGAGATGAGCACCATC 3068
QY 555 ArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGlu 574
Db 3069 CGGCAGAACCTGGGGTCTGTCCCCAGCATATAACGCTGTGTTGACATGCTGACTGTGAA 3128
QY 575 GluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGlu 594
Db 3129 GAACACATCTGGTTCATGCCCCGCTTGAAGGGCTCTCTRAGAAGCAGCTGAAAGCGGAG 3188
QY 595 ValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLys---AspAsnGlnAlaLys 613
Db 3189 ATGGAGCAGATGGCCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAAGCAAAACAAGC 3248
QY 614 LysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnPro 633
Db 3249 CAGCTGTTCAGGTGGATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTGTTCGGGGGATCT 3308
QY 634 LysIleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleVal 653
Db 3309 AAGTKGTCTATTCTGGATGAACCCACAGCTGTGTGGACCCCTTACTCCCGCAGGGGAATA 3368
QY 654 TrpAsn---LeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPhe 672
Db 3369 TGGGAGCTGCTGCTGAAATACCGACAA---GGCCGCACCATTTATTTCTCTACACACCAC 3425
QY 673 MetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLys 692
Db 3426 ATGGATGAAGCGGACGCTCCTGGGKACAGGATTGCCATCATCTCCCATGGGAAGCTGTGC 3485
QY 693 CysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMet 712
Db 3486 TGTGTGGGCTCCTCCCTGTTTCTGAAGAACCCAGYTGGAACAGGCTACTACCTGACCTTG 3545
QY 712 ----- 712
Db 3546 GTCAAGAAAGATGTGGAATCCTCCCTCAGTTCTCTGCAGAAACAGTAGTACTGTGTCA 3605
QY 713 TyrIleAspLysTyrCysAla----- 719
Db 3606 TACCTGAAAAAGGAGGACAGTGTTCCTCAGAGCAGTTCTGATGTGGCCTGGGACGAGC 3665
QY 720 -----ThrGluSerLeuSerSerLeuValLysGlnHis 730
Db 3666 CATGASAGTGACACGCTGACCATCGATGTCCTGCTATCTTCCAACTCATCAGGAAGCAT 3725
QY 731 IleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeuProphe 750
Db 3726 GTGTCTGAAGCCCGGCTGGTGGAAAGACATAGGGCATGAGCTGACCTATGTGTGCCATAT 3785
QY 751 LysAspMetAspLys-----PheSerGlyLeuPheSerAlaLeuAspSerHis---Ser 767
Db 3786 GARGCTGCTAAGGAGGAGCGCTTTGTGGAACTCTTTTCATGAGATTGATGACCGRCTCTCA 3845

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QY 1160 Tyr-----Thr 1161
Db 5269 ATTAATGGCAGCGTGGCCACCTTTGTCTGAGCTGTTTCACYGACAATAAGCTGAATAAT 5328
QY 1162 IleAlaThrIleLeuHisTyrAlaPheCysIleIleProIleTyrProLeuLeuGly 1181
Db 5329 ATCMATGATATCCTGAAGTCCGTGTTCTC---TGATCTTCCACATTTTTCCTGGGACGA 5385
QY 1182 CysLeuIleSerPheIleLys----- 1188
Db 5386 GGGCTCATCGACATGGTGAAAAAACAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAG 5445
QY 1189 -----IleSerTrpLysAsnValArgLysAsnValAspThrTyrAsn 1202
Db 5446 AATCGCTTTGTGTACCATATATCTTGGGACTTGGTGGAAGAACTCTTCGCC----- 5499
QY 1203 ProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeuTrpIle 1222
Db 5500 -----ATGCGCGTGAAGGGGTGTCTTCTCTCATTACTGTT----- 5538
QY 1223 PheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAspProPhe 1242
Db 5539 ---CTGATCCAGTAC-----AGATTC 5556
QY 1243 PheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAspAsnGlu 1262
Db 5557 TTC-----ATCAGGCCCAGACCTGTAAATGCAAAAGCTA-----TCTCCTCTGAAT--- 5601
QY 1263 AspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGlyCysGln 1282
Db 5602 GATGAAGATGAAGATGTGAGGCGGGAAGACAGAGAATCTTGTATGGTGAGGC----- 5655
QY 1283 CysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLys 1302
Db 5656 -----CAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATATAY----- 5697
QY 1303 LysAspPheLeuLeuSerArgLysValLysValAlaThrLysTyrIleSerPheCys 1322
Db 5698 -----AGAAGGAAGCGGAAGCTGCTGTTGACAGGATTTGCGTGSGC 5739
QY 1323 ValLysLysGlyGluIleLeuGlyLeuGlyProAsnGlyAlaGlyLysSerThrIle 1342
Db 5740 ATTCTCTCCTGGTGAGTCTTTGGGCTCCTGGGAGTTAATGGGCTGGAATAATCATCAACT 5799
QY 1343 IleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyr 1362
Db 5800 TTCAAGATGTTAAACAGGAGATACCACCTGTTACCAGAGGAGATGCTTTCCTT---AACAAA 5856
QY 1363 SerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIle 1382
Db 5857 AATAGTATCTTATCAAAACATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTT 5916
QY 1383 AsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLys 1402
Db 5917 GATGCCATCACAGAGCTGTTGACTGGGAGAGAACACGTGGAGTCTTTGCCCTTTTGAGA 5976
QY 1403 GlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeu 1422
Db 5977 GGAGTCCCAGAGAAAGAGTTGGCAAGTTGGTGAGTGGGCGGATTCGGAAACTGGGCCCTC 6036
QY 1423 LysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCys 1442
Db 6037 GTGAAGTATGGAGAAAAAATATGCTGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCT 6096
QY 1443 PheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGly 1462
Db 6097 ACAGCCATGGCTTGATCGGYGGGCTCTCTGTGGTGTCTTCTGGATGAACCCACACAGGC 6156
QY 1463 MetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArg 1482
Db 6157 ATGGATCCCAAAGCCGCGGTTCTTGTGAATGTGCCCTAAGTGTGTCAAG---GAG 6213
QY 1483 LysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArg 1502
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QY 1503 ValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSer 1522
Db 6274 ATGGCAATCATGGTCAATGGAAGGTTTCAGTGCCCTTGGCAGTGTCCAGCATCTAAAAAAT 6333
QY 1523 LysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGlu 1542
Db 6334 AGGTTTGAGATGGTTATACAATAGTTGTACGAATAGCAGGG-----TCCAACCCYRGAC 6387
QY 1543 ValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGluSer 1562
Db 6388 CTGAAGCCTGTCCAGGATTTCTTTGGACTTGCATTTCTCTGGAAGTGTCTAAAAGAGAAA 6447
QY 1563 PheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSer 1582
Db 6448 CACCGGAACATGCTACAATACCAGCTTCCA---TCTTCATTATCTTCTGTGCCAGGATA 6504
QY 1583 PhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGln 1602
Db 6505 TTCAGCATCTCTCCAGAGCAAAAAGCGACTCCACATAGAGACTACTCTGTCTTCTCAG 6564
QY 1603 AlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAspAsn--- 1621
Db 6565 ACAACACTTGACCAGATATTGTGAACCTTGCCAAAGGACCAAGTGATGATGATGATGATG 6624
QY 1622 -----SerCysGlyThrLeuAsnSerThr 1629
Db 6625 AAAGACCTCTCATTAACAAAAACCAGACAGTAGTGGAMGTTGCAGTTCTCATCTTTT 6684
QY 1630 LeuTrpTrpGluArgThrGlnGluAsp-----ArgValValPhe 1642
Db 6685 CTACAGGATGAGAAAGTGAAAGAAAGCTATGTATGAAGAAATCCTGTTC 6732

RESULT 13
US-10-796-307-78
; Sequence 78, Application US/10796307
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001509
; CURRENT APPLICATION NUMBER: US/10/796,307
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 44201
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 10247
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-307-78

Alignment Scores:
Pred. No.: 3.58e-130 Length: 10247
Score: 1439.00 Matches: 485
Percent Similarity: 41.88% Conservative: 309
Best Local Similarity: 25.58% Mismatches: 632
Query Match: 17.08% Indels: 470
DB: 6 Gaps: 64

US-10-090-458-5 (1-1642) x US-10-796-307-78 (1-10247)
QY 89 SerSerIleMetGlnLysValSerThrAspHisLeuProAspValIleIleThrGluGlu 108
Db 1650 TCTCGCTTTCATGGAGTGTGTCAACCTGAACCTGAACAAGCTR---GAACCCATAGCAACAGAGTC 1706
QY 109 TyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLysProSerAsnPheValGly 128
Db 1707 TGGCTCATCAACAAGTCCATG-----GAGCTGTGGATGAGAGGAAGTTCTGGGCTGGT 1760
QY 129 ValValPhe-----LysAspSerMetSerTyrGlu 138
:::|||||
```


Db 3148 TGGGAGCTGCTGCTGAAATACCGACAA--GGCCGACCACTATTCTCTCTACACACCAC 3204
 QY MetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLys 692
 Db ATGGATGAAGCGGACGCTCTGGGKACAGGATTGCCATCATCTCCCATGGGAAGCTGTGC 3264
 QY CysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMet 712
 Db TGTGTGGGCTCCTCCCTGTTCTGAAGAACCAAGTGGAAACAGGCTACTACCTGACCTTG 3324
 QY 712 ----- 712
 Db 3325 GTCAAGAAAGATGTGGAAATCCTCCCTCAGTTCCTGCAGAAACAGTAGTAGCACTGTGTCA 3384
 QY TyrIleAspLysTyrCysAla----- 719
 Db 3385 TACCTGAAAAGAGGAGACAGTGTTCCTCAGAGCAGTTCTGATGCTGGCCTGGGCAGCGAC 3444
 QY 720 -----ThrGluSerLeuSerSerLeuValLysGlnHis 730
 Db 3445 CATGASAGTGACACGCTGACCATCGATGCTCTGCTATCTCCAACCTCATCAGGAAGCAT 3504
 QY IleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnLeuValTyrSerLeuProPhe 750
 Db GTGTCTGAAGCCCGGCTGGTGAAGACATAGGGCATGAGCTGACCTATGTCTGCCATAT 3564
 QY LysAspMetAspLys-----PheSerGlyLeuPheSerAlaLeuAspSerHis---Ser 767
 Db GARGCTGCTAAGGAGGGAGCCCTTTGTGGAACCTCTTCATGAGATTGATGACCGRCTCTCA 3624
 QY AsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLys 787
 Db GACCTGGGCATTTCTAGTTATGGCATCTCAGAGACGACCCCTGGAAGAAATATTCTCTCAAG 3684
 QY leuGluValGluAlaGluIleAsp----- 795
 Db 3685 GTGGCCGAAGAGAGTGGGTGGATGCTGAGACCTCAGATGGTACCTTGGCAGCAAGACGA 3744
 QY 796 -----GlnAlaAspTyrSerValPheThrGln----- 804
 Db 3745 AACAGCGGGCCCTTCGGGACAAAGCAGAGCTGTCTTCGCCCGTTCACTGAAGATGATGCT 3804
 QY ---GlnProLeuGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeu 823
 Db GCTGATCCAAATGATTCTGACATAGACCCAGAAATCC-----AGAGACAGACTTG 3855
 QY LeuIleLeuSerGluThrLysAlaSerLeu---ValSerThrMetSerLeuTrpLysGln 842
 Db CTCAGTGGGATGGATGGCAAGGRTCTCTACCAGGTGAAGGCTGGAAACTTACACAGCAA 3915
 QY GlnMetTyrThrIleAlaLysPheHisPheThrLeuLysArgGluSerLysSerVal 862
 Db CAGTTTGTGGCCCTTTTGTGAAGAGACTGTCTAATTGCCAGCGGAGTCCGAAAGGATTT 3975
 QY ArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuVal 882
 Db TTTGCTCAGATTGCTTGGCAGCTGTGTTTGTCTGCATTGCCCTTGTGTTTGTGCTGATC 4035
 QY HisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeu----- 899
 Db 4036 -----GTGCCACCCTTTGGCAAGTACCCAGCTCCAGCGGAGTCCGAACTTCAG 4074
 QY 900 -----TyrPheLeuLysProGlyAspLysProHisLysTyrLys 912
 Db 4075 CCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCTCCTCAGGACACGGGA 4134
 QY ThrSerLeuLeuLeu----- 917
 Db 4135 ACCCTGGAACCTCTTAAACGCCCTCACCAAGACCCCTGGCTTCGGGACCCGCTGTATGGAA 4194
 QY 917 ----- 917
 Db 4195 GGAAACCCAATCCCGACACACRCCCTGCCAGGCGAGGGAGGAAGATGGACCACCTGCCCCA 4254

QY 917 ----- 917
 Db 4255 GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCCCTTCA 4314
 QY 918 -----GlnAsnSerAlaAsp----- 922
 Db 4315 CTGTCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCTCCCCAGGK 4374
 QY 923 -----SerAspIleSerAspLeuIleSerPhePhe 932
 Db 4375 GCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAAACACTGCAGATATCTCTCAGGACCTG 4434
 QY ThrSerGlnAsnIleMetValThrMet----- 941
 Db 4435 ACAGGAAGAAACATTTYGGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC 4494
 QY 941 ----- 941
 Db 4495 TTAAAGAAACAAGATCTGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGT 4554
 QY 942 -----IleAsnAspSer-----Asp 946
 Db 4555 AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCAYCAAAACAATGAAGAAA 4614
 QY TyrValSerValAlaProHisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyr 966
 Db CACCTAAAGCTGGCCAAGACAGTTCTGCAGATCGATTCTCAACAGCTTGGGAAGATTT 4674
 QY Val-----PheAlaAlaValPheAsnSerThrMetValTyr 978
 Db 4675 ATGACAGGACTGGACACCAARAATAATGTCAAGGTGTGGTTCAATAACAAGGCTGGCAT 4734
 QY SerLeuProIleLeuValAsnIleIle----- 987
 Db 4735 GCAATCAGCTCTTTCCTGAATGTATCATCAACRATGCCATTCTCCGGGCCAACCTGCAAAAG 4794
 QY 988 -----SerAsnTyr-----TyrLeuTyrHisLeuAsnValThrGlu 999
 Db 4795 GGAGAGAACCCCTAGCCATTATGGAATTACTGCTTCAATCATCCCTGAATCTCACCAAG 4854
 QY ThrIleGlnIleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLysIle 1019
 Db CAG---CAGCTCTCAGAGTGGCTCYGATGACCAACATCAGTGGATGTCTGTGTCCATC 4911
 QY GluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPhe 1039
 Db TGTGTCATCTTT-----GCAATGTCTTCCGTCGCCAGCCAGCTTT 4950
 QY AlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGly 1059
 Db 4951 GTCGTATTCTGTATCCAGGAGCGGGTCAGCAAGCAAAACACCTGCAGTTCATCAGTGA 5010
 QY LeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIle 1079
 Db GTGAAGCCTGTCTACTGGCTCTCTAATTGCTCTGGGATATGTGCAATTACGTTGTC 5070
 QY IleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThr 1099
 Db 5071 CTGCCCACACTGGTCATTATCATCTTTCATCTGCTCCAGCAGAGTCCCTATGTCTCCTCC 5130
 QY ValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPhe 1119
 Db ACCAATCTGCCTGTGTAGCCCTTCTACTTTTGTGTGTTGGTGGTCAATCACACCTCTC 5190
 QY ThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPhe 1139
 Db ATGTACCCAGCCTCCTTTGTGTTCAAG----- 5217
 QY IleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGly 1159
 Db -----ATCCCCAGCACAGCCTATGTGTGTGCTCACCGGTGAACCTCTTTCATTGGC 5268

; CURRENT APPLICATION NUMBER: US/10/796,307
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 44201
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 10026
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-307-75

Alignment Scores:
Pred. No.: 3.45e-130 Length: 10026
Score: 1439.00 Matches: 485
Percent Similarity: 41.88% Conservative: 309
Best Local Similarity: 25.58% Mismatches: 632
Query Match: 17.08% Indels: 470
DB: 6 Gaps: 64

US-10-090-458-5 (1-1642) x US-10-796-307-75 (1-10026)

QY 89 SerSerIleMetGlnLysValSerThrAspHisLeuProAspValIleIleThrGluGlu 108
Db 1429 TCTCGCTTCATGGAGTGTGTCAACCTGAACAAGCTR--GAACCCATAGCAACAGAGTC 1485
QY 109 TyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLysProSerAsnPheValGly 128
Db 1486 TGGCTCATCAACAAGTCCATG-----GAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGT 1539
QY 129 ValValPhe-----LysAspSerMetSerTyrGlu 138
Db 1540 ATTGTGTTCACTGGAAATTACTCCAGGCAGYATTGAGCTGCCCATCATGTCACAGTACAAG 1599
QY 139 LeuArgPhePheProAspMetIle-----ProValSerSerIleTyrMetAsp 154
Db 1600 ATCCGAATGGACATTGACAATGTGGAGAGGACAAATAAATCAAGGATGGGTACTGGGAC 1659
QY 155 -----SerArgAlaGlyCysSerLysSerCysGluAlaAlaGlnTyrTrpSerSerGly 172
Db 1660 CCTGGTCTCGAGCT-----GACCCCTTTGAGGACATGCGGTACTCTSGGGGGC 1710
QY 173 PheThrValLeuGlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSer 192
Db 1711 TTCGCCTACTTGCRCGATGTGGTGGAGCAGGCAATCATCAGGTGCTGACGGGCACC--- 1767
QY 193 LeuTrpLysGluLeuGluSerThrLysAlaValIleMetGlyGluThrAlaValGlu 212
Db 1768 -----GAGAAGAAACTGGTGCTATATGCAACAGATG----- 1800
QY 213 IleAspThrPheProArgGlyValIleLeuIleTyrLeuValIleAlaPheSerProphe 232
Db 1801 -----CCCTATCCCTGTTASGTTGATGACATCTTTCTGCGGTGATGAGCCCGTCAATG 1854
QY 233 GlyTyrPheLeuAlaIle-----HisIleVal 241
Db 1855 CCCCTCTTCATGACGCTGGCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATYGTG 1914
QY 242 AlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThrAla 261
Db 1915 TATGAGAAGGAGGRCGCGCTGAAAGAGACCATTGCGGATCATGGCGCTGGAACAACAGCATM 1974
QY 262 PheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMet-----Ser 278
Db 1975 CTCTGGTTTAGCTGGTTTCATT-----AGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGC 2028
QY 279 LeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPhePheProGlnSerSerIleVal 298
Db 2029 CTGCTAGTGGTTCATCCTGAAGTTAGGAAACCTGCTG---CCCTACAGTATCCAGCGTG 2085
QY 299 IlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThr 318
Db 2086 GTGTTTGTCTTCCTGTCGCTGTTTGTGTGTGAGACAATCCTGCAGTGTCTCCTGATTAGC 2145
QY 319 ProLeuPheLysLysSerLysHisVal-----GlyIleValGluPhePheVal 334

Db 2146 ACACCTCTTCTCCAGAGCCCAACCTGGCAGCAGCCTGTGGGGCATCATCTACTACGCTG 2205
QY 335 ThrValAlaPhe-----GlyPheIleGlyLeuMetIleIleLeu 347
Db 2206 TACCTGCCCTACGTCTGTGTGTGGCATGGCAGGACTACRTGGCTTCMCACTCAAGATC 2265
QY 348 IleGluSerPheProLysSerLeuValTrpLeuPheSerPropheCysHisCysThrPhe 367
Db 2266 TTCGCTAGC-----CTGCTGTCTCCT-----GTGGCTTTT 2295
QY 368 ValIleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSerPheSer 387
Db 2296 GGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGAGCAGGGCATTTGGAGTGCAGTGGGAC 2355
QY 388 AsnLeuThrAlaGlyPro-----TyrProLeuIleIleThrIleIleMet 402
Db 2356 AACCTGTTTGAGAGTCTCTGTGGAGGAAGATGGCTTCAATCTCACCACCTTCGRTCTCCATG 2415
QY 403 LeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnValIlePro 422
Db 2416 ATGCTGTTTRACACCTTCTCTATGGGTGATGACCTGGTACATTGAGGCTGTCTTTCCA 2475
QY 423 GlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp----- 440
Db 2476 GGCAGTACGGAATTCACAGGCCCTCGTATTTTCTTGACCAAGTCTCTACTGGTTTGGC 2535
QY 441 -----SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsn 454
Db 2536 RAGAAAGTGATGAGAGAGCCACCTCGTTTCCAAAGAGAGAAATRTCAGAA----- 2589
QY 455 ValAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPheValGly 474
Db 2590 -----ATCTGCATGGAGGAG-----GAACCCACCCACTTG----- 2619
QY 475 LysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnVal 494
Db 2620 AAGCTGGCGTGTCCATTGAGAACCTGGTAAAGTCTAC---YCATGGGATGAAGGTG 2676
QY 495 GluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGly 514
Db 2677 ---GCTGTGATGGCTGGCACTGAATTTTATGAGGGCCAGATCACTCTCTCTCTGGGC 2733
QY 515 HisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSer 534
Db 2734 CACAATGGAGYGGRAAGACAGCACCATCATGTCAATCTGACCGGTTGTTCCTCCCGGACC 2793
QY 535 AspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAla 554
Db 2794 TCGGCACYGCCTACATCTGGGAAAGACATTCGC-----TCTGAGATGAGCACCATC 2847
QY 555 ArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGlu 574
Db 2848 CGGCAGAACCTGGGGTCTGTCTCCCGCAGCATAACTGTTTGACATGCTGACTGTGAA 2907
QY 575 GluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGlu 594
Db 2908 GAACACATCTGGTTCTATGCCCGCTTGAAGAGGCTCTCTRAGAAGCACGCTGAAGCGGAG 2967
QY 595 ValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLys---AspAsnGlnAlaLys 613
Db 2968 ATGGAGCAGATGGCCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAGCAAAACAAGC 3027
QY 614 LysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnPro 633
Db 3028 CAGCTGTGAGGTGGAATGCAGAGAAAGCTATCTGTGGCCTTGTGGCCTTTGTGGGGGATCT 3087
QY 634 LysIleLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleVal 653
Db 3088 AAGTGTGTCATTCTGGATGAACCCACAGCTGTGTGGACCCCTTACTCCCGCAGGGGAATA 3147
QY 654 TrpAsn---LeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPhe 672

Db 4876 GGCTCCGATGACCACATCATCAGTGGATGTCCTTGTGTCCATCTGTGTCTATCTTT-----4927

QY 1026 aLeuLeuGlyllelleValThrAlaMetProProTyrPheAlaMetGluAsnAlaGluAs 1046

Db 4928 -----GCAATGTCCTTCGTCCAGCCAGCTTTGTCTATTCCTGTATCCAGGA 4974

QY 1046 nHisLyslleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAlaTyrTr 1066

Db 4975 GCGGGTCAGCAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCTACTCTG 5034

QY 1066 pIleGlyGlnAlaValAlaValAspIleProLeuPhePheIlelleLeuLeuMetLeuGl 1086

Db 5035 GCTCTCTAATTTTGTCTGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCAATTAT 5094

QY 1086 ySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPheLeuAlaValVa 1106

Db 5095 CATCTTCATCTGCTCCAGCAGAAAGTCCATATGTCTCCACCAATCTGCCTGTGCTAGC 5154

QY 1106 lPheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSerPheTh 1126

Db 5155 CTTTCTACTTTTGTCTGATGGGTGGTCAATCACACCTCTCATGTATCCAGCCTCTTTGT 5214

QY 1126 rPheLysLyslleLeuAsnThrLysGluPheTrpSerPheIleTyrSerValAlaAlaLe 1146

Db 5215 GTTCAAG-----ATCCCCAGCAC 5232

QY 1146 uAlaCyslleAlaIleThrGluIleThrPhePheMetGlyTyr-----ThrIleAlaTh 1164

Db 5233 AGCCTATGTGTGCTCACAGCGTGAACCTCTTCATTTGGCATTAATGGCAGCGTGGCCAC 5292

QY 1164 r-----IleLeuHisTy 1168

Db 5293 CTTTGTGCTGGAGCTGTTCACCGACAATAAGCTGAATAATATCAATGATATCTGAAGTC 5352

QY 1168 rAlaPheCysllelleProIleTyrProIleTyrProLeuLeuGlyCysLeuIleSerPheIleLy 1188

Db 5353 CGTGTTC---TTGATCTTCCACATTTTGGCTGGCAGGAGGCTCATCGACATGGTGAA 5409

QY 1188 s-----11 1189

Db 5410 AAACCAAGCAATGGCTGATGCCCTGGAAAGTTTGGGGAGAAATCGCTTGTGTCACCATT 5469

QY 1189 eSerTrpLysAsnValArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSerVa 1209

Db 5470 ATCTTGGGACTTGGTGGGACGAAACCTCTTCGCC-----ATGGCCGT 5511

QY 1209 lAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTrGl 1229

Db 5512 GGAAGGGTGGTGTCTCTCTCATTAAGT-----CTGATCCAGTAC-----5554

QY 1229 uLysLysTyrGlyArgSerIleArgLysAspProphePheArgAsnLeuSerThrLy 1249

Db 5555 -----AGATTCTTC-----ATCAGGCCCCAG 5574

QY 1249 sSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspVally 1269

Db 5575 ACCTGTAATGCAAGCTA-----TCTCCTCTGAAT---GATGAAGATGAAGATGTGAG 5625

QY 1269 sAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysProse 1289

Db 5626 GCGGGAAGACAGAGAATTCTTGATGGTGGAGGC-----CAGAATGACAT 5670

QY 1289 rIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerAr 1309

Db 5671 CTTAGAAATCAAGGAGTTGACGAAGATATAT-----AG 5703

QY 1309 gLysValLysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLe 1329

Db 5704 AAGGAACGGAAGCCTGCTGTGTGACAGGATTTGCGTGGSCATTCCTCCTGGTGTGCTT 5763

QY 1329 uGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAs 1349

Db 5764 TGGGCTCTGGGAGTTAATGGGCTGGAAATCATCACTTTCAAGATGTTTAACAGGAGA 5823

QY 1349 pIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAs 1369

Db 5824 TACCACCTGTACCAGAGAGATGCTTTCCTT---AACAGAAATAGTATCTTATCAACAT 5880

QY 1369 pAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspTh 1389

Db 5881 CCATGAAGTACATCAGAACATGGGTACTGCCCTCAGTTTGATGCCATCAGAGCTGTT 5940

QY 1389 rThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMe 1409

Db 5941 GACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGT 6000

QY 1409 tLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysTh 1429

Db 6001 TGGCAAGTTGTGTAGTGGCGATTTCGAAACTGGCCCTCGTGAAGTATGGAGAAATA 6060

QY 1429 rValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGl 1449

Db 6061 TGCTGGTAACATATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATCGG 6120

QY 1449 yAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGl 1469

Db 6121 CGGGCCTCCTGTGTGTTTCTGGATGAACCCACACAGGCATGGATCCCAAGCCCGCG 6180

QY 1469 nHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaIleLeuTh 1489

Db 6181 GTTCTTGTGGAATTCTGCCCTTAAGTTGTGTAAG---GAGGGGAGATCAGTAGTCTTAC 6237

QY 1489 rThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMetValSerGl 1509

Db 6238 ATCTCATAGTATGGAAGAATGTGAAGCTCTTTCACACTAGGATGGCAATCATGGTCAATGG 6297

QY 1509 yGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPh 1529

Db 6298 AAGGTTCAAGTGCCTGGCAGTGTCCAGCATCTAAATAATAGTTTGGAGATGTTTATAC 6357

QY 1529 eLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArgGl 1549

Db 6358 AATAGTTGTACGAATAGCAGGG-----TCCAAACCCGGACCTGAAGCCTGTCCAGGATTT 6411

QY 1549 uIleGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerIleLeuAlaTy 1569

Db 6412 CTTTGGACTTGCATTTCTCTGGAAGTGTTCCTGAGGAGAAACACCCGGAACATGCTACAATA 6471

QY 1569 rLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeuGluAl 1589

Db 6472 CCAGCTTCCA---TCTTCATTATCTTCTCTGGCCAGGATATTCAGCATCCTCTCCCAGAG 6528

QY 1589 aLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPh 1609

Db 6529 CAAAAAGCGACTCCACATAGAAGACTACTCTGTCTTCTCAGACAAACACTTGACCAAGTATT 6588

QY 1609 eValGluLeuThrLysGluGlnGluGluGluAspAsn-----1621

Db 6589 TGTGAACCTTGGCAAGGACCAAAAGTGTATGATGACCACTTAAAGACCTCTCATACACAA 6648

QY 1622 -----SerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGl 1636

Db 6649 AAACCAGACAGTAGTGGACGTTGCAGTTCTTCACATCTTTTCTACAGGATGAGAAAAGTGAA 6708

QY 1636 nGluAsp-----ArgValValPhe 1642

Db 6709 AGAAAGCTATGTATGAAGAATCCTGTTTC 6736

RESULT 12

US-10-796-307-75

; Sequence 75, Application US/10796307

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001509


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RESULT 11
US-10-465-498-96
; Sequence 96, Application US/10465498
; GENERAL INFORMATION:
; APPLICANT: DENEFFE, Patrice
; APPLICANT: ROSIER-MONTUS, Marie-Francoise
; APPLICANT: ARNOULD-REGUIGNE, Isabelle
; APPLICANT: PRADES, Catherine
; APPLICANT: NAUDIN, Laurent
; APPLICANT: LEMOINE, Cendrine
; APPLICANT: DUVERGER, Nicolas
; APPLICANT: ASSMANN, Gerd
; APPLICANT: RUST, Stephan
; APPLICANT: FUNKE, Harold
; APPLICANT: BREWER, Bryan
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS CORRESPONDING TO HUMAN GENE ABC1
; FILE REFERENCE: ST99020USCNT1
; CURRENT APPLICATION NUMBER: US/10/465,498
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: FR99 07684
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/FR00/01595
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US10/018,714
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; PRIOR APPLICATION NUMBER: US10/269,780
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96
; LENGTH: 9495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6763)..(6763)
; OTHER INFORMATION: n is a, c, g, or t
US-10-465-498-96

Alignment Scores:
Pred. No.: 3,76e-132 Length: 9495
Score: 1458.50 Matches: 491
Percent Similarity: 43.33% Conservative: 328
Best Local Similarity: 25.98% Mismatches: 613
Query Match: 17.31% Indels: 458
DB: 6 Gaps: 68

US-10-090-458-5 (1-1642) x US-10-465-498-96 (1-9495)
Qy 89 SerSerIleMetGlnLysValSerThrAspHisLeuProAspValIleIleThrGluGlu 108
Db 1435 TCTCGCTTCATGGAGTGTGTCAACCTGAACAAGCTA---GAACCCATAGCAACAGAAGTC 1491
Qy 109 TyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLysProSerAsnPheValGly 128
Db 1492 TGGCTCATCAACAAGTCCATG-----GAGCTGCTGGATGAGAGGAAGTCTCTGGGCTGGT 1545
Qy 129 ValValPhe-----LysAspSerMetSerTyrGlu 138
Db 1546 ATTGTGTTCACTGGAATTACTCCAGGCAGCATTTGAGCTGCCCATCATGTCAAGTACAAG 1605
Qy 139 LeuArgPheProAspMetIle-----ProValSerSerIleTyrMetAsp 154
Db 1606 ATCCGAATGGACATTGACAATGTGGAGAGGACAAATAAATCAAGGATGGGTACTGGGAC 1665
Qy 155 -----SerArgAlaGlyCysSerLysSerCysGluAlaAlaGlnTyrTrpSerSerGly 172
Db 1666 CCTGGTCTCGAGCT-----GACCCCTTTGAGGACATCGGTACGTCTGGGGGGC 1716
Qy 173 PheThrValLeuGlnAlaSerIleAspAlaAlaIleIleGlnLeu-----Lys 188
Db 1717 TTCGCCTACTTGCAGGATGTGGTGAGCAGGCAATCATCAGGGTGCTCGGGCACCAGAA 1776
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Qy 189 ThrAsnValSerLeuTrpLysGluLeuGluSerThrLysAlaValIleMetGlyGluThr 208
Db 1777 GAAAACTGGTGTCTATAT-----GCAACAGATGCCCTA----- 1809
Qy 209 AlaValValGlu-IleAspThrPheProArgGlyVal-----IleLeuIleTyrLe 225
Db 1810 TCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATGCCCTCTTCAT 1869
Qy 225 uValIleAlaPheSerPropheGlyTyrPheLeuAlaIle-----HisIleValAl 242
Db 1870 GACGCTGGCCTGGATT-----TACTCAGTGGCTGTGATCATCAAGGGCATCGTGTA 1920
Qy 242 aGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThrAlaPh 262
Db 1921 TGAGAAAGGAGGACCGGTGAAAGAGACCATCGGGATCATGGGCCTGGACAACAGCATCCT 1980
Qy 262 eTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMet-----SerLe 279
Db 1981 CTGGTTTAGTGGTTCATT-----AGTAGCCTCATTCCTCTCTTGTGAGCGCTGGCCT 2034
Qy 279 uLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerIleValI 299
Db 2035 GCTAGTGGTTCATCCTGAAGTTAGGAACCTGCTG---CCCTACAGTATCCAGCGTGGT 2091
Qy 299 ePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrPr 319
Db 2092 GTTGTCTTCTCGTCCGTTGTTGCTGTGGTGACAATCCTGCAGTGTCTCTGATTAGCAC 2151
Qy 319 cLeuPheLysLysSerLysHisVal-----GlyIleValGluPhePheValTh 335
Db 2152 ACTCTTCTCCAGAGCCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTACGCTGTA 2211
Qy 335 rValAlaPhe-----GlyPheIleGlyLeuMetIleIleLeuI 348
Db 2212 CCTGCCCTACGTCCTGTGTGGCATGGCAGACTACGTGGCTTCACACTCAAGATCTT 2271
Qy 348 eGluSerPheProLysSerLeuValTrpLeuPheSerPropheCysHisCysThrPheVa 368
Db 2272 CGCTAGC-----CTGCTGTCTCCT-----GTGGCTTTTGG 2301
Qy 368 lIleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSerPheSerAs 388
Db 2302 GTTGGCTGTGAGTACTTTCCTCTTTTGGAGGAGCAGGCGCATTTGGAGTGCAGTGGGACAA 2361
Qy 388 nLeuThrAlaGlyPro-----TyrProLeuIleIleThrIleIleMetLe 403
Db 2362 CCTGTTTGAGAGTCTCTGTGGAGGAAGATGGCTTCAATCTCACCACTTCGCTCTCCATGAT 2421
Qy 403 uThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnValIleProGl 423
Db 2422 GTGTTTGACACCTTCTCTATGGGTGATGACCTGGTACATTCAGGCTGTCTTCCAGG 2481
Qy 423 yGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp----- 440
Db 2482 CCAGTACGGAATTCCAGGCCCTGGTATTTTCTCTTGACCAAGTCTCTACTGTTGGCGA 2541
Qy 441 -----SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnVa 455
Db 2542 GGAAAGTGATGAGAGAGAGCCACCTGGTTTCCAAACCAGAGAGAAATATCAGAA----- 2593
Qy 455 lAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPheValGlyLy 475
Db 2594 -----ATCTGCATGGAGGAG-----GAACCCACCCACTTG-----AA 2625
Qy 475 sGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGl 495
Db 2626 GCTGGCGGTGTCCATTGAGAACCTGGTAAAGTCTACCGA---GATGGGATGAAGGTG-- 2680
Qy 495 uAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHi 515
Db 2681 -GCTGTTCGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACCTCTCTCTCTGGGCCA 2739
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QY	993	----	TyrHisLeuAsnValThrGluThrIleGlnIleTrpSer	1000
DB	4819	TATGGAATTACTGCTTTCAATCATCCCTGAATCTCACC	AAAGCAG---CAGCTCTCAGAG	4875
QY	1006	ThrProphePheGlnGluIleThrAspIleValPheLysIleGluLeuTyrPheGlnAla	1025	
DB	4876	GTGGCTCCGATGACCACATCAGTGGATGCTCTGTGTCCATCTGTGTCACTCTT	-----	4929
QY	1026	AlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsnAlaGlu	1045	
DB	4930	-----GCAATGCTCTTCGTCGCCAGCCAGCTTTGTCGATATTCCTGATCCAG	4974	
QY	1046	AsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAlaTyr	1065	
DB	4975	GAGCGGGTCAGCAAAAGAAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTGCTATC	5034	
QY	1066	TrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeuIleLeuMetLeu	1085	
DB	5035	TGGCTCTCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACCTGGTCATT	5094	
QY	1086	GlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPheLeuAlaVal	1105	
DB	5095	ATCATCTTCATCTGCTTCCAGCAGAAAGTCCCTATGTGTCTCCACCAATCTGCCTGTGCTA	5154	
QY	1106	ValPheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSerPhe	1125	
DB	5155	GCCCTTCTACTTTTGTGTATGGTGGTCAATCAACACCTCTCATGTACCCAGCCTCCTTT	5214	
QY	1126	ThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIleTyrSerValAlaAla	1145	
DB	5215	GTGTTCAAG-----	5232	
QY	1146	LeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr-----	1163	
DB	5233	ACAGCCTATGTGGTGTCCACCAGCGTGAACCTCTTCATTGGCATTAAATGGCAGCGTGGCC	5292	
QY	1164	Thr-----	1167	
DB	5293	ACCTTTGTGCTGGAGCTGTTTACCAGCAATAAGCTGAATAATATCAATGATATCTGAAG	5352	
QY	1168	TyrAlaPheCysIleIleIleProIleTyrProLeuLeuGlyCysLeuIleSerPheIle	1187	
DB	5353	TCCGTGTTCTC-----TTGATCTTCCCACATTTTTCCTGGGACGAGGGCTCATCGACATGGTG	5409	
QY	1188	Lys-----	1188	
DB	5410	AAAAACAGGCAATGGCTGATGCCCTGGAAAGGTTGGGAGAAATCGCTTTGTGTCAACA	5469	
QY	1189	IleSerTrpLysAsnValArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSer	1208	
DB	5470	TTATCTTGGACTTGTGTGGGACGAAACCTCTTCGCC-----	5511	
QY	1209	ValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyr	1228	
DB	5512	GTGGAAGGGTGTGTCTTCTCCTCATTA	5556	
QY	1229	GluLysLysTyrGlyArgSerIleArgLysAspProphePheArgAsnLeuSerThr	1248	
DB	5557	-----AGATTCTTC-----	5574	
QY	1249	LysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspVal	1268	
DB	5575	AGACCTGTAATGCAAGCTA-----TCTCCTCTGAAT--GATGAAGATGAAGATGTG	5625	
QY	1269	LysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysPro	1288	
DB	5626	AGCGGGAAAGACAGAGAATTCTTGATGGTGGAGGC-----	5670	
QY	1289	SerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSer	1308	
DB	5671	ATCTTAGAAATCAAGGAGTTGACGAAGATATAT-----	5703	
QY	1309	ArgLysValLysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluIle	1328	

[illegible]

RESULT 10
US-10-465

2626	Db	AA	GCTGGCGGTGTC	CAATTCAGAAACCTGGTAAAAAGTCTACCGA	---GATGGGATGAAGGTG	2688
495	QY	GU	AlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGly			514
2683	Db	---	GCTGTCGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACCTCCTTCTCTGGGC			2739
515	QY	HI	SerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSer			534
2740	Db	CA	CAATGGAGCGGGAGACGACCAACCATGTCAATCCTGACCGGTTGTTCCCCCGGACC			2799
535	QY	AS	GlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAla			554
2800	Db	TC	GGCACCGCCTACATCTGGGAAAAAGACATTGCG	-----TCTGAGATGAGCAACCATC		2853
555	QY	AR	GlyMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGlu			574
2854	Db	CG	CAGAACCTGGGGTCTGTCTCCAGCATAAACGTGCTGTTTGACATGCTGACTGCGAA			2913
575	QY	GL	AsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGlu			594
2914	Db	GA	ACACATCTGGTTCTATGCGCGCTTGAAAGGGCTCTCTGAGAAGCACCGTGAAGCGGAG			2973
595	QY	VA	GlnLysValLeuLeuAspLeuAspMetGlnThrIleLys	---AspAsnGlnAlaLys		613
2974	Db	AT	GGACGATGGCCCTGGATGTTGGTTGGCTTCCCATCAACCAAGCTGAAAAGCAAAACAAGC			3033
614	QY	LY	SerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnPro			633
3034	Db	CA	GCTGTCAGGTGGAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTTGTCGGGGGATCT			3093
634	QY	LY	SerLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleVal			653
3094	Db	AA	GGTTGTCTCTGGATGAACCCACAGCTGGTGTGGACCTTACTCCCGCAGGGGAATA			3153
654	QY	TR	Asn---LeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPhe			672
3154	Db	TG	GAGCTGCTGCTGAAATACCGACAA---GGCCGCGACCATTTATTTCTCTACACACCAC			3210
673	QY	ME	AspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLys			692
3211	Db	AT	GATGAAGCGGACGCTCTGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGC			3270
693	QY	CV	ValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMet			712
3271	Db	TG	TGTGGGCTCTCCCTGTTTCTGAAGAACCAAGCTGGGAAACAGGCTACTACCTGACCTTG			3330
712	QY	---	-----	-----	---	712
3331	Db	GT	CAAGAAAGATGTGGAATCTCCTCAGTTCTCTGCAGAAAAACAGTAGTACACTGTGTCA			3390
713	QY	TY	AspLysTyrCysAla	-----	-----	719
3391	Db	TAC	CTGAAAAGGAGGACAGTGTCTCTCAGAGCAGTTCTGATGCTGGCCTGGSCAGCGAC			3450
720	QY	---	-----	-----	-----	730
3451	Db	CAT	GAGTGACACGCTGACCATCGATGTCTCTGCTATCTCCAACTCATCAGAAAGCAT			3510
731	QY	IL	ProGlyAlaThrLeuLeuGlnAsnAspGlnLeuValTyrSerLeuProphe			750
3511	Db	GT	GCTGAAGCCCGGCTGGTGAAGACATAGGGCATGAGCTGACCTATGTGTGCTCCATAT			3570
751	QY	LY	AspMetAspLys	-----PheSerGlyLeuPheSerAlaLeuAspSerHis	---Ser	767
3571	Db	GA	AGCTGCTAAGGAGGAGCGCCTTTGTGGAACTCTTTCATGAGATTGATGACCGCTCTCA			3630
768	QY	AS	LeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLys			787
3631	Db	GAC	CTGGGCATTTCTAGTTATGGCATCTCAGAGACGACCCCTGGAAAGAAATATTCTCTCAAG			3690
788	QY	LE	GluValGluAlaGluIleAsp	-----	-----	795
3691	Db	GT	GGCCGAAGAGAGTGGGTGGATGCTGAGACCTCAGATGGTACCTTGCCAGCAAGACGA			3750

QY	796	-----GlnAlaAspTyrSerValPheThrGln-----	804
DB	3751	AACAGGCGGCCCTTCGGGGACAAGCAGAGCTGCTTCGCCCGTTCTCCTGAAGATGATGCT	3810
QY	805	---GlnProLeuGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeu	823
DB	3811	GCTGATCCAAATGATTCTGACATAGACCCAGAATCC-----AGAGAGACAGACTTG	3861
QY	824	LeuIleLeuSerGluThrLysAlaSerLeu---ValSerThrMetSerLeuTrpLysGln	842
DB	3862	CTCAGTGGGATGGATGGCAAAAGGTCCTTACCAGGTGAAAGGCTGGAACTTACACAGCAA	3921
QY	843	GlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLysSerVal	862
DB	3922	CAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAANTGCCAGCGGAGTCGGAAGAGGATTT	3981
QY	863	ArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuVal	882
DB	3982	TTTGCTCAGATTGCTGCCAGCTGTGTTTGTCTGCATTGCCCTTGTGTTCAGCCTGATC	4041
QY	882	-----	882
DB	4042	GTGCCACCCTTTGGCAAGTACCCAGCCTGGAACTTCAGCCCTGGATGTACAAACGAACAG	4101
QY	882	-----	882
DB	4102	TACACATTGTGACGAATGATGCTCTCTGAGGACACGGGAACCCCTGGAACCTTTAAACGCC	4161
QY	882	-----	882
DB	4162	CTCACAAAGACCCTGGCTTCGGGACCCCGCTGTATGGAAGGAAACCCCAATCCAGACACG	4221
QY	883	-----HisHisSerPheLysAsnAlaValValProIleLysLeuValPro	897
DB	4222	CCCTGCCAGGCAGGGAGGAAGAGTGGACCACTGCCCCAGTTCCTCC--CAGACCATCATG	4278
QY	898	AspLeuTyr-----	900
DB	4279	GACCTCTTCCAGAATGGAACTGGACAATGCAGAAACCTTCACCTGCATGCCAGTGTAGC	4338
QY	901	-----PheLeuLysProGly-----Asp	906
DB	4339	AGCGACAAATCAAGAAGATGCTGCCTGTGTCTCCCGAGGGCAGGGGGCTGCCTCCT	4398
QY	907	LysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAspIleSer	926
DB	4399	CCACAAAGAAAACAAACACTGCAGATATCTCTCAGGACCTGCACGGAAGAAACATTTTCG	4458
QY	927	Asp-----LeuIleSerPhePheThrSerGlnAsnIleMet	938
DB	4459	GATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAGCTTAAAGAAACAAGATCTGG	4518
QY	939	ValThr-----	940
DB	4519	GTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTGAGTAATACTCAAGCACTTCCT	4578
QY	941	-----MetIleAsnAspSer-----AspTyrValSerValAlaPro	952
DB	4579	CCGAGTCAAGAGAGTTAATGATGCCACCAAAACAATGAAGAAACACCTTAAAGCTGGCCAAG	4638
QY	953	HisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyrVal-----	967
DB	4639	GACAGTTCTGCAGATCGATTCTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACC	4698
QY	968	-----PheAlaAlaValPheAsnSerThrMetValTyrSerLeuProIleLeuVal	984
DB	4699	AGAAATAATGTCAAGGTGTGTTTCAATAACAAGGGCTGGCATGCCAATCAGCTCTTTTCCTG	4758
QY	985	AsnIleIleSerAsnTyrTyrLeu-----	992
DB	4759	AATGTTCATCAACATGCCATTCTCCGGGCCAACCTCGCAAAAGGGAGAGAACCTTAGCCAT	4818

Qy 907 LysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAspIleSer 926
Db 2759 CTTCCCCAGGAACCCGTAACAGCCTGTTGATCATCAATAACACAGAAATCAATATTGAA 2818
Qy 927 AspLeuIleSerPhePheThrSerGlnAsnIleMetValThrMet----- 941
Db 2819 GATTTTATAAAATCCTGAAGCATCAAAATATATCTTTGGAAAGTAGATGACTTTTGAAAAAC 2878
Qy 942 IleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMetHis 961
Db 2879 AGAAATGGTACTGATGGCCTCTCA-----TACAATGGAGCTATCATAGTTTCTGGT 2929
Qy 962 SerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeuPro 981
Db 2930 AAACAAAAGGATTATAGATTTTCAGTTGTGTGTAATACCAAGAGATTGCAGCTGTTTCCA 2989
Qy 982 IleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThrIle 1001
Db 2990 ATTCTTATGAATATTATCAGCAATGGCTACTTCAAAATGTTTAAATCACACACATATT 3049
Qy 1002 GlnIleTyrSerThrProPhePheGlnGluIleThrAspIleValPheLysIleGluLeu 1021
Db 3050 CGAATTGAGTCAAGCCCATTT-----CCTCTTAGCCACATAGGACTCTGGACTGGGTTG 3103
Qy 1022 TyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMet 1041
Db 3104 COGGATGGTTCCCTTTTCTTATTTTGGTTCTATGTAGCATTTCTCCTATATCACCATG 3163
Qy 1042 GluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeu 1061
Db 3164 GGCAGCATCAGTGATTACAGAAAAATGCTAAGTCCAGCTATGGATTTCAGGCCCTCTAC 3223
Qy 1062 ProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeu 1081
Db 3224 ACTTCTGCTTACTGTTGGTGGCAGGCACCTAGTGGAGCTCAGCTTCTTCTATTTAATCTC 3283
Qy 1082 IleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLys 1101
Db 3284 CTTTAAATG-----TATTTAATTTCTACATAGAAAAACATGCAGTACCTTCTTATT 3334
Qy 1102 PheLeuAlaValPheCysLeuIle-----GlyTyrValProSerValIle 1117
Db 3335 ACAAGCCAAATGTGTTTGTGTTTGGTTATAGTTACTCCTGGTTATGCAGCTTCTCTGTC 3394
Qy 1118 LeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrp 1137
Db 3395 TTCTTCATATATATGATATCATTTATTTTCGAAAAGGAGAAAAACAGTGGCCTTTGG 3454
Qy 1138 SerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePhe 1157
Db 3455 TCATTTTACTTCTTTTTCCTCCACCATCATGTTTCCATCATCTTTAATCAATCATTTT 3514
Qy 1158 ---MetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIle 1176
Db 3515 GACCTRAGTATATTGATTACCACCATG-----GTATGGTTCCCTTCA 3556
Qy 1177 TyrProLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLys 1196
Db 3557 TATACCTTGCTTGA---TTTAAAACTTTTTCGAAAGTG-----AGA 3595
Qy 1197 AsnValAspThrTyrAsnProTrpAspArgLeuSer----- 1208
Db 3596 GACCAGGAGCCTACAGAGAAATTTCCAGAGGCAAAATTTTGAATTTGATGCCACTGATTTT 3655
Qy 1209 ValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyr 1228
Db 3656 CTAGTCTGCTTCATACCTACTTTTCAGACTTTGCTATTTCGTTTTTGTCTTAAGATGCATG 3715
Qy 1229 GluLysLysTyrGlyArgSerIleArgLysAspPropPhePheArgAsnLeuSerThr 1248
Db 3716 GAACTAAATGTGGAAGAAAAAGATGCGAAAAAGATCCTGTTTTTCAGA---ATTTCCCCC 3772

Qy 1249 LysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspVal 1268
Db 3773 CAAAGTAGAGATGCTAAG--CCAATCCAGAGAAACCCATAGATGAAGATGATATT 3829
Qy 1269 LysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysPro 1288
Db 3830 CAAACAGAAAAGAAATAAGAACAGCCACTGCTCTGACCACTTCAATCTTAGATGAGAAACCT 3889
Qy 1289 SerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSer 1308
Db 3890 GTTATAATTGCCAGCTGTCTACACAAAAGAAATATGAGGCCAGAGAAAAGTTGCTTTTCA 3949
Qy 1309 ArgLysValLysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluIle 1328
Db 3950 AAGAGGAAGAAGAAATAAGCAGCAAGAAATATCTCTTCTGTGTTCAAGAGGTGAAATT 4009
Qy 1329 LeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGly 1348
Db 4010 TTGGATTGCTAGGACCCARTGGTGTGTAAGAAAGTTTCATCTATTAGAAATGATATCTGG 4069
Qy 1349 AspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGlu 1368
Db 4070 ATCACAAGCCAACCTGCTGGAGAGGTGGAACCTGAAAGCTGCAGTTCA----- 4117
Qy 1369 AspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAsp 1388
Db 4118 -----GTTTTGGCCACCTGGGTACTGCTCCTCAAGAGAACGTGCTGTGCCCCATG 4168
Qy 1389 ThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAsp 1408
Db 4169 CTGACGTTGAGGGAACACCTGGAGGTGTATGTCGCTCAAGGGCTCAGAAAGCGGAC 4228
Qy 1409 MetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLys 1428
Db 4229 GCGAGGCTCGCCATCGCAAGATTAGTGAGTGCTTCAAACTGCATGAGCAGCTGAATGTT 4288
Qy 1429 ThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeu 1448
Db 4289 CCTGTGCAGAAATTAAACAGCAGGAATCACGAGAAAGTTGTGTTTGTGCTGAGCCTCCTG 4348
Qy 1449 GlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLysAlaLys 1468
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Qy 1469 GlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaIleLeu 1488
Db 4409 CAGCAAAATGTGGCAGCAATCCAGGCAGTCAGTCAGTGTAAAAACACAGAGAGAGGTGCTCCTG 4468
Qy 1489 ThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMetValSer 1508
Db 4469 ACCACCCATAACCTGGCTGAGGGGGAAGCCTTGTGTGACCGTGTGGCCATCATGGTGTCT 4528
Qy 1509 GlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyr 1528
Db 4529 GGAAGGCTTAGATGCTTGGCTCCATCCACACACCTGAAAAACAAACTTGGCAAGGATTAC 4588
Qy 1529 PheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArg 1548
Db 4589 ATTCTAGAGCTAAAAGTGAAG-----GAAACGTCTCAAGTGACTTTGTTGCCACACT 4639
Qy 1549 GluIleGlnTyrIlePheProAsnAlaSerArgGlnGlnSerPheSerSerIleLeuAla 1568
Db 4640 GAGATTCTGAAGCTTTCCACAGGCTGCAGGCGAGGAAAGGTATTCTCTTGTGTTAAC 4699
Qy 1569 TyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeuGluGlu 1588
Db 4700 TATAAGCTGCCCGTGGCAGACGTTTACCTCTCTATCACAGACCTTTTCAAAATTAGAAGCA 4759
Qy 1589 AlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnVal 1608
Db 4760 GTGAAGCATAACTTTAACCTGGAAGAAATACAGCCTTCTCAGTGCACACTGGAGAAGGTA 4819
Qy 1609 PheValGluLeuThrLysGluGlnGluGluAsnSerCysGlyThrLeuAsnSer 1628

707	TTACAAACAGCTATTAACTAGCCATTATAGAAATCACAAACCAATCACCCCTGTGATGGAG	766	1763	TTGTCTGTTCACACAGAAGGATCAGTTACCATCTATAATAAAAAATCTCTCTCTGAAATGCAA	1822
196	GlueuGluSerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThr	215	550	GluMetPheGluAlaArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAsp	569
767	GAGTGTGATGTAGTTACTGTCTAACTATGAAGACATTACCTTTTCATAACTAAATAATCTT	826	1823	GACCTTGGAGGAATCAGAAAGATAACTGGCGTCTGTCTCAATCAATGTTCAATTTTGAC	1882
216	pheProArgGlyValIleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPhe	235	570	ValLeuThrValGluGluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsn	589
827	CTTCACAATGAGATGTTTATTTATCTCTTCTGCTTCATTTCTCCCACTTGTATATTT	886	1883	ATACTCACCGTGAAGGAAACCTCAGCCTGTTTGCTAAAAATAAAGGGATTTCATCTAAAG	1942
236	LeuAlaIleHisIleValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMet	255	590	AsnIleIleGlnGluValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLysAsp	609
887	ATATCACTCAATGTAACAAAGAGAGA--AAAAAGTCTAAGAATTTGATGAAATGATG	943	1943	GAAGTGGAAACAAGAGGTACAACGAATATATTGGAATTGGACATGCAAAACATTCAGAT	2002
256	GlyLeuHisAspThrAlaPheTyrLeuSerTyrValLeuLeuTyrThrSerLeuIlePhe	275	610	AsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaVal	629
944	GGTCTCCAAGATTGAGCATTTCTGGCTCTCTGGGTCTAATCTATGCTGGCTTCATCTTT	1003	2003	AACCTTGCTAAACATTTAAGTGAAGGACAGAAAAAGAAAGCTGACTTTTGGGATTACCAT	2062
276	LeuMetSerLeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSer	295	630	LeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSer	649
1004	ATTATTTCCATATTCTTTACAAATTATCATAACATTCACCCAAATTATAGTCATGACTGGC	1063	2063	TTAGGAGATCCTCAA-----	2077
296	SerIleValIlePheLeuLeuPheLeuTyrGlyLeuSerSerValPhePheAlaLeu	315	650	ArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsnArgValThrValPheSer	669
1064	TTCATGGTCATATTATACTCTTTTATATGGCTTATCTTTTGGTAGCTTTGGTGTTTC	1123	2077	-----	2077
316	MetLeuThrProLeuPheLysLysSerLysHisValGlyIleValGluPhePheValThr	335	670	ThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGly	689
1124	CTGATGAGTGTCTGTTAAAGAAAGCTGCTCCTCACCAATTGGTGTGTTTCTCCCTACC	1183	2078	-----TCCATGGATGAGGCTGACATCCTGGCTGATAGAAAAGTGATCATGTCCAATGGG	2131
336	ValAlaPheGlyPheIleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeu	355	690	MetLeuLysCysValGlySerSerMetPheLeuLysSerLysTyrGlyIleGlyTyrArg	709
1184	CTCTTTTGGGATGTCGGGA--TTCACTGTATTTTATGAACAACCTTCCTTCATCTCTG	1240	2132	AGACTGAAGTGTCCAGGTTCTTCTATSTTTTGAAGAAGGTGGGTCTTGGATATCAC	2191
356	ValTrpLeuPhe-----SerPropheCysHisCysThrPheValIleGlyIleAla	372	710	LeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeuSerSerLeuValLysGln	729
1241	GAGTGGATTTCGAATATTGTAGCCCTTT-----GCCTTTACTACTGGAATGATT	1291	2192	CTAAGTTTACATAGGAATGAAATATGTAAACCCAGAACAAATAACATCCTTCTACTCAT	2251
373	GlnValMetHisLeuGluAspPheAsn--GluGlyAlaSerPheSerAsnLeuThrAla	391	730	HisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeuPro	749
1292	CAGATTATCAAACTG--GATTATACTGAATGGTGTAAATTTTCTCTGACCCCTTCAGGA	1348	2252	CACATCCCCGATGCTAAATTAATAACAGAAACAGAAAGCTTGTATATATACTTTTGCCA	2311
392	GlyProTyrProLeuIleIleThrIleLeuMetLeuThrLeuAsnSerIlePheTyrVal	411	750	PheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeuAspSerHisSerAsnLeu	769
1349	GACTCATATACAATGATAGCAACTTTTCTATGTTGCTTTTGGATGGTCTCATCTACTTG	1408	2312	CTGGAAGGACAAATACATTTCCAGATCTTTTCCAGATCTTGGATAAGTGTCTTGACCAG	2371
412	LeuLeuAlaValTyrLeuAspGlnValIleProGlyGluPheGlyLeuArgArg-----	429	770	GlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLysLeuGlu	789
1409	CTATTGGCATATATCTTTTGACAAATTTTACCC-----TATGGAGATGAGCGCCATTAT	1462	2372	GGAGTGACAGGTTATGACATTTCCATGTCACTCTAAATGAAGTCTTTATGAAACTGGAA	2431
430	SerSerLeuTyrPheLeuLysProSerTyrTrpSerLysSerLysArgAsnTyrGluGlu	449	790	ValGluAlaGluIleAspGlnAlaAspTyrSerValPheThrGlnGlnProLeuGluGlu	809
1463	TCTCCTTTATTTTCTTGAATTCATCATCTGTTTCCAAACACCAAGGACTAATGCTAAG	1522	2432	GGACAGTCAACTATCGAACAA--GATTTC-----GAACAAGTGGAGATG	2473
450	LeuSerGluGlyAsnValAsnGlyAsnIleSerPheSerGluIleIleGluProValSer	469	810	GluMetAspSerLysSerPheAspGluMetGluGlnSerLeuLeuIleLeuSerGluThr	829
1523	GTTATTGAGAAAGAAATCGATGCTGAGCATCCCTCTGATGATTATTTTGAACCAGTAGCT	1582	2474	ATAAGAGACTCAGAAAGCCTCAATGAATGGAGCTGGCTCACTCTTCTCTCTGAAATG	2533
470	SerGluPheValGlyLysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLys	489	830	LysAlaSerLeuValSerThrMetSerLeuTyrLysGlnGlnMetTyrThrIleAlaLys	849
1583	CCTGAATTCACAGAAAGAGCCATCAGAAATGTTAAGAAGGAATATAAAGGA	1642	2534	CAGACAGCT--GTAGTGCATGGCCCTCTGGAGAATGCAAGTCTTTGCCATGGCACGG	2590
490	LysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIle	509	850	PheHisPhePheThrLeuLysArgGluSerLysSerValArgSerValLeuLeuLeuLeu	869
1643	AAATCTGGAAGAGTGAAGCATTTGAAAGGCTTGCTCTTTGACATATATGAAGGTCAAATC	1702	2591	CTCCGTTTCTTAAAGTTAAACAGTCAAACTAAA-----GTGTTATTGACCCCTA	2638
510	ThrAlaLeuLeuGlyHisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGly	529	870	LeuIlePhePheThrValGlnIlePheMetPheLeuValHis-----HisSerPhe	886
1703	ACGGCAATCCTGGGTACAGTGGAGCTGGCAAAATCTTCACTGCTAAATATTTCTTAATGGA	1762	2639	TTATTGGTATTGGAAATCGCAATATTTCCCTTTGATTGTTGAAAAATATATATATGCTATG	2698
530	LeuCysProProSerAspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAsp	549	887	LysAsnAlaValProIleLysLeuValProAspLeuTyrPheLeuLysProGlyAsp	906
			2699	TTAAATGAAAAGATCGATTGGGAATTTAAAAACCAATTTGATTTTCTCTCTCTCTGGACAA	2758

QY	1235	ArgSerIleArgLysAspPropPhePheArgAsnLeuSerThrLysSerLysAsnArgLys	1254
DB	3697	AAATCAATGAGAAAGGATCCTTCTTTAGAAATTTCTCAAGAAAGTAGTGATGTGTCAA	3756
QY	1255	LeuProGluProProAspAsnGluAspGluAspValLysAlaGluArgLeuLys	1274
DB	3757	AATCCAGAAAGAACCA-----GAAGGAGAGGATGAAGATGTTCCAGATGGAAGAGAGTGAGA	3810
QY	1275	ValLysGluLeuMetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAsn	1294
DB	3811	ACAGCAAATGCCTTGAATCTACTAATTTTGATGAGAAAGCCAGTCATCATTCGCCAGCTGT	3870
QY	1295	LeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysVal	1314
DB	3871	CTACGCAAGGAGTATGCAGGGAAGAGAAAGGCTGTTTTTCCAAGAGGAAGATAAAGATA	3930
QY	1315	AlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyPro	1334
DB	3931	GCCACGAGAAATGTCCTCTCTGTGTTAGAAAAGGTGAAGTTTATAGGATTATTAGGACAC	3990
QY	1335	AsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSer	1354
DB	3991	AATGGAGCTGGTAAAGACATCCATTAAAGGTGATAAATGGAGACACAAAACCAACTGCT	4050
QY	1355	GlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLys	1374
DB	4051	GGACAAGTGCTACTG-----AAAGGAGCGGTGGAGGGGATGCCCTGGAG	4095
QY	1375	CysMetGlyTyrCysProGlnIleAsnProLeuTyrProAspThrThrLeuGlnGluHis	1394
DB	4096	TTCTTGGGTACTGCCCTCAGGAGAACCGCTGTGGCCCAACCTGACAGTGAGGACGAC	4155
QY	1395	PheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSer	1414
DB	4156	CTGGAGGTGTACGCCCGCTGAAAGGGCTGAGGAAAGGGGATGCTGAGGTTGCCATCACA	4215
QY	1415	ArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPro	1434
DB	4216	CGGTTAGTGATCGCTCAAGCTGCAGGACCAGCTGAAGTCTCCGGTGAAGACCCTGTCA	4275
QY	1435	AlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThr	1454
DB	4276	GAGGGAATAAAGAGAAAGCTGTGCTTTGTCTTGAGCATACTGGGGAACCCGTCAGTGGTG	4335
QY	1455	LeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTyrArgAla	1474
DB	4336	CTTCTGGATGAGCCGTCGACCGGATGGACCCCGAGGGGAGCAGCAAAATGTGGAGGCC	4395
QY	1475	IleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGlu	1494
DB	4396	ATCCGGGCCACCTTTAGAAACACGGAAAGGGGTGCCCTCTTAACCCACCTACATGGCA	4455
QY	1495	GluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIle	1514
DB	4456	GAGGCTGAGGCCGTGTGTGACCGAGTGGCCATCATGTTGTTCTGGAGGTTGAGATGTATC	4515
QY	1515	GlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeu	1534
DB	4516	GGTTCCATCCAAACACCTGAAAAGCAAATTTGGCAAAGATTACCTGCTGGAGATGAAGGTG	4575
QY	1535	LysAspTrpIleGluAsnLeu---GluValAspArgLeuGlnArgGluIleGlnTyrIle	1553
DB	4576	AAG-----AACCTGGCACAAGTGGAGCCCTCCATGCAGAGATCCTGAGGCTT	4623
QY	1554	PheProAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLys	1573
DB	4624	TTCCCCCAGGCTGCTCGGCAGAAAGGTACTCTCTCTGATGGTTTATAAGTTGCCAGTG	4683
QY	1574	GluAspValGlnSerLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPhe	1593
DB	4684	GAAATGTGCAACCTTTAGCCCAAGCTTTCTTCAAATTAAGAAAGGTTAAACACAGAGCTTT	4743

QY 1594 AlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThr 1611
 Db 4744 GACCTAGAGGAGTACAGCCTCTCACAGTCTACCCCTGGAGCAGGTTTTCTCGAGCTCTCC 4803

QY 1614 LysGluGlnGlu-----GluGluAsp 1620
 Db 4804 AAGGAGCAGGAGCTGGGTGATTTTGAGGAGGAT 4836

RESULT 8
 US-10-796-280-369
 ; Sequence 369, Application US/10796280
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001510
 ; CURRENT APPLICATION NUMBER: US/10/796,280
 ; CURRENT FILING DATE: 2004-03-10
 ; NUMBER OF SEQ ID NOS: 68533
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 369
 ; LENGTH: 5185
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-796-280-369

Alignment Scores:
 Pred. No.: 1.87e-281 Length: 5185
 Score: 2967.50 Matches: 664
 Percent Similarity: 59.22% Conservative: 322
 Best Local Similarity: 39.88% Mismatches: 548
 Query Match: 35.22% Indels: 131
 Db: 6 Gaps: 34

US-10-090-458-5 (1-1642) x US-10-796-280-369 (1-5185)

QY 5 IleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLysAsnTyrLeuLeu 24
 Db 182 ATGAACACAGAAAGCGTGTATCAGCAACCAAGCAGCTTCTGTGCAAGAATTTTCTTAAG 241

QY 25 LysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeuPhePheLeuPhe 44
 Db 242 AAATGGAGGATGAAAGAGAGAGAGCTTATTGGAATGGGGCTCTCAATACTTCTAGGACTG 301

QY 45 TrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGluValProAsnIle 64
 Db 302 TGTATTGCTCTGTTTCCAGTCCATGAGAAATGTCAGTTTCTGGAATGGCTCCTCAG 361

QY 65 GluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProVal 84
 Db 362 AATCTGGGAAGGTAGATAAATTAAATAGCTCTTCTTAAATGTTGTGTATACACCAATA 421

QY 85 ThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu-----Pro 101
 Db 422 TCTAATTAAACCCAGCAGATAAATGAATAAACAGCAGCTTGCTCTTTTGAAGGAACA 481

QY 102 AspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSer 121
 Db 482 AGTGTCATTGGGGCACCAATAAAACACACATGAGCAAAATACTTCTGGAAAATTACCA 541

QY 122 LysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArgPhe 141
 Db 542 TATGCT-----ATGGGAATCATCTTTAATGAAACTTCTCTTATAAGTTAATAATT 592

QY 142 PheProAspMetIleProValSerSerIleTyrMet---AspSerArgAlaGlyCys--- 159
 Db 593 TTCCAGGGATAT-----AACAGTCCACTTTGGAAGAAAGAGATTCTCAGCTCATTTGCTGG 646

QY 160 -----SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrVal 175
 Db 647 GATGGATATGGTGAGTTTTCATGTACATTGACCAAACTACTGGAATAGAGGATTTGTGGCT 706

QY 176 LeuGlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLys 195

Db 1654 ATTTACGAAGGCCAAATCACTGCAATACCTTGGTACAGTGGAGCTGGAAGTCAACACTG 1713
QY 524 MetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIleTyrGlyHis 543
Db 1714 CTAACATTTCTAGTGGTTGTCTGTTCACCAAAAGGTTTCAGTCCACCATCTATAACAAT 1773
QY 544 ArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIleCysProGln 563
Db 1774 AAGCTTTCAGAAATGGCTGACCTAGAAAATCTCAGCAAGCTGACCGGAGTTGTCCACAA 1833
QY 564 LeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeuAlaSerIle 583
Db 1834 TCCAATGTGCAATTTGACTTCCTCACTGTAAAGAGAAACCTCAGACTCTTTGCTAAATA 1893
QY 584 LysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeuAspLeuAsp 603
Db 1894 AAAGGGATT-----CTGCCACAAGAGTGGATAA----- 1923
QY 604 MetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeu 623
Db 1923 ----- 1923
QY 624 SerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAla 643
Db 1924 -----GAGATTTTCCTGTTGGATGAACCAACTGCT 1953
QY 644 GlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsn 663
Db 1954 GGATGGATCCCTTTTCAAGACACCAAGTATGGAACCTTCTGAAAGAACCGCAAAACAGAC 2013
QY 664 ArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLys 683
Db 2014 CGCGTGATCCTCTTCAGTACCCAGTTTCATGGATGAGCCGACATCCTGGCGACAGGAAA 2073
QY 684 AlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeuLysSerLys 703
Db 2074 GTATTTCTCTCCCAAGGGAAGCTAAAGTCCGCGGCTCTCTTTGTTTCTAAAGAAGAAA 2133
QY 704 TrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeu 723
Db 2134 TGGGGATTGGATATACCTTAAGCTTGCAAGTTAAATGAAATATGTTGTGAGGAAACATA 2193
QY 724 SerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGln 743
Db 2194 ACATCACTTGTAAACAGCACATCCCTGATGCCAAATATCAGCCAAAGCGAAGGAAAA 2253
QY 744 LeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeu 763
Db 2254 CTTATTTATACATTACCTTAGAAAAGAACAAATAAATTTCCAGAACTTTACAAGGATCTT 2313
QY 764 AspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAsp 783
Db 2314 GATAGCTATCCTGACCTAGGAATTGAGAATTATGGTGTTCATGACAACTTTGAATGAA 2373
QY 784 ValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThr 803
Db 2374 GTATTCCTGAAGCTAGAAGGAAATCTACAATTAAATGATCGGACATTGCTATTTGGGA 2433
QY 804 GlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeu 823
Db 2434 GAAGTACAAGCGGAAAAAGCTGACGACACTGAAAGGCTTGTGAGATGGAACAAGCTCCTC 2493
QY 824 LeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGln 843
Db 2494 TCTTCACCTTAACAAGATGAGAAAGACA--ATAGGTGGTGGCTCTCTGGCGACAGCAA 2550
QY 844 MetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLysSerValArg 863
Db 2551 ATCTGCGCAATTGCAAGGTTTCGTTGTTAAAGTTAAAGCATGAAGAAAGCTCTTTTA 2610
QY 864 SerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHis 883

Db 2611 GCACTGCTATTATTAATTTGCTGGATTTGCCCCCTCTTCTTGTGGAGTATACCATGGTG 2670
QY 884 HisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLys 903
Db 2671 AAAATATATCAAAACAGTTACACC--TGGGAACCTTCTCCTCATTTGTATTCTCTTGCT 2727
QY 904 ProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSerAlaAspSer 923
Db 2728 CCTGGACAACAACCATGACCTCTCACTCACTCACTGATCATCAATAAAACAGGGGCA 2787
QY 924 AspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThrMet----- 941
Db 2788 ACCATTGATGACTTTATACAGTCTGTGGAGCACCAGAACATAGCTTTAGAAAGTGGATGCA 2847
QY 942 -----IleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsn 958
Db 2848 TTTGGAACCTAGAAATGGCACAGATGACCCATCT-----TATAATGGAGCCATCACA 2898
QY 959 ValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyr 978
Db 2899 GTGTGTTGTAATGAAAAGAATTACAGCTTTTCGTAGCATGCAATGCCAAAAGATTGAAT 2958
QY 979 SerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThr 998
Db 2959 TGCTTCCCAGTTCTTATGGACATTGTTAGTAATGGGCTACTTGGAAATGGTTAAACCATCA 3018
QY 999 GluThrIleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLys 1018
Db 3019 GTACATATCCGAACCTGAAAGAGTACATTTTTCGAGAAATGGACAGGACAAATCCAATCGGA 3078
QY 1019 IleGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyr 1038
Db 3079 TTCCTGGCATATATCATGTTCTGGCTG-----GTTTTAACATCGAGTTGCCACCTTAC 3132
QY 1039 PheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSer 1058
Db 3133 ATTGCCATGAGCAGCATCGATGATTATAAGAACAGAGCTCGTCCCAGCTACGGATTTC 3192
QY 1059 GlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePhe 1078
Db 3193 GGACTCTCCCCTTCTGCTTACTGGTTTGGGAGCGCTGGTGGATGTTTCCCTGTACTTC 3252
QY 1079 IleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyr 1098
Db 3253 TTTGGTCTCGTTTTTATATATTTAATGAGCTACATTTCAAACCTTCGAAGACATGCTACTT 3312
QY 1099 ThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeu 1118
Db 3313 ACAATAATTCAATATTATTTCAAATCCCATGTGCTGTGGTTATTCCTTTTCCCTCATCTTC 3372
QY 1119 PheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSer 1138
Db 3373 ATGACATACGTGATTTCTCTCATCTTTTCGAAGGGGAGAGAAAAATAGTGGCATTTGGTCA 3432
QY 1139 PheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMet 1158
Db 3433 TTTTGTTCATGTTGTACATGATTTCTGTGGCTGGATTTGCGTTTCAGTATCTTC--- 3489
QY 1159 GlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrPro 1178
Db 3490 -----GAAAGTGATATTCATTTATCTTCACTTTTAAATACCACCTGCCACA 3537
QY 1179 LeuLeuGlyCysLeuIle-----SerPheIleLysIleSer-----TrpLysAsnVal 1194
Db 3538 ATGATTGGCTGTTTGTTCATTATCTTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3597
QY 1195 ArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerPro 1214
Db 3598 CGAATGGATGTACAGCCATTT-----CTGGTATTCCTTAATTCCT 3636
QY 1215 TyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGly 1234
Db 3637 TTCCITTCATTTTATCATTTTTTCTTTTACTCTTCGATGCTCGAATGGAAGTTGGAAG 3696

Db 4684 GAAGATGTGCAACCTTTAGCCCAAGCTTTCTTCAAATTAGAGAAAGGTTAAACAGAGCTTT 4743
Qy 1594 AlaileGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThr 1613
Db 4744 GACCTAGAGGAGTACAGCTCTCACAGTCTACCTGGAGCAGGTTTCTCTGGAGCTCTCC 4803
Qy 1614 LysGluGlnGlu-----GluGluAsp 1620
Db 4804 AAGGAGCAGGAGCTGGGTGATTTTGAGGAGGAT 4836
RESULT 7
US-10-788-792-45
; Sequence 45, Application US/10788792
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
; FILE REFERENCE: 5152
; CURRENT APPLICATION NUMBER: US/10/788,792
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,655
; PRIOR FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 45
; LENGTH: 5677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-788-792-45
Alignment Scores:
Pred. No.: 3e-295 Length: 5677
Score: 3108.00 Matches: 672
Percent Similarity: 60.02% Conservative: 319
Best Local Similarity: 40.70% Mismatches: 536
Query Match: 36.89% Indels: 124
DB: 6 Gaps: 26
US-10-090-458-5 (1-1642) x US-10-788-792-45 (1-5677)
Qy 6 ArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLysAsnTyrLeuileLys 25
Db 148 AGAAGATCAGTGTGTCAACAACTTGGGCTTATTATGCAAGAACTTTCTTAAAAA 207
Qy 26 CysArgThrLysLysSerSerValGlnGluLeuLeuPheProLeuPhePheLeuPheTrp 45
Db 208 TGGAGATGAAAAGAGAGCTCTTAATGGAATGGCTGAATTCATTGCTCCTACTACTTTGT 267
Qy 46 LeuileLeuileSerMetMetHisProAsnLysLysTyrGluGluValProAsnileGlu 65
Db 268 TTGTATATATATCCCTCATAGTCATCAAGTAAATGATTTTCTTCACTGCTTACCATGGAC 327
Qy 66 LeuAsnProMetAspLysPheThrLeuSerAsnLeuileLeuGlyTyrThrProValThr 85
Db 328 CTGGGACGGGTAGATACATTTAATGAATCCAGATTTTCTGTTGTATACACACCTGTCACC 387
Qy 86 AsnIleThrSerSerIleMetGlnLysValSerThrAsp----- 98
Db 388 AACAGACCCACAGATAATGAATAAAGTAGCCTCTACTCCCTTCCCTGGCAGGTAAAGAG 447
Qy 99 -----HisLeuProAspValileIleThrGluGluTyrThrAsnGluLysGluMetLeu 116
Db 448 GTCTTGGGACTGCCAGATGAGGAAAGTATTAAAGAAATTCACA----- 489
Qy 117 ThrSerSerLeuSerLysProSerAsnPheValGlyValValPheLysAspSerMetSer 136
Db 490 -----GCAATATATCTGAAGAAATAGTAAGAGTCACTCCTTACTAATACTACTCA 540
Qy 137 TyrGluLeuArgPhe---PheProAspMetIleProValSerSerIleTyrMetAspSer 155
Db 541 TATCATTTGAAGTTCTTGCTAGGACATGGAATGCCAGCAAGAGAGGAGCACCAAGGACCAT 600

Qy 156 ArgAlaGlyCysSerLysSer-----CysGluAlaAlaGlnTyrTrpSer 170
Db 601 ACAGCTCATTTGTTATGAAACAAATGAAGATGTTTACTGTGAAGTTTCAGTATTTTGGAG 660
Qy 171 SerGlyPheThrValLeuGlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsn 190
Db 661 GAAGGTTTGTGGCTCTTCAAGCTGCCAATTAATGCTGCTATTATAGAAATCACAAACAAT 720
Qy 191 ValSerLeuTrpLysGluLeuGluSerThrLysAlaValIleMet----- 205
Db 721 CACTCAGTGATGGAGGAGCTGATGTCACTTACTGGAAAAAATATGAAGATGCTATTCCTTC 780
Qy 206 ---GlyGluThrAlaValValGluIleAspThrPheProArgGlyValIleLeuIleTyr 224
Db 781 ATTGGTCAATCAGGAGTTATA-----ACTGATTTGTACCTTTTTC 822
Qy 225 LeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIleValAlaGluLys 244
Db 823 TGCATTATTTTCATTTCTCTCATTTACTTATGTCATCTGTTAATGTCCAGAGAGAGG 882
Qy 245 GluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThrAlaPheTrpLeu 264
Db 883 ---AAAAGGATGAAGCCTTGATGACAATGATGGGTCTTCGGGATTCAGCGTTCCTGGCTC 939
Qy 265 SerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeuMetAlaValIle 284
Db 940 TCCTGGGGTTTGTCTATGCTGGTTTCATCTTCATTATGGCCCTTTTCTTGGCACTTGTT 999
Qy 285 AlaThrAlaSerLeuLeuPheProGlnSerSerIleValIlePheLeuLeuPhePhe 304
Db 1000 ATAAGATCTACCCAGTTTATCATTTTGTCTGGTTCATGGTAGTCTTCAGCCTCTTCTC 1059
Qy 305 LeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeuPheLysLysSer 324
Db 1060 CTGTATGGATTATCTTTGGTAGCTTTGGCTTTCTTAAATGAGCATCTCTGTAAGAAATCT 1119
Qy 325 LysHisValGlyIleValGluPhePheValThrValAlaPheGlyPheIleGlyLeuMet 344
Db 1120 TTCCTCACCGCCTGTGTGTCTCCTCCTCACTGTCTTTTGGGGTGTCTGGGG---TTC 1176
Qy 345 IleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSerProPheCysHis 364
Db 1177 ACATCACTGTACAGACACACTTCTCGATCCTCTGGAGTGGATTTTAAAGCTTGTAGTCCC 1236
Qy 365 CysThrPheValIleGlyIleAlaGlnValMetHisLeuGlu---AspPheAsnGluGly 383
Db 1237 TTTGCCCTTCATGCTTGAATGGCCAGCTTTTACACTTGGACTATGATTTGAATTTCTAAT 1296
Qy 384 AlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleIleMetLeu 403
Db 1297 GCA---TTTCCTCATCCATCGGACGGCTCAAATCTCATTTGTAGCAACAATAATTCATGTTG 1353
Qy 404 ThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnValIleProGly 423
Db 1354 GCATTTGACACTTGCTCTATCTGGCATTTGGCGATTACTTTGAAAAAATTTTGCCAAAT 1413
Qy 424 GluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrpSerLysSer 443
Db 1414 GAATATGGACATCGACGTCACCTTTGTTTCTTCTGAAGTCCCTCATTTTGGTCTCAAACA 1473
Qy 444 LysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSerPheSerGlu 463
Db 1474 CAAAGACTGATCAGTGGCCCTTGAAGATGAATGGATGCCGATCCTTCATTTCATGAC 1533
Qy 464 IleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIleSerGlyIle 483
Db 1534 TCTTTTGAACAAGCCCTCCAGAAATTCCAAGGGAAGAGCCCATCAGAAATGTT 1593
Qy 484 GlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAsp 503
Db 1594 ACAAAAGAATATAAGGAAGCCCTGATAAATAAGAGCCCTTGAAGATCTGGTATTTGAC 1653
Qy 504 IleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLysSerThrLeu 523

Db 541 TATCATTTGAAGTTCTTGCTAGGACATGGAAATGCCAGCAAAGAGGAGCACAAGGACCAT 600
QY 156 ArgAlaGlyCysSerLysSer-----CysGluAlaAlaGlnTyrTrpSer 170
Db 601 ACAGCTCATTTGTTATGAACAACAATGAAGATGTTTACTGTGAAGTTTCAGTATTTTGGAAAG 660
QY 171 SerGlyPheThrValLeuGlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsn 190
Db 661 GAAGGTTTGTGGCTCTTCAAGCTGCCATTAAATGCTGCTATTATAGAAATCACAACAAAT 720
QY 191 ValSerLeuTrpLysGluLeuGluSerThrLysAlaValIleMet----- 205
Db 721 CACTCAGTGATGGAGAGCTGATGTCAGTTACTGGAAAAAATATGAAGATGCATTCCTTC 780
QY 206 ---GlyGluThrAlaValValGluIleAspThrPheProArgGlyValIleLeuIleTyr 224
Db 781 ATTGGTCAATCAGGAGTTATA-----ACTGATTTGTACCTTTTTC 822
QY 225 LeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIleValAlaGluLys 244
Db 823 TGCATTATTTTCATTTCTCTCATTCATTACTATGATCATCTGTTAATGTCAAGAGAGAGG 882
QY 245 GluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThrAlaPheTrpLeu 264
Db 883 ---AAAAGGATGAAGGCCTTGATGACAAATGATGGGTCTTCGGGATTCAGCGTTCTGGCTC 939
QY 265 SerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeuMetAlaValIle 284
Db 940 TCCTGGGTTTGTCTATGCTGCTGTTTTCATCTTCATTATGGCCCTTTCTTGGCATTGTT 999
QY 285 AlaThrAlaSerLeuLeuPheProGlnSerSerIleValIlePheLeuLeuPhePhe 304
Db 1000 ATAAGATCTACCCAGTTTATCATTTTGTCTGGCTTCATGGTAGTCTTCAGCCTCTTTCTC 1059
QY 305 LeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeuPheLysLysSer 324
Db 1060 CTGTATGGATTATCTTTGGTAGCTTTGGCTTCTTAAATGAGCATCTTGTAAGAAATCT 1119
QY 325 LysHisValGlyIleValGluPhePheValThrValAlaPheGlyPheIleGlyLeuMet 344
Db 1120 TTCCTCACCGGCCTGGTGTGTTCTCCTCCTCACTGTCTTTGGGGTGTCTGGG---TTC 1176
QY 345 IleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSerProPheCysHis 364
Db 1177 ACATCACTGTACAGACACACTTCCTGCATCCTTGGAGTGGATTAAAGCTTGCTAGTCCC 1236
QY 365 CysThrPheValIleGlyIleAlaGlnValMetHisLeuGlu---AspPheAsnGluGly 383
Db 1237 TTTGCCCTTCATGCTTGGAAATGGCCAGCTTTTACACTTGGACATGATTTGAATTTCTAAT 1296
QY 384 AlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIleIleMetLeu 403
Db 1297 GCA---TTTCTCATCCATCGGACGGCTCAAAATCTCATTTGTAGCAACAAATTTTCATGTTG 1353
QY 404 ThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnValIleProGly 423
Db 1354 GCATTTGACACTTGCCTCTATCTGGCATTGGCGATTACTTTGAAAAAATTTTGCCAAAT 1413
QY 424 GluPheGlyLeuArgSerSerLeuTyrPheLeuLysProSerTyrTrpSerLysSer 443
Db 1414 GAATATGGACATCGACGCTCCACCTTTGTTTCTCTGAAGTCCCTCATTTTGGTCTCAAAACA 1473
QY 444 LysArgAsnTyrGluGluLeuSerGlyAsnValAsnGlyAsnIleSerPheSerGlu 463
Db 1474 CAAAAGACTGATCACGTGGCCCTTGAAGATGAAATGGATGCCATCCTTCATTTTCATGAC 1533
QY 464 IleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIleSerGlyIle 483
Db 1534 TCTTTGAACAAGCGCCCTCCAGAATTCCAAGGGAAGAAAGCCATCAGAAATGTT 1593
QY 484 GlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAsp 503
Db 1594 ACAAAAGAAATATAAAGGAAAGCCTGTATAAAATAGAGCCTTGAAGATCTGGTATTGAC 1653

QY 504 IleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLysSerThrLeu 523
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QY 524 MetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIleTyrGlyHis 543
Db 1714 CTAAACATTTCTTAGTGGTTGTCTGTTCCACCAAGGTTTCAGTCAACATCTATAACAAT 1773
QY 544 ArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIleCysProGln 563
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QY 564 LeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeuAlaSerIle 583
Db 1834 TCCAATGTGCAATTGACTTCTCTCACTGTAAAGAGAAACCTCAGACTCTTTTGCTAAAATA 1893
QY 584 LysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeuAspLeuAsp 603
Db 1894 AAAGGATT-----CTGCCACAAGAAGTGGATAAA----- 1923
QY 604 MetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeu 623
Db 1923 ----- 1923
QY 624 SerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAla 643
Db 1924 -----GAGATTTTCTGTGGATGAACCAACTGCT 1953
QY 644 GlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsn 663
Db 1954 GGATTGGATCCCTTTTCAAGACACCAAGTATGGAACCTTCTGAAAGAACGCAAAACAGAC 2013
QY 664 ArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLys 683
Db 2014 CGCGTGATCCTCTTCAGTACCCAGTTCATGGATGAGCCGACATCTGGCGGACAGGAAA 2073
QY 684 AlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeuLysSerLys 703
Db 2074 GTATTTCTCTCCCAAGGGAAGCTAAAGTCCGCGGCTCTTCTTTGTTCTAAAGAAGAAA 2133
QY 704 TrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeu 723
Db 2134 TGGGGGATTGGATATCACTTAAGCTTGCACTTAAATGAAATATGTTGTTGAGGAAAACATA 2193
QY 724 SerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGln 743
Db 2194 ACATCACTTGTAAAACAGCACATCCCTGATGCCAAATATATCAGCCAAAAGCGAAGGAAA 2253
QY 744 LeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeu 763
Db 2254 CTTATTTATACATTACCCTTAGAAAAGAACAAAATAAATTTCCAGAACTTTACAGGATCTT 2313
QY 764 AspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAsp 783
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QY 784 ValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThr 803
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QY 804 GlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeu 823
Db 2434 GAAGTACAAGCGGAAAAAGCTGACGACACTGAAAGGCTTGTGTGATGGAACAAGTCCCTC 2493
QY 824 LeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGln 843
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Qy 1255 LeuProGluProProAspAsnGluAspGluAspValLysAlaGluArgLeuLys 1274
Db 3757 AATCCAGAAGAACCA-----GAAGGAGAGGATGAAGATGTTTCAGATGGAAGAGTGAGA 3810
Qy 1275 VallysGluLeuMetGlyCysGlnCysGluGluLysProSerIleMetValSerAsn 1294
Db 3811 ACAGCAAAATGCCTTGAATTTACTAATTTTGTATGAGAAGCCAGTCATCATTCAGCTGT 3870
Qy 1295 LeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysVal 1314
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Qy 1315 AlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyPro 1334
Db 3931 GCCACGAGAAATGTCTCTCTGTGTGTAGAAAAGGTGAAGTTTTTAGGATATTAGGACAC 3990
Qy 1335 AsnGlyAlaGlyLysSerThrIleIleAsnIleValGlyAspIleGluProThrSer 1354
Db 3991 AATGGAGCTGGTAAAGACATCCATTAAAGGTGAAGTGTTCAGGATATTAGGACAC 4050
Qy 1355 GlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLys 1374
Db 4051 GGACAAAGTGCTACTG-----AAAGGAGCGGTGGAGGGGATGCCCTGGAG 4095
Qy 1375 CysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHis 1394
Db 4096 TTCCTGGGGTACTGCCCTCAGGAGAACCGCTGTGGCCCAACCTGCAGTGAGGCAGCAC 4155
Qy 1395 PheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSer 1414
Db 4156 CTGGAGGTGTACGCCCGCGTGAAGGGCTGAGGAAAGGGGATGCTGAGGTTGCCATCACA 4215
Qy 1415 ArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPro 1434
Db 4216 CGGTAGTGGATGCGCTCAAGCTGCAGGACCGAGTGAAGTCTCCGGTGAAGACCTTGTCA 4275
Qy 1435 AlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThr 1454
Db 4276 GAGGGAATAAAGAGAAAGCTGTGCTTTGTCTGAGCATACTGGGGAACCGTCACTGGTG 4335
Qy 1455 LeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAla 1474
Db 4336 CTTCTGGATGAGCCGTCGACCGGATGACCCCGGGGCGAGCAGCAAAATGTGGCAGGCC 4395
Qy 1475 IleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGlu 1494
Db 4396 ATCCGGGCCACCTTTAGAAACACGGAAGGGTGGCTCTCCTAACCACCCACTACATGGCA 4455
Qy 1495 GluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIle 1514
Db 4456 GAGGCTGAGGCCGTGTGACCGAGTGGCCATCATGATCTCTGGAGGTTGAGATGTATC 4515
Qy 1515 GlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeu 1534
Db 4516 GGTTCATCCACACCTGAAAAGCAAATTTGGCAAAGATTACCTGCTGGAGATGAAGGTG 4575
Qy 1535 LysAspTrpIleGluAsnLeu--GluValAspArgLeuGlnArgGluIleGlnTyrIle 1553
Db 4576 AAG-----AACCTGGCACAAAGTGGAGGCCCTCCATGCAGAGATCCTGAGGCTT 4623
Qy 1554 PheProAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLys 1573
Db 4624 TTCCCCCAGGCTGCTCGGCAGGAAAGGTACTCTCTGTATGTTTATAAGTTGCCAGTG 4683
Qy 1574 GluAspValGlnSerLeuSerGlnSerPhePheLysLeuGluGluAlaLysHisAlaPhe 1593

Db 4684 GAAGATGTGCAACCTTTAGCCCAAGCTTTCTTCAAATTAGAGAAGGTTAAACAGAGCTTT 4743
Qy 1594 AlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThr 1613
Db 4744 GACCTAGAGGAGTACAGCCTCTCACAGTCTACCTGGAGCAGGTTTTTCTCTGGAGCTCTCC 4803
Qy 1614 LysGluGlnGlu-----GluGluAsp 1620
Db 4804 AAGGAGCAGGAGCTGGGTGATTTTGAGGAGGAT 4836
RESULT 6
US-10-764-425-40
; Sequence 40, Application US/10764425
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: US/10/764,425
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 5677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-764-425-40
Alignment Scores:
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Qy 6 ArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLysAsnTyrLeuIleLys 25
Db 148 AGAAAGATCAGTGTGTCTCAACAACTTGGGCCCTTATTATGCAAGAACTTCTTAAAAA 207
Qy 26 CysArgThrLysLysSerSerValGlnGluIleLeuPheProLeuPheLeuPheTrp 45
Db 208 TCGAGAATGAAAAGAGAGTCTCTTAATGGAATGGCTGAATTCAATTGCTCTACTACTTGT 267
Qy 46 LeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGluValProAsnIleGlu 65
Db 268 TTGTATATATATCTCATAGTCATCAAGTAAATGATTTTCTTCTCCTGCTTACCATGGAC 327
Qy 66 LeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProValThr 85
Db 328 CTGGGACGGGTAGATACATTTAATGAATCCAGATTTCTGTTGTATACACACCTGTCAAC 387
Qy 86 AsnIleThrSerSerIleMetGlnLysValSerThrAsp----- 98
Db 388 AACACGACCCCAACAGATAATGAATAAAGTAGCTCTACTCCCTTCTCTGGCAGGTAAGAG 447
Qy 99 -----HisLeuProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeu 116
Db 448 GTCTTGGGACTGCCAGATGAGGAAAGTATTAAAGAATTACACA----- 489
Qy 117 ThrSerSerLeuSerLysProSerAsnPheValGlyValValPheLysAspSerMetSer 136
Db 490 -----GCAATATATCTGAAGAAATAGTAAGAGTCAACCTTTACTAATACTACTCA 540
Qy 137 TyrGluLeuArgPhe--PheProAspMetIleProValSerSerIleTyrMetAspSer 155

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Db 1654 ATTTACGAAGGCCAAATCACTGCAATACTTGGTCACAGTGGAGCTGGAAGTCAACACTG 1713
QY 524 MetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIleTyrGlyHis 543
Db 1714 CTAAACATTCTTAGTGGTGTCTGTTCCCAACCAAGGTTTCAGTCACCATCTATAACAAT 1773
QY 544 ArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIleCysProGln 563
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QY 564 LeuAspIleHisPheAspValLeuThrValGluGlnAsnLeuSerIleLeuAlaSerIle 583
Db 1834 TCCAATGTGCAATTGTCTCTCACTGTGAAGAGAAACCTCAGACTCTTTGCTAAATA 1893
QY 584 LysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeuAspLeuAsp 603
Db 1894 AAAGGATT-----CTGCCACAAGATGGATAA----- 1923
QY 604 MetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeu 623
Db 1923 ----- 1923
QY 624 SerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAla 643
Db 1924 -----GAGATTTTCCTGTTGGATGAACCAACTGCT 1953
QY 644 GlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsn 663
Db 1954 GGATGGATCCCTTTTCAAGACACCAAGTATGGAACCTTCTGAAAGAACGCCAAACAGAC 2013
QY 664 ArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLys 683
Db 2014 CCGGTGATCCTCTTCAGTACCAGTTTCATGGATGAGGCCGACATCCTGGCGGACAGGAA 2073
QY 684 AlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeuLysSerLys 703
Db 2074 GTATTTCTCTCCCAAGGAAGCTAAAGTGCGGGCTCTTTGTTTCTAAAGAAGAA 2133
QY 704 TrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeu 723
Db 2134 TGGGGATTGGATATCACTTAAGCTTGCAAGTTAAATGAATATGTGTTGAGGAAACATA 2193
QY 724 SerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGln 743
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QY 744 LeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeu 763
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QY 764 AspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAsp 783
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QY 784 ValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThr 803
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Db 2434 GAAGTACAAGCGGAAAAGCTGACGACACTGAAGCTTGTGAGATGGAACAAGTCCCTC 2493
QY 824 LeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGln 843
Db 2494 TCTTCACTTAACAAGATGAGAAAGACA--ATAGGTGGTGTGGCTCTCTGGCGACAGCAA 2550
QY 844 MetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLysSerValArg 863
Db 2551 ATCTGCGCAATTGCAAGGTTGCTTGTGTTAAAGTTAAAGCATGAAGAAAGCTCTTTTA 2610

QY 864 SerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHis 883
Db 2611 GCACTGCTATTAATCTAATGGCTGGATTTTGCCTCTTCTTGTGGAGTATACCATGGTG 2670
QY 884 HisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLys 903
Db 2671 AAAATATATCAAAACAGTTACACC--TGGGAACCTTCTCCTCATTTGTATTTCTTGCT 2727
QY 904 ProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSerAlaAspSer 923
Db 2728 CTGGACAACAACCATGACCTCTCACTCAACTACTGATCATCAATAAAACAGGGGCA 2787
QY 924 AspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThrMet----- 941
Db 2788 AGCATTGATGACTTTTATACAGTCTGTGGAGCACCAACATAGCTTTAGAAAGTGGATGCA 2847
QY 942 -----IleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsn 958
Db 2848 TTGGAACTAGAAATGGCACAGATGACCCATCT-----TATAATGGAGCCATCACA 2898
QY 959 ValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyr 978
Db 2899 GTGTGTTGTAATGAAAGAAATTACAGCTTTTCGTAGCATGCAATGCCAAAGATTGAAT 2958
QY 979 SerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThr 998
Db 2959 TGCTTCCAGTTCTTATGGACATTTGTAGTAATGGCTACTTGGAAATGGTTAAACCATCA 3018
QY 999 GluThrIleGlnIleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLys 1018
Db 3019 GTACATATCCGAACCTGAAAGAAGTACATTTTGGAGAATGGACAGGACAAATCCAATCGGA 3078
QY 1019 IleGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyr 1038
Db 3079 TTCTCTGGCATATATCATGTTCTGGCTG-----GTTTAAACATCGAGTTGCCACCTTAC 3132
QY 1039 PheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSer 1058
Db 3133 ATTGCCATGACGACGATCGATGATTATAAGAACAGAGCTCGTCCCAGCTACGATTTC 3192
QY 1059 GlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePhe 1078
Db 3193 GGACTCTCCCTTCTGCTTACTGTTTGGGCGAGCGCTGGTGGATGTTTCCCTGTACTTC 3252
QY 1079 IleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyr 1098
Db 3253 TTGGTCTTGGTTTTTATATATTTAATGAGCTACATTTCAAACCTTCGAAGACATGCTACTT 3312
QY 1099 ThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeu 1118
Db 3313 ACAATAATTCAATATTAATCAATCCCATGTGCTGTTGGTTATTCCTTTTCCCTCATCTTC 3372
QY 1119 PheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSer 1138
Db 3373 ATGACATACGTGATTTCTTTCATCTTTTCGCAAGGGAGAAAAAATAGTGGCATTTGGTCA 3432
QY 1139 PheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMet 1158
Db 3433 TTTGTTTCTATGTTGTCACCTGATTTCTCTGTGGCTGGATTTGGCTTCAGTATCTTC--- 3489
QY 1159 GlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrPro 1178
Db 3490 -----GAAAGTGATATTCATTTATCTTTCATCTTTTAAATACCACCTGCCACA 3537
QY 1179 LeuLeuGlyCysLeuIle-----SerPheIleLysIleSer-----TrpLysAsnVal 1194
Db 3538 ATGATTGGCTGTTTGTCTTATCTTCTCATCTCTCTCTTTTCTCTCTCTCTCTCTCTCTCT 3597
QY 1195 ArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerPro 1214
Db 3598 CGAATGGATGTACAGCCATTT-----CTGGTATTCCTTAATTCCT 3636

Db 2551 ATCTGGCAATTGCAAGGGTTTCGCTTGTAAAGTTAAAGCATGAAGAAAGCTCTTTTA 2610
Qy 864 SerValleuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuValHis 883
Db 2611 GCACTGCTATTAAATCTTAATGGCTGGATTTCGCCCTCTTCTTGTGGAGTATACCATGGTG 2670
Qy 884 HisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLys 903
Db 2671 AAAATATATCAAAACAGTTACACC---TGCGAATCTTCTCCTCATTTGTATTCTCTTGCT 2727
Qy 904 ProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSer 923
Db 2728 CCTGGACAACACACATGACCCCTCTCACTCAACTACTGATCATCAATAAAACAGGGGCA 2787
Qy 924 AspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThrMet----- 941
Db 2788 AGCATTGATGACTTTATACAGTCTGTGGAGCACCAACATAGCTTTAGAAAGTGGATGCA 2847
Qy 942 -----IleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsn 958
Db 2848 TTTGGAAC TAGAAATGGCACAGATGACCCATCT-----TATAATGGAGCCATCACA 2898
Qy 959 ValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyr 978
Db 2899 GTGTGTTGTAATGAAAGAATAACAGCTTTCGTTAGCATGTCATGCCAAAAGATTGAAT 2958
Qy 979 SerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThr 998
Db 2959 TGCTTCCCAGTCTTATGGACATTGTTAGTAATGGGCTACTTGGAAATGGTTAAACCATCA 3018
Qy 999 GluThrIleGlnIleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLys 1018
Db 3019 GTACATATCCGAACTGAAAGAAGTAGATACATTTTGGAGAATGGACAGACAATCCAATCGGA 3078
Qy 1019 IleGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyr 1038
Db 3079 TTCCTGGCATATATCATGTTCTGGCTG-----GTTTTAACATCGAGTGGCCACCTTAC 3132
Qy 1039 PheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSer 1058
Db 3133 ATTGCCATGAGCAGCATGATGATTATAGAACACAGAGCTCGGTCCAGCTACGGATTTC 3192
Qy 1059 GlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePhe 1078
Db 3193 GGACTCTCCCTTCTGCTTACTGTTTGGCAGGCGCTGGTGGATGTTCCCTGTACTTC 3252
Qy 1079 IleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyr 1098
Db 3253 TTGGTCTTCGTTTTATATATTTAATGAGCTACATTTCAAACCTTCGAAGACATGCTACTT 3312
Qy 1099 ThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeu 1118
Db 3313 ACAATAATTCAATATATTCAAATCCCATGCTGTTGGTTATTCCTTTTCCCTCATCTTC 3372
Qy 1119 PheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSer 1138
Db 3373 ATGACATACGTGATTCTTCATCTTTTCGCAAGGGAGAAAAAATAGTGGCATTTGGTCA 3432
Qy 1139 PheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMet 1158
Db 3433 TTTTGTTCATGTTGTCACTGATTTCTCTGTGGCTGGATTTGGCGTTCAGTATCTTC--- 3489
Qy 1159 GlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrPro 1178
Db 3490 -----GAAAGTGATATTCCATTTATCTTCACTTTTTHAATACCACTGCCACA 3537
Qy 1179 LeuLeuGlyCysLeuIle-----SerPheIleLysIleSer-----TrpLysAsnVal 1194
Db 3538 ATGATTGGCTGTTTGTCTTATCTTCTCATCTTCTCTTCTTCTCTCTCTCTCTCTCTCTCT 3597
Qy 1195 ArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerPro 1214

Db 3598 CGAATGGATGTACAGCCATTT-----CTGGTATTCCTAATTCCT 3636
Qy 1215 TyrLeuGlnCysValleuLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGly 1234
Db 3637 TTCCTTTCATTTTATCTTTTCTTTTACTCTTCGATGTCCTGAATGGAAGTTTGGAAAG 3696
Qy 1235 ArgSerIleArgLysAspProphePheArgAsnLeuSerThrLysSerLysAsnArgLys 1254
Db 3697 AAATCAATGAGAAAGGATCCCTTTCTTTTAGAATTTCTCCAAGAAGTAGTGTTGTGTCAA 3756
Qy 1255 LeuProGluProProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLys 1274
Db 3757 AATCCAGAAGAACCA-----GAAGGAGAGGATGAAGATGTTTCAGATCGAAAGAGTGAGA 3810
Qy 1275 ValLysGluLeuMetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAsn 1294
Db 3811 ACAGCAAAATGCCCTTGAATTTCTACTAATTTTGTATGAGAAGCCAGTCAATTCGCCAGCTGT 3870
Qy 1295 LeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysVal 1314
Db 3871 CTACGCAAGGAGTATGCAGGGAAGAGGAAAGGCTGTTTTTCCAAGAGGAATAAGATA 3930
Qy 1315 AlaThrLysTyrIleSerPheCysValLysGlyGluIleLeuGlyAspIleGluProThrSer 1334
Db 3931 GCCACGAGAAATGCTCTCTTCTGTGTAGAAAAGGTGAAGTTTTTAGGATTATTAGGACAC 3990
Qy 1335 AsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSer 1354
Db 3991 AATGGAGCTGGTAAAGCACATCCATTAAAGTGATAAATCTGGAGACACAAAACCACTGCT 4050
Qy 1355 GlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLys 1374
Db 4051 GGACAAGTGTCTACTG-----AAAGGAGCGGTGGAGGGGATGCCCTGGAG 4095
Qy 1375 CysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHis 1394
Db 4096 TTCCTGGGTACTGCCCTCAGGAGAACCGCGTGTGGCCCAACCTGACAGTGAGGCAGCAC 4155
Qy 1395 PheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSer 1414
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Qy 1415 ArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPro 1434
Db 4216 CGGTAGTGGATGGCTCAAGCTGCAGGACCAGCTGAAGTCTCCGGTGAAGACCTTGTCAC 4275
Qy 1435 AlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThr 1454
Db 4276 GAGGGAATAAGAGAAAGCTGTGCTTTGTCTGAGCATACTGGGGAACCCGTCAGTGGTG 4335
Qy 1455 LeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAla 1474
Db 4336 CTTCTGGATGAGCCGTCGACCGGATGGACCCGAGGGGCGAGCAGCAAAATGTGGCAGGCC 4395
Qy 1475 IleArgThrAlaPheLysAsnArgLysArgAlaIleLeuThrThrHisTyrMetGlu 1494
Db 4396 ATCCGGGCCACCTTTAGAAACACGGAAGGGGTGCCCTCTCAACCAACCATACATGGCA 4455
Qy 1495 GluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIle 1514
Db 4456 GAGGCTGAGGCCGCTGTGTGACCGAGTGGCCATCATGTTCTGGAGGTTGAGATGTATC 4515
Qy 1515 GlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeu 1534
Db 4516 GGTTCATCCAACACCTGAAAGCAAAATTTGGCAAAAGATTACCTGCTGAGATGAAGGTG 4575
Qy 1535 LysAspTrpIleGluAsnLeu---GluValAspArgLeuGlnArgGluIleGlnTyrIle 1553
Db 4576 AAG-----AACCTGGCACAAAGTGGAGCCCTCCATGTCAGAGATCCTGAGGCTT 4623
Qy 1554 PheProAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLys 1573
Db 4624 TTCCCCCAGGCTGCTCGGCAGGAAAGGTACTCTCTCTGTATGGTTTTATAAGTTGCCAGTG 4683

Db 3767 CTAGTCTGCTTCATACCCCTACTTTTCAGACTTTGCTATTGCTTTTGTCTTAAGATGCATG 3826
Qy 1229 GluLysLysTyrGlyArgSerIleAArgLysAspProphePheArgAsnLeuSerThr 1248
Db 3827 GAACTAAATGTGGAAGAGAAAGAAATGCGAAAGATGCTGTTTTCAGA---ATTCCCCC 3883
Qy 1249 LysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspVal 1268
Db 3884 CAAAGTAGAGATGCTAAG---CCAAATCCAGAGAACCCCATAGATGAAGATAT 3940
Qy 1269 LysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysPro 1288
Db 3941 CAAACAGAAAGAAATAAGACAGCCACTGCTCTGACCCTTCAATCTTAGATGAGAAACCT 4000
Qy 1289 SerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSer 1308
Db 4001 GTTATAATTGCCAGCTGTCTACACAAAGAAATATGCGGCCAGAGAAAGTTGCTTTTCA 4060
Qy 1309 ArgLysValLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluile 1328
Db 4061 AAGAGGAAGAGAAATAGCAGCAAGAAATATCTCTTTCTGTGTTCAAGAAAGGTGAAATT 4120
Qy 1329 LeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGly 1348
Db 4121 TTGGATTGCTAGGACCCARTGGTGTCTGGAAGTTTCATCTATTAGAATGATATCTGG 4180
Qy 1349 AspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGlu 1368
Db 4181 ATCACAAAGCCAACTGCTGGAGAGGTGGAACCTGAAAGGCTGCAGTTCA----- 4228
Qy 1369 AspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAsp 1388
Db 4229 -----GTTTGTGGCCACCTGGGTACTGCGCTCAAGAGAACGTGCTGTGGCCCATG 4279
Qy 1389 ThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAsp 1408
Db 4280 CTGACGTTGAGGGAACACCTGGAGGTGTATGCTGCGTCAAGGGGCTCAGGAAAGCGGAC 4339
Qy 1409 MetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLys 1428
Db 4340 GCGAGGCTGCCCATCGCAAGATTAGTGAGTGCTTTCAAACCTGCATGAGCAGCTGAATGT 4399
Qy 1429 ThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeu 1448
Db 4400 CCTGTGCAGAAATTAAACAGCAGGAATCACGAGAAAGTTGTGTTTGTGCTGAGCCTCTG 4459
Qy 1449 GlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLysAlaLys 1468
Db 4460 GGAACCTCACCTGTCTTCTGCTGATGAACCATCTACGGGCATAGACCCACAGGGCAG 4519
Qy 1469 GlnHisMetTyrArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeu 1488
Db 4520 CAGCAATGTGGCAGGCAATCCAGGCAGTYGTTTAAACACACAGAGAGAGGTGTCCTCTG 4579
Qy 1489 ThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMetValSer 1508
Db 4580 ACCACCCATAACCTGGCTGAGGCGGAAGCCTTGTTGTGACCGTGTGGCCCATCATGTTGCT 4639
Qy 1509 GlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyr 1528
Db 4640 GGAAGGCTTAGATGCAATTGGCTCCATCCAACACCTGAAACAAACCTTGGCAAGGATTAC 4699
Qy 1529 PheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArg 1548
Db 4700 ATTCTAGAGCTAAAGTGAAG-----GAAACGCTCTCAAGTGACTTTGCTCCACACT 4750
Qy 1549 GluileGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerIleLeuAla 1568
Db 4751 GAGATTCTGAAGCTTTTCCACAGGCTGCAGGGCAGGAAAGGTATTCCCTTTTGTTAACC 4810
Qy 1569 TyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeuGlu 1588

Db 4811 TATAAGCTGCCCCGTGGCAGACGTTTACCCCTCTATCATCAGACCTTTACAAATTAGAAGCA 4870
Qy 1589 AlAlysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnVal 1608
Db 4871 GTCAAGCATAACTTTAACCTGGAAGAAATACAGCCTTTCTCAGTGCACACTGGAGAAGGTA 4930
Qy 1609 PheValGluLeuThrLysGluGlnGluGluAspAsnSerCysGlyThrLeuAsnSer 1628
Db 4931 TTCTTAGAGCTTTCTAAAGAACAG--GAAGTAGGAAATTTTGATGAAGAAATTGATACA 4987
Qy 1629 ThrLeuTrpTrpGlu 1633
Db 4988 ACAATGAGATGAAA 5002
RESULT 4
PCT-US04-02188-40
; Sequence 40, Application PC/TUS0402188
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eveleigh, Deepa
; APPLICANT: Bigwood, Douglas
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
; FILE REFERENCE: 5151
; CURRENT APPLICATION NUMBER: PCT/US04/02188
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: 60/442,582
; PRIOR FILING DATE: 2003-01-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 5677
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-02188-40
Alignment Scores:
Pred. No.: 3e-295 Length: 5677
Score: 3108.00 Matches: 672
Percent Similarity: 60.02% Conservative: 319
Best Local Similarity: 40.70% Mismatches: 536
Query Match: 36.89% Indels: 124
DB: 1 Gaps: 26
US-10-090-458-5 (1-1642) x PCT-US04-02188-40 (1-5677)
Qy 6 ArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLysAsnTyrLeuIleLys 25
Db 148 AGAAGATCAGTGTGTGTCAACAAACTTGGGCCCTATTATGCAAGAACTTCTTAAAAA 207
Qy 26 CysArgThrLysLysSerValGlnGluIleLeuPheProLeuPhePheLeuPheTrp 45
Db 208 TGGAGAATGAAAAGAGAGAGTCCTTAATGGAATGGCTGAATTCATTGCTCCTACTTGT 267
Qy 46 LeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluValProAsnIleGlu 65
Db 268 TTGTATATATATCCTCATAGTCATCAAGTAAATGATTTTCTTCACTGCTTACCATGGAC 327
Qy 66 LeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProValThr 85
Db 328 CTGGACGGGTAGATACATTAAATGAATCCAGATTTTCTGTGTATACACACCTGTCAAC 387
Qy 86 AsnIleThrSerSerIleMetGlnLysValSerThrAsp----- 98
Db 388 AACACGACCCCAACAGATATGAATAAAGTAGCCTCTACTCCCTTCTGCGAGGTAAAGAG 447
Qy 99 -----HisLeuProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeu 116
Db 448 GTCTTGGGACTGCCAGATGAGGAAAGTATTAAAGAAATTCACA----- 489
Qy 117 ThrSerSerLeuSerLysProSerAsnPheValGlyValValPheLysAspSerMetSer 136
Db 490 -----GCAAATTATCTCTGAAGAAATAGTAAGAGTCACCTTTACTAATACACTCA 540


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Db 4905 TTCCCCCAGGCTGCTCGGCAGGAAGGGTACTCTCTGTGATGGTTTATAAGTTGCCAGTG 4964
QY 1574 GluAspValGlnSerLeuSerGlnSerPhePheLeuGluGlnAlaLysHisAlaPhe 1593
Db 4965 GAAGATGTGCAACCTTTAGCCCAAGCTTCTCGAATTAGAGAAGGTTAAACAGGGCTTT 5024
QY 1594 AlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThr 1613
Db 5025 GACCTAGAGGAGTACAGCCTCTCACAGTCTACCTGGAGCAGGTTTCTCTGGAGCTCTCC 5084
QY 1614 LysGluGlnGlu-----GluGluAsp 1620
Db 5085 AAGGAGCAGGAGCTGGGTGATTTTGAGGAGGAT 5117
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RESULT 3

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US-10-796-280-368
; Sequence 368, Application US/10796280
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001510
; CURRENT APPLICATION NUMBER: US/10/796,280
; CURRENT FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 68533
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 5296
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-796-280-368
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Alignment Scores:

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Pred. No.: 6.84e-296 Length: 5296
Score: 3114.00 Matches: 687
Percent Similarity: 60.96% Conservative: 328
Best Local Similarity: 41.26% Mismatches: 556
Query Match: 36.96% Indels: 94
DB: 6 Gaps: 33
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US-10-090-458-5 (1-1642) x US-10-796-280-368 (1-5296)

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QY 5 IleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLysAsnTyrLeuIle 24
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QY 25 LysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeuPhePheLeuPhe 44
Db 242 AAATGGAGGATGAAAGAGAGAGAGCTTATTGGAATGGGCCCTCTCAATACTTCTAGGACTG 301
QY 45 TrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGluValProAsnIle 64
Db 302 TGTATTGCTCTGTTTCCAGTTCCATGAGAAATGTCCAGTTTCCCTGGAATGGCTCCTCAG 361
QY 65 GluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProVal 84
Db 362 AATCTGGGAAGGTAGATAAAATTAATAGCTCTTCTTTAATGGTTGTGTATACACCAATA 421
QY 85 ThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu-----Pro 101
Db 422 TCTAATTTAACCAGCAGAGATAATGATAAAACAGCACTTGCTCTCTCTTTTGAAGGAACA 481
QY 102 AspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSer 121
Db 482 AGTGTCAATTGGGCACCAATAAAACACACATGACGAAATACTTCTGGAAATTTACCA 541
QY 122 LysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArgPhe 141
Db 542 TATGCT-----ATGGGAATCATCTTTAATGAAACTTTCTCTTATAAGTTAATATT 592
QY 142 PheProAspMetIleProValSerSerIleTyrMet---AspSerArgAlaGlyCys--- 159
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Db 593 TTCCAGGGATAT-----AACAGTCCACTTTGGAAAGAAGATTTTCTCAGCTCATTTGCTGG 646
QY 160 -----SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrVal 175
Db 647 GATGGATATGGTGAGTTTTCATGTACATTGACCAATACTGGAATAGAGGATTTGTGGCT 706
QY 176 LeuGlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLys 195
Db 707 TTACAAACAGCTATTAACTACTGCCATTATAGAAATCACAAACCAATCACCTGTGATGGAG 766
QY 196 GluLeuGluSerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThr 215
Db 767 GAGTTGATGTCAGTTACTGCTATACTATGAAGACATTACCTTTTCATAACTAAAAATCTT 826
QY 216 PheProArgGlyValIleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPhe 235
Db 827 CTTCACAATGAGATGTTTATTTTATCTTCTTGCTTCATTTCTCCCACTTGTATATTTT 886
QY 236 LeuAlaIleHisIleValAlaGluLysGluLysIleLysGluPheLeuLysIleMet 255
Db 887 ATATCACTCAATGTAAACAAAGAGAGA---AAAAAGCTTAAGATTTTGATGAAATGATG 943
QY 256 GlyLeuHisAspThrAlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePhe 275
Db 944 GGTCTCCAAGATTCAGCATTTCTGGCTCTCTGGGCTCTAATCTATCTATGCTGGCTTCATCTTT 1003
QY 276 LeuMetSerLeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSer 295
Db 1004 ATTATTTCCATATTCRTTACAATTTATCAATACATTCACCCAAATATATAGTCATGCTGGC 1063
QY 296 SerIleValIlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeu 315
Db 1064 TTCATGGTCAATATTTATCTCTTTTATATGCTTATCTTTGCTAGCTTTTGGTGTTTC 1123
QY 316 MetLeuThrProLeuPheLysLysSerLysHisValGlyIleValGluPhePheValThr 335
Db 1124 CTGATGAGTGTGCTGTTAAAGAAAGCTGTCTCTCACCAATTTGGTGTGTTTCTCCTTACC 1183
QY 336 ValAlaPheGlyPheIleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeu 355
Db 1184 CTCTTTTGGGATGTCTGGGA---TTCACGTGATTTTATGAACAACTTCCTTCATCTCTG 1240
QY 356 ValTrpLeuPhe-----SerProPheCysHisCysThrPheValIleGlyIleAla 372
Db 1241 GAGTGGATTTTGAATATTTGTAGCCCTTTT-----GCCTTTACTACTGGAATGATT 1291
QY 373 GlnValMetHisLeuGluAspPheAsn---GluGlyAlaSerPheSerAsnLeuThrAla 391
Db 1292 CAGATTATCAAACTG---GATTATACTGAATGGTGTAAATTTTCTGACCCCTTCAGGA 1348
QY 392 GlyProTyrProLeuIleIleThrIleIleMetLeuThrLeuAsnSerIlePheTyrVal 411
Db 1349 GACTCATATACATGATAGCAACTTTTCTATGTTGCTTTTGGATGGTCTCATCTACTTG 1408
QY 412 LeuLeuAlaValTyrLeuAspGlnValIleProGlyGluPheGlyLeuArgArg----- 429
Db 1409 CTATTGGCATTTATCTTTGACAAAATTTTACCC-----TATGGAGATGAGCGCCATTAT 1462
QY 430 SerSerLeuTyrPheLeuLysProSerTyrTrpSerLysSerLysArgAsnTyrGluGlu 449
Db 1463 TCTCCTTTTATTTTCTTGAATTCATCTCTGTTGTTTCCAAACACCAAGGACTAATGCTAAG 1522
QY 450 LeuSerGluGlyAsnValAsnGlyAsnIleSerPheSerGluIleIleGluProValSer 469
Db 1523 GTTATTGAGAAAGAAATCGATGCTGAGCATCCCTCTCTGATGATTATTTTGAACCAAGTAGCT 1582
QY 470 SerGluPheValGlyLysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLys 489
Db 1583 CCTGAATTCAGGAAAGAAAGCCCATCAGAAATGTTAAGAGGAATATAAAGGA 1642
QY 490 LysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIle 509
Db 1643 AAATCTGGAAAAGTGAAGCATTGAAAGGCTTGCTCTTTGACATATATGAAGGTCAAATC 1702
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[illegible]

QY	1195	ArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerPro	1214
DB	3879	CGAATGGATGTACAGCCATT-----CTGGTATTCCTAATTCCT	3917
QY	1215	TyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGly	1234
DB	3918	TTCCTTCATTTTATCATTTTCTTTTCTTTTACTCTCGATGTCTGGAATGGAAGTTTGGAAAG	3977
QY	1235	ArgSerIleArgLysAspProphePheArgAsnLeuSerThrLysSerLysAsnArgLys	1254
DB	3978	AAATCAATGAGAAAGGATCCTTTCTTTTAGAATTTCTCCAAGAAAGTAGTGATGTGTCAA	4037
QY	1255	LeuProGluProProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLys	1274
DB	4038	AATCCAGAAGAACCA-----GAAGGAGAGATGAAGATGTTTCAGATGGAAGAGTGAAGA	4091
QY	1275	ValLysGluLeuMetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAsn	1294
DB	4092	ACAGCAAATGCCTTGAATTCTACTAATTTTGTAGAGAAGCCAGTCATCATTCGCCAGCTGT	4151
QY	1295	LeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysVal	1314
DB	4152	CTACCGAAGGAGTATGCAGGAAGAGGAAAGCTGTTTTTCCAAAGAGGAAGATAAGATA	4211
QY	1315	AlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyPro	1334
DB	4212	GCCACGAGAAATGTCCTCTCTGTGTTAGAAAAGGTGAAGTTTATAGGATTATTAGGACAC	4271
QY	1335	AsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSer	1354
DB	4272	AATGGAGCTGGTAAAGCACATCCATTAAAGGTGATACTGGAGACACAAAACCAACTGCT	4331
QY	1355	GlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLys	1374
DB	4332	GGACAAGTGCTACTG-----AAAGGGAGCGGTGGAGGGGATGCCCTGGAG	4376
QY	1375	CysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHis	1394
DB	4377	TTCCTGGGGTACTGCCCTCAGGAGAACCGCTGTGGCCCCAACCTGACAGTGGAGCCAC	4436
QY	1395	PheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSer	1414
DB	4437	CTGGAGGTGTACGCCCGCGTCAAGCTGCAGGACCAGCTGAAGTCTCCCGTGAAGACCTGTCA	4496
QY	1415	ArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPro	1434
DB	4497	CGGTTAGTGATCGCTCAAGCTGCAGGACCAGCTGAAGTCTCCCGTGAAGACCTGTGTC	4556
QY	1435	AlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThr	1454
DB	4557	GAGGGAATAAGAGAAAGCTGTGCTTTGTCTTGAGCATACTGGGGAACCCGTCAGTGGTG	4616
QY	1455	LeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAla	1474
DB	4617	CTTCTGGATGAGCCGTCGACCGGGATGGACCCCGAGGGGCAGCAGCAAAATGTGGCAGGCC	4676
QY	1475	IleArgThrAlaPheLysAsnArgLysArgAlaIleLeuThrThrHisTyrMetGlu	1494
DB	4677	ATCCGGGCCACCTTTAGAAACACGGAAAGGGGTGCCCTCCTAACCCACCATACATGGCA	4736
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DB	4737	GAGGCTGAGGCCGTGTGACCGAGTGGCCATCATGGTATCTGGGAGCTTGAGATGTATC	4796
QY	1515	GlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeu	1534
DB	4797	GGTTCCATCCAACACCTGCAAAGCAAATTTGGCAAAGATTACCTGCTGGAGATGAAGGTG	4856
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Qy 171 SerGlyPheThrValLeuGlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsn 190
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Qy 191 ValSerLeuTrpLysGluLeuGluSerThrLysAlaValIleMet----- 205
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Qy 206 ---GlyGluThrAlaValValGluIleAspThrPheProArgGlyValIleLeuIleTyr 224
Db 942 ARTGGTCAATCAGGAGTTATA-----ACTGATTGTACCTTTTTTCC 983
Qy 225 LeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIleValAlaGluLys 244
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Qy 325 LysHisValGlyIleValGluPhePheValThrValAlaPheGlyPheIleGlyLeuMet 344
Db 1281 TTCCTCACCGGCTGGTCGTGTTCTCTCACTGTCTTTAGGGGTGTCGGG---TTC 1337
Qy 345 IleIleLeuIleGluSerPhePrCLysSerLeuValTrpLeuPheSerProPheCysHis 364
Db 1338 ACATCACTGTACAGACACCTTCCTGCATCCTTGGAGTGGATTTTAAGCTTGTAGTCCC 1397
Qy 365 CysThrPheValIleGlyIleAlaGlnValMetHisLeuGlu---AspPheAsnGluGly 383
Db 1398 TTTGCCTTTCATGCTTGGATGGCCCGAGCTTTTACACTTGGACTATGATTTGAATTCTAAT 1457
Qy 384 AlaSerPheSerAsnLeuThrAlaGlyProTyrProTyrProLeuIleIleThrIleIleMetLeu 403
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Qy 404 ThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnValIleProGly 423
Db 1515 GCATTTGACACTTGCCTCTATCTGGCATTTGGCGATTACTTTGAAAAAATTTTGCCAAAT 1574
Qy 424 GluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrpSerLysSer 443
Db 1575 GAATATGGACATCGACGCTCCACCTTTGTTTTCCTGAAGTCTCATTTTGGTCTCAAACA 1634
Qy 444 LysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSerPheSerGlu 463
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Qy 464 IleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIleSerGlyIle 483

Db 1695 TCCTTTGAACAAGCGCTCCAGAAATTCCAAGGGGAAAGAGCCATCAGAAATCAGAAATGTT 1754
Qy 484 GlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAsp 503
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Qy 524 MetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIleTyrGlyHis 543
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Db 1995 TCCAATGTGCAATTTGGACTTCCTCACTGTAAAGAGAAAAACCTCAGACTCTTTGCTAAAAATA 2054
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RESULT 2

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; Sequence 57, Application PC/TUS0407967
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: LEE, Ernestine A.; RICHARDSON, Thomas W.;
; APPLICANT: ELLIOTT, Vicki S.; GRIFFIN, Jennifer A.;
; APPLICANT: HAFALIA, April J.A.; DING, Li;
; APPLICANT: CHAWLA, Narinder K.; YANG, Junming;
; APPLICANT: BAUGHN, Mariah R.; THORNTON, Michael B.;
```

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; APPLICANT: GIETZEN, Kimberly J.; MARQUIS, Joseph P.
; APPLICANT: TRIBOULEY, Catherine M.; ISON, Craig H.;
; APPLICANT: RAMKUMAR, Jayalakmi; JIN, Pei;
; APPLICANT: CHIEN, David; BECHA, Shanya D.;
; APPLICANT: WILSON, Amy D.; HAWKINS, Phillip R.;
; APPLICANT: KHARE, Reena; BHATIA, UMESH G.
; APPLICANT: BLAKE, Julie J.; BURRILL, John D.;
; APPLICANT: HO, Anne; LEE, Sally;
; APPLICANT: ZHENG, Wenjin
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PF-1517 PCT
; CURRENT APPLICATION NUMBER: PCT/US04/07967
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US 60/456,169
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 60/462,271
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/465,412
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/475,073
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/476,492
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/502,391
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/524,102
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PERL Program
; SEQ ID NO 57
; LENGTH: 5396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7520474CB1
PCT-US04-07967-57

Alignment Scores:
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Score: 3229.00 Matches: 689
Percent Similarity: 61.60% Conservative: 328
Best Local Similarity: 41.73% Mismatches: 550
Query Match: 38.32% Indels: 84
DB: 1 Gaps: 24

US-10-090-458-5 (1-1642) x PCT-US04-07967-57 (1-5396)
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 12, 2004, 21:52:05 ; Search time 325 Seconds
(without alignments)
3300.409 Million cell updates/sec

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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delopt 6.0 , Delext 7.0

Searched: 1355633 seqs, 326623912 residues

Total number of hits satisfying chosen parameters: 2711266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10090458 @CGN 1 1 75 @runat 08042004_121554_25634 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents NA New:
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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:
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7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3231	38.3	5235	1	PCT-US04-07967-55 Sequence 55, Appl
2	3229	38.3	5396	1	PCT-US04-07967-57 Sequence 57, Appl
3	3114	37.0	5296	6	US-10-796-280-368 Sequence 368, App
4	3108	36.9	5677	1	PCT-US04-02188-40 Sequence 40, Appl
5	3108	36.9	5677	1	PCT-US04-07268-45 Sequence 45, Appl
6	3108	36.9	5677	6	US-10-764-425-40 Sequence 40, Appl
7	3108	36.9	5677	6	US-10-788-792-45 Sequence 45, Appl
8	2967.5	35.2	5185	6	US-10-796-280-369 Sequence 369, App
9	1475	17.5	9497	6	US-10-465-498-91 Sequence 91, Appl
10	1473.5	17.5	9593	6	US-10-465-498-94 Sequence 94, Appl
11	1458.5	17.3	9495	6	US-10-465-498-96 Sequence 96, Appl

12	1439	17.1	10026	6	US-10-796-307-75	Sequence 75, Appl
13	1439	17.1	10247	6	US-10-796-307-78	Sequence 78, Appl
14	1439	17.1	10405	6	US-10-796-307-77	Sequence 77, Appl
15	1363	16.2	6705	5	US-09-032-438C-5	Sequence 5, Appl
16	1352	16.0	6705	6	US-10-336-215A-5	Sequence 5, Appl
17	1352	16.0	6705	6	US-10-336-219A-5	Sequence 5, Appl
18	1352	16.0	6705	6	US-10-340-097B-5	Sequence 5, Appl
19	1350	16.0	6819	5	US-09-032-438C-2	Sequence 2, Appl
20	1350	16.0	7488	5	US-09-032-438C-1	Sequence 1, Appl
21	1339	15.9	6701	6	US-10-603-187-1	Sequence 1, Appl
22	1337	15.9	6819	6	US-10-336-215A-2	Sequence 2, Appl
23	1337	15.9	6819	6	US-10-336-219A-2	Sequence 2, Appl
24	1337	15.9	6819	6	US-10-340-097B-2	Sequence 2, Appl
25	1337	15.9	7318	6	US-10-783-528-12	Sequence 12, Appl
26	1337	15.9	7783	6	US-10-336-215A-1	Sequence 1, Appl
27	1337	15.9	7783	6	US-10-336-219A-1	Sequence 1, Appl
28	1337	15.9	7783	6	US-10-340-097B-1	Sequence 1, Appl
29	1295.5	15.4	6027	6	US-10-775-920-5	Sequence 5, Appl
30	1295.5	15.4	6174	6	US-10-775-920-6	Sequence 6, Appl
31	1295.5	15.4	6588	6	US-10-775-920-4	Sequence 4, Appl
32	1295.5	15.4	6704	6	US-10-775-920-3	Sequence 3, Appl
33	1291.5	15.3	6704	6	US-10-775-920-1	Sequence 1, Appl
34	1249.5	14.8	5811	6	US-10-100-683-3889	Sequence 3889, Ap
35	546	6.5	1879	6	US-10-775-920-7	Sequence 7, Appl
36	479	5.7	1501	6	US-10-775-920-2	Sequence 2, Appl
37	407	4.8	4254	7	US-60-554-981-1303	Sequence 1303, Ap
38	400.5	4.8	4646	6	US-10-775-169-198	Sequence 198, App
39	399	4.7	4192	6	US-10-782-413-53	Sequence 53, Appl
40	395.5	4.7	4669	6	US-10-680-516-1	Sequence 1, Appl
41	365	4.3	6129	6	US-10-769-619-1	Sequence 1, Appl
42	365	4.3	6129	6	US-10-782-413-44	Sequence 44, Appl
43	364	4.3	4572	6	US-10-790-273-1	Sequence 1, Appl
44	360.5	4.3	6126	6	US-10-769-619-3	Sequence 3, Appl
45	358	4.2	6129	6	US-10-769-619-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

PCT-US04-07967-55
; Sequence 55, Application PC/TUS0407967
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
; APPLICANT: LEE, Ernestine A.; RICHARDSON, Thomas W.;
; APPLICANT: ELLIOTT, Vicki S.; GRIFFIN, Jennifer A.;
; APPLICANT: HAFALIA, April J.A.; DING, Li;
; APPLICANT: CHAWLA, Narinder K.; YANG, Junning;
; APPLICANT: BAUGHN, Mariah R.; THORNTON, Michael B.;
; APPLICANT: GIETZEN, Kimberly J.; MARQUIS, Joseph P.
; APPLICANT: TRIBOULEY, Catherine M.; ISON, Craig H.;
; APPLICANT: RAMKUMAR, Jayalaxmi; JIN, Pei;
; APPLICANT: CHIEN, David; BECHA, Shanya D.;
; APPLICANT: WILSON, Amy D.; HAWKINS, Phillip R.;
; APPLICANT: KHARE, Reena; BHATIA, UMESH G.
; APPLICANT: BLAKE, Julie J.; BURRILL, John D.;
; APPLICANT: HO, Anne; LEE, Sally;
; APPLICANT: ZHENG, Wenjin
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PF-1517 PCT
; CURRENT APPLICATION NUMBER: PCT/US04/07967
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US 60/456,169
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US 60/462,271
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 60/465,412
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/475,073
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/476,492
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/502,391
; PRIOR FILING DATE: 2003-09-12

Qy 1238 gLysAspProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluPr 1258
Db 1711 AAAAGATCCCTTTTTCAGAAACCTTTCAACGAAGCTTAAAAATAGGAAGCTTCAGAAC 1770
Qy 1258 oProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLe 1278
Db 1771 ACCAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCT 1830
Qy 1278 uMetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysG1 1298
Db 1831 GATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATATATGGTCAGCAATTTGCATAAAGA 1890
Qy 1298 uTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTy 1318
Db 1891 ATATGATGACAAGAAAGATTTCCTTCTTCAAGAAAAAGTAAAGAAAGTGCGCAACTAAATA 1950
Qy 1318 rIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaG1 1338
Db 1951 CATCTCTTTCTGTGTGAAAAAGGAGAGAGATCTTAGGACTATTGGGTCCAAATGGTGCTGG 2010
Qy 1338 yLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPh 1358
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Qy 1358 eLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTy 1378
Db 2071 TTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGTGATGGGTTA 2130
Qy 1378 rCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTy 1398
Db 2131 CTGTCTCAGATAAACCCCTTTGTGGCCAGATACTACATTCAGGAACATTTTGAATTTA 2190
Qy 1398 rGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHi 1418
Db 2191 TGGAGCTGTCAAAGGAATGAGTCAAGTGACATGAAAGAAGTCATAAGTCGAATAACACA 2250
Qy 1418 sAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLy 1438
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Qy 1438 sArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspG1 1458
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Qy 1458 uProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAl 1478
Db 2371 ACCATCTACAGGTATGGATCCCAAGCCCAACAGCACATGTGGCGAGCAATTGGAAGTGC 2430
Qy 1478 aPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAl 1498
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Qy 1538 eGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSe 1558
Db 2611 AGAAAAACCTAGAAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAATGCAAG 2670
Qy 1558 rArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSe 1578
Db 2671 CCGTCAGGAAAGTTTTCCTTCTATTTTGGCTCATAAAAATTCCTAAGGAAGATGTTTCAGTC 2730
Qy 1578 rLeuSerGlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTy 1598
Db 2731 CCTTTCACAATCTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAATA 2790
Qy 1598 rSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluG1 1618

Db 2791 TAGCTTTTCTCAAGCAACATTGGAAACAGGTTTTTTGTAGAACTCACTAAAGAACAAAGAGGA 2850
Qy 1618 uGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAs 1638
Db 2851 GGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAACACAAGAAGA 2910
Qy 1638 pArgValValPhe 1642
Db 2911 TAGAGTAGTATTT 2923

Search completed: April 13, 2004, 04:14:16
Job time : 7815 secs

Db 4549 ATAGACTAGTATTT 4562
RESULT 15
US-10-108-260A-160
; Sequence 160, Application US/10108260A
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 3347
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-160
Alignment Scores:
Pred. No.: 0 Length: 3347
Score: 4930.50 Matches: 966
Percent Similarity: 98.17% Conservative: 1
Best Local Similarity: 98.07% Mismatches: 2
Query Match: 58.52% Indels: 17
DB: 45 Gaps: 2
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QY 684 AlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeuLysSerLys 703
Db 62 GCTGTGATATACAAAGGAATGCTGAAATGTGTGGTTCTTCAATGTTCTCAAAAGTAAA 121
QY 704 TrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeu 723
Db 122 TGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATGTGCCACAGAAATCTCT 181
QY 724 SerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGln 743
Db 182 TCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTAACAACAGAAATGACCAACAA 241
QY 744 LeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeu 763
Db 242 CTTGTGTATAGTTCCTTTCAAGGACATGGACAAAATTTTCAGGTTTGTTCCTGCCCCA 301
QY 764 AspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAsp 783
Db 302 GACAGTCATTCAAAATTTGGGTGTCAITTCATGGTGTTCCTTCCATGACGACTTTTGGAGAC 361
QY 784 ValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThr 803
Db 362 GTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTTGACCAAGCAGATATAGTGTATTTACT 421
QY 804 GlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeu 823
Db 422 CAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGAATGAATGGAACAGAGCTTA 481
QY 824 LeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGln 843
Db 482 CTTATTTCTGAAACCAAGGTTTCATTTCTTACCTTGAACGTTGAAAGTAAATCAGTGAGA 541
QY 844 MetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLysSerValArg 863
Db 542 ATGTATACAATAGCAAAAGTTTCATTTCTTACCTTGAACGTTGAAAGTAAATCAGTGAGA 601
QY 864 SerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHis 883
Db 602 TCAGTGTGCTTCGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTTTTGGTTTCAT 661

QY 884 HisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLys 903
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QY 904 ProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAla----- 921
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QY 922 -----AspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMe 938
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Db 842 GGTGACGATGATTAAATGACAGTACTATGTATCCGTGGCTCCCATAGTGGCTTTAAA 901
QY 958 nValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTy 978
Db 902 TGTGATGCATTCAGAAAAGGACTATGTTTTCAGCTGTTTTCACACAGTACTATGGTTTA 961
QY 978 rSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValTh 998
Db 962 TTCTTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCATTTAAATGTGAC 1021
QY 998 rGluThrIleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLy 1018
Db 1022 TGAACCATCCAGATCTGGAGTACCCCATCTTTTCAGAAATTACTGATATAGTTTTAA 1081
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QY 1058 rGlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePh 1078
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QY 1078 eIleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTy 1098
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QY 1098 rThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLe 1118
Db 1291 TACTGTAAAGTTCTTGTGTGGTTTTCCTTATGTTATGTTCCATCAGTTATTTCT 1350
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Db 1411 ATTTATCTATTCTGTGGCAGCGTTGGCTGTATTGCAATCACTGAAATAAATTTCTTTAT 1470
QY 1158 tGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrPr 1178
Db 1471 GGGATACACAATTCGAATCTTCTTCAATATGCTTTTGTATCATCATTCCTCAATCTATCC 1530
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Db 1531 ACTTCTAGTTGCTGTATTTCTTTCAAAAAATTTCTTGGAGAATGTACGAAAAAATGT 1590
QY 1198 lAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCy 1218
Db 1591 GGACACCTATATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCTTACCTGCAGTG 1650
QY 1218 sValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGlyArgSerIleAr 1238
Db 1651 TGTACTGTGGATTTTCTCTTACAAATACTATGAGAAAAAATATGAGGCGCAGATCAATAAG 1710

QY 920 rAla-----AspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMe 938
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Db 2491 TGCTGGTGAGAACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAAGCCAGACATAAT 2550
QY 938 tValThrMetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAs 958
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Db 2551 G----- 2551
QY 958 nValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTy 978
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Db 2552 -----GACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTA 2592
QY 978 rSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValTh 998
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Db 2593 TTCTTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCATTTAAATGTGAC 2652
QY 998 rGluThrIleGlnIleTyrPhePheGlnGluIleThrAspIleValPheLy 1018
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Db 2653 TGAACCATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAATGATATAGTTTTAA 2712
QY 1018 sIleGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTy 1038
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Db 2713 AATTGAGCTGTATTTTCAAGCAGCTTTGCTTTGGAATCAATGTTACTGCAATGCCACCTTA 2772
QY 1038 rPheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSe 1058
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Db 2773 CTTTGCCATGGAAAAATGCAGAGATCATAAAGATCAAAGCTTATACCTCAACTTAAACTTTC 2832
QY 1058 rGlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePh 1078
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Db 2833 AGGTCTTTTGCCATCTGCATATTGGATGGACAAGCTGTTGTGATATCCCTTATTTT 2892
QY 1078 eIleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTy 1098
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Db 2893 TATCATCTTATTTTGTATGCTAGGAAGCTTATTGGCATTTTCATATGGAATATATTTTA 2952
QY 1098 rThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLe 1118
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Db 2953 TACTGTAAAGTTCCTTGCTGTGGTTTTTGGCTTATTGGTTATGTTCCATCAGTTATCT 3012
QY 1118 uPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSe 1138
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Db 3013 GTTCACCTTATATGCTTTTCCACCTTTAAGAAATTTTAAATACCAAGAAATTTTGGTC 3072
QY 1138 rPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMe 1158
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Db 3073 ATTTATCTATTCTGTGGCAGCGTTGGCTGTATTGCAATCACTGAAATAACTTTCTTTAT 3132
QY 1158 tGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrPr 1178
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Db 3133 GGGATACAAATGCAACTATTCTTCATTATGCCTTTTGTATCATCATTTCCAATCTATCC 3192
QY 1178 oLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnVa 1198
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Db 3193 ACTTCTAGGTGCTGTATTCTTTTCATAAAGATTCTTTGGAAGAAATGTACGAAAAAATGT 3252
QY 1198 lAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCy 1218
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Db 3253 GGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTGTATATCGCCTTACCTGCAGTG 3312
QY 1218 sValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGlyArgSerIleAr 1238
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Db 3313 TGTACTGTGGATTTTCTCTTTACATACTATGAGAAAAAATATGGAGGCAGATCAATAAG 3372
QY 1238 gLysAspPropPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluPr 1258
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Db 3373 AAAAGATCCCTTTTTCAG-----TCTAAAAATAGGAAGCTTCCAGAAC 3416
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Db 3477 GATGGTTGCCAGTGTGTGTGAGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGA 3536
QY 1298 uTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysValAlaThrLysTy 1318
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Db 3537 ATATGATGACAAAGAAATTTTCTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATA 3596
QY 1318 rIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGl 1338
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Db 3597 CATCTCTTTCTGTGTGAAAAAAGGCT--ATCTTAGGACTATTGGGTCCAAATGGTCTGG 3654
QY 1338 yLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPh 1358
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Db 3655 CAAAAGCACAATATTATATTCTGTTGGTGATATTGAACCAACTTCAGGCCAGGTATT 3714
QY 1358 eLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTy 1378
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Db 3715 TTTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGATTCACTGAAGTGTATGGTTA 3774
QY 1378 rCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTy 1398
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Db 3835 TGGAGCTGTCAAAGGAATGAGTCAAGTGACATGAAAGAGTCAATAAGTCAATAACACA 3894
QY 1418 sAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLy 1438
|||
Db 3895 TGCACCTTGATTTAAAGAAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAA 3954
QY 1438 sArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGl 1458
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QY 1458 uProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAla-IleArgThrA 1478
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Db 4015 ACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATG-----TGCAATTGCAACTG 4068
QY 1478 lAPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluA 1498
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Db 4069 CATTTAAAAACAGAAAGCGGGCTGTATTCTGACCACTCACTATATATGAGGAGGCAGAGG 4128
QY 1498 lAValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValG 1518
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Db 4129 CTGTCTGTGATCGAGTAGCTATCATGTTCTGTTGTTCTGGCAGTTAAGATGTATCGGAACAGTAC 4188
QY 1518 lNHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpI 1538
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Db 4189 AACATCTAAAGAGTAAATTTGGAAAAAGGCTACTTTTTTGGAAATTAATTTGAAGGACTGGA 4248
QY 1538 leGluAsnLeuGluValAlaAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaS 1558
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Db 4249 TAGAAAACTTAGAAGTAGACCCGCCCTTCAAAAGAGAAATTCAGTATATTTTCCCAAAATGCAA 4308
QY 1558 erArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnS 1578
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Db 4309 GCCGTGAGGAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGT 4368
QY 1578 erLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPheAlaIleGluGluT 1598
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Db 4369 CCCTTTTCACAATCTTTTTTAAAGCTGGAAGAAAGCTAAACATGCTTTTGGCATTGAAGAAAT 4428
QY 1598 yrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluG 1618
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Db 4429 ATAGCTTTTCTCAAGCAACATTGGAAACAGGTTTTTGTAGAACTCACTAAAGAAACAAGAGG 4488
QY 1618 luGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluA 1638
|||
Db 4489 AGGAAGATAATAATAGTTGTGGAACTTTAAACAGCACACTTTTGGTGGGAACGAACACAAGAG 4548
QY 1638 spArgValValPhe 1642

Db 655 |||||GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTGAAGGAGCTGGAGTCAACT 714
QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 715 AAAGCTGTATTATGGGAGAACTGCTGTGTAGAAATAGATACCTTTCCCGAGAGTA 774
QY 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240
Db 775 ATTTTAAATACCTAGTTATAGCAATTTTACACCTTTTGGATACCTTTTGGCAATTCATATC 834
QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 835 GTAGCAGAAAAA----- 846
QY 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 846 ----- 846
QY 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerIleValIlePhe 300
Db 846 ----- 846
QY 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 846 ----- 846
QY 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 846 ----- 846
QY 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 846 ----- 846
QY 361 PropheCysHisCysThrPheValIleGlyIleAlaGln-ValMetHisLeuGluAspPh 380
Db 847 -----GAAAGTCATGCTTTAGAAAGATT 870
QY 380 eAsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrI 400
Db 871 TAAAGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAAT 930
QY 400 eIleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVa 420
Db 931 TATCATGCTCACACTTAATAGTATATTCTATGTCCTCTTGGTGTCTATCTTTGATCAAGT 990
QY 420 IileProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysPProSerTyrTr 440
Db 991 CATTCAGGGGAATTGGCTTACGGAGATCATCTTTATATATTTTCTGAAGCCTTCATATTG 1050
QY 440 pSerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSe 460
Db 1051 GTCAAAGAGCAAAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAG 1110
QY 460 rPheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIl 480
Db 1111 TTTTAGTGAATATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAGAAAT 1170
QY 480 eSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLe 500
Db 1171 TAGTGGTATTTCAGAAGACATACAGAAAGAGGGTGAAAAATGTGGAGGCTTTTGAGAAATT 1230
QY 500 uSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLy 520
Db 1231 GTCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTTGGCCACAGTGGAAACAGGAA 1290
QY 520 sSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIl 540
Db 1291 GAGTACATTGATGAATATTCTTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTAT 1350
QY 540 eTyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIl 560
|||

Db 1351 ATATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCAT 1410
QY 560 eCysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLe 580
Db 1411 TTGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAGAAGAAAAATTTATCAATTTT 1470
QY 580 uAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLe 600
Db 1471 GGCTTCAATCAAAGGGATACCAGCCAACAATATAATACAAGAAAGTGCAGAAAGTTTACT 1530
QY 600 uAspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLy 620
Db 1531 AGATTTAGACATGCAGACTATCAAAAGATAAACCAAGCTAAAAAATTAAGTGGTGGTCAAAA 1590
QY 620 sArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGl 640
Db 1591 AAGAAAGCTGTCAATTAGGAATTGCTGTTCTTTGGGAACCCAAAGATACTGCTGCTAGATGA 1650
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Db 1651 ACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGATGGAATCTTTTAAAAATACAG 1710
QY 660 gLysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAl 680
Db 1711 AAAAGCCAAATCGGTGACAGTGTTCAGTACTCATTTTCATGATGAAGCTGACATTTCTGC 1770
QY 680 aAspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLe 700
Db 1771 AGATAGGAAAGCTGTGATATCAAGAAGAAATGCTGAAATGTGTGGTTCTTTCAATGTTCT 1830
QY 700 uLysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaTh 720
Db 1831 CAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCAC 1890
QY 720 rGluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAs 740
Db 1891 AGAATCTCTTTCTTCACCTGGTTAAACAACATATACCTGGAGTACTTTATTACAACAGAA 1950
QY 740 nAspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPh 760
Db 1951 TGACCAACAACCTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCAGGTTTGT 2010
QY 760 eSerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrTh 780
Db 2011 TTCTGCCCTAGACAGTCAATTCAAATTTGGGTGTCAATTTCTTATGTTGTTTCCATGACGAC 2070
QY 780 rLeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSe 800
Db 2071 TTTTGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTGACCAAGCAGATTATAG 2130
QY 800 rValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGl 820
Db 2131 TGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTTCAAAATCTTTTGATGAAATGGA 2190
QY 820 uGlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTr 840
Db 2191 ACAGAGCTTACTTATTTCTTGAAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTG 2250
QY 840 pLysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLy 860
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QY 860 sSerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPh 880
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QY 880 eLeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTy 900
Db 2371 TTTGGTTTCATCACTCTTTTAAAAATGCTGTGTTTCCCATCAAACTTGTTCAGACTTATA 2430
QY 900 rPheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSe 920
Db 2431 TTTTCTAAAAACCTGGAGACAAACCAATAAAATACAAAAACAAGTCTGCTTCTTCAAAATTC 2490
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QY 1258 oProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLe 1278
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QY 1278 uMetGlyCysGlnCysCysGlnGluLysProSerIleMetValSerAsnLeuHisLysG1 1298
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QY 1298 uTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTy 1318
DB 3537 ATATGATGACAAAGAAATTTCTCTTTCAAGAAAGCTAAAGAAAGTGGCAACTAAATA 3596
QY 1318 rIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaG1 1338
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QY 1338 yLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPh 1358
DB 3655 CAAAAGCACAAATTATTATATCTGTGGTGGTGATATGAACCAACTTCAGGCCAGGTATT 3714
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DB 3715 TTTAGGAGATTATTCTTCAGACACAAGTGAAGATGATGATTCCTGAAGTGTATGGTTA 3774
QY 1378 rCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTy 1398
DB 3775 CTGTCTTCAGATAAACCCCTTTGTGGCCAGATACATTCAGGAACATTTTGAAATTTA 3834
QY 1398 rGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHi 1418
DB 3835 TGGAGCTGTCAAAGGAATGAGTGAAGTGACATGAAAGAGTCATAAGTCGAATAACACA 3894
QY 1418 sAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLy 1438
DB 3895 TGCACCTTGATTTAAAGAAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAA 3954
QY 1438 sArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspG1 1458
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QY 1458 uProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAla-IleArgThrA 1478
DB 4015 ACCATCTACAGGTATGGATCCCAAAGCCAAACAGCACATG-----TGCAATTGCAACTG 4068
QY 1478 lApeLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluA 1498
DB 4069 CATTTAAAAACAGAAAGCGGGTGTCTATTCTGACCACTCACTATATATGGAGGAGGAGG 4128
QY 1498 lAValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValG 1518
DB 4129 CTGTCTGTGATCGAGTAGTATCATGTTCTGTGGCAGTTAAGATGTATCGGAACAGTAC 4188
QY 1518 lHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpi 1538
DB 4189 AACATCTAAAGAGTAAATTTGAAAAAGGCTACTTTTTGAAAAATTAAATTGAAGGACTGGA 4248
QY 1538 lGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlas 1558
DB 4249 TAGAAAAACCTAGAAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAA 4308
QY 1558 eArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnS 1578
DB 4309 GCCGTGAGGAAAGTTTTTCTTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGT 4368
QY 1578 erLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPheAlaIleGluGluT 1598
DB 4369 CCCTTTCACAATCTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTTTGCCATTGAAGAT 4428
QY 1598 yrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluG 1618
DB 4429 ATAGCTTTTCTCAAGCAACATTGGAAACAGGTTTTTTGTAGAACTCACTAAAGAACAGAGG 4488
QY 1618 luGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluA 1638

DB 4489 AGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGACACAGAAG 4548
QY 1638 sArgValValPhe 1642
DB 4549 ATAGAGTAGTATTT 4562
RESULT 14
US-60-466-412-2441
; Sequence 2441, Application US/60466412
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001466
; CURRENT APPLICATION NUMBER: US/60/466,412
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 429241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2441
; LENGTH: 5595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-466-412-2441
Alignment Scores:
Pred. No.: 0 Length: 5595
Score: 7377.00 Matches: 1474
Percent Similarity: 89.67% Conservative: 2
Best Local Similarity: 89.55% Mismatches: 5
Query Match: 87.55% Indels: 167
DB: 103 Gaps: 5
US-10-090-458-5 (1-1642) x US-60-466-412-2441 (1-5595)
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DB 115 ATGTCCTCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACATTTCTACTGAAG 174
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
DB 175 AATTACTTAATTAATGCAGAACCAAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA 234
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
DB 235 TTTTTTTTATTTTGGTTAATATAATTAATAGCATGATGCATCCAAATAAGAAATATGAAGAA 294
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
DB 295 GTGCCTAATATAGAACTCAATCCTATATGGACAAAGTTTACTCTTTCTAATCTAATCTTGA 354
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
DB 355 TATACTCCAGTGACTAATAATTAACAAGCAGCATCATGMAGAAAAGTGTCTACTGATCATCTA 414
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
DB 415 CCTGATGTCATAATTAATGAAGAATAATACAAATGAAAAAGAAATGTTAACATCCAGTCTC 474
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
DB 475 TCTAAGCCGAGCAACTTTGTAGTGTGGTTTTTCAAAAGACTCCATGTCTTATGAACCTCGT 534
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
DB 535 TTTTTTCTTGATATGATTCAGTATCTTCTATTTATATATGATTCAGAGCTGGCTGTCTCA 594
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
DB 595 AAATCATGTGAGGCTGCTCAGTACTGTCTCTCCTCAGGTTTCACAGTTTTTACAAGCATCCATA 654
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200

Db 1291 GAGTACATTGATGAATATTCTTTGTGGACTCTGCCCCACCTTCTGATGGGTTTGCACTAT 1350
QY 540 eTyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 1351 ATATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAGAAATAATGATTGGCAT 1410
QY 560 eCysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLe 580
Db 1411 TTGTCCACAGTTAGATATACACTTTGTATGTTTGGACAGTAGAAGAAATTTATCAATTT 1470
QY 580 uAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLe 600
Db 1471 GGCTTCAATCAAAGGGATACCAGCCCAATATATATACAAAGAGTGCAGAAAGTTTACT 1530
QY 600 uAspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLy 620
Db 1531 AGATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAATTAAAGTGGTGCATAA 1590
QY 620 sArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGl 640
Db 1591 AAGAAAGCTGTCATTAGGAATTGCTGTTTGGGAACCCAAAGATACTGCTGCTAGATGA 1650
QY 640 uProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLysTyrAr 660
Db 1651 ACCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATAACAG 1710
QY 660 gLysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAl 680
Db 1711 AAAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTCITGC 1770
QY 680 aAspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLe 700
Db 1771 AGATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGTTCTTCAATGTTCTT 1830
QY 700 uLysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaTh 720
Db 1831 CAAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCAC 1890
QY 720 rGluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAs 740
Db 1891 AGAATCTCTTCTTCACTGGTTAAACAAACATATACCTGGAGTACTTTATTACAACAGAA 1950
QY 740 nAspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPh 760
Db 1951 TGACCAACAACCTTGTTGATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAGGTTTGT 2010
QY 760 eSerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrTh 780
Db 2011 TTCTGCCCTAGACAGTCAATCAAATTTGGGTGTCAATTTCTTATGGTGTTCATGACGAC 2070
QY 780 rLeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSe 800
Db 2071 TTTGGAAGACGATTTTAAAGCTAGAGTTGAAGCAGAAATTGACCAAGCAGATTATAG 2130
QY 800 rValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGl 820
Db 2131 TGTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGA 2190
QY 820 uGlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTr 840
Db 2191 ACAGAGCTTACTTATTTCTGAAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTG 2250
QY 840 pLysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLy 860
Db 2251 GAAACAACAGATGTATACAAATAGCAAAAGTTTCATTTCTTTACCTTGAACGTTGAAAGTAA 2310
QY 860 sSerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPh 880
Db 2311 ATCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTT 2370
QY 880 eLeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTy 900
Db 2371 TTTGGTTCACTCTTTTAAAAATGCTGTGGTTGCCATCAAACTTGTTCAGACCTTATA 2430

QY 900 rPheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSe 920
Db 2431 TTTTCTAAACCTGGAGACAAACACATAAATACAAACAAAGTCTGCTTCTTCAAATTC 2490
QY 920 rAla-----AspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMe 938
Db 2491 TGCTGGTGAGAACTCAGATATCAGTGATCTTATTAGCTTTTTCACAGCCAGACATAAT 2550
QY 938 tValThrMetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAs 958
Db 2551 G----- 2551
QY 958 nValMetHisSerGluLysAspTyrValPheAlaValPheAsnSerThrMetValTy 978
Db 2552 -----GACTATGTTTTCAGCTGTTTTCAGCTGTTTTCAGCTACTATGGTTTA 2592
QY 978 rSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValTh 998
Db 2593 TTCTTTTACCTATATTAGTGAATATCATTAGTAACTACTATCTTTATCATTTAAATGTGAC 2652
QY 998 rGluThrIleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLy 1018
Db 2653 TGAACCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTACTGATATAGTTTTTAA 2712
QY 1018 sIleGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTy 1038
Db 2713 AATTGAGCTGTATTTTCAAGCAGCTTGTCTTGAATCATTTGTACTGCAATGCCACCTTA 2772
QY 1038 rPheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSe 1058
Db 2773 CTTTGCCATGGAAAAATGCAGAGAAATCATAAGATCAAAGCTTATACTCAACTTAAACTTTC 2832
QY 1058 rGlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePh 1078
Db 2833 AGGTCTTTTGCCATCTGCATATTGGATTGGACAAAGCTGTTGTGATATCCCTTATTTT 2892
QY 1078 eIleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTy 1098
Db 2893 TATCATTTCTTATTGTATGCTAGGAAGCTTATTTGGCATTTTCATTTATGATATATTTT 2952
QY 1098 rThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLe 1118
Db 2953 TACTGTAAAGTTCCTTGTGTGGTTTTTTTGGCTTATTTGGTTATGTCTCCATCAGTTATTC 3012
QY 1118 uPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSe 1138
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QY 1138 rPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMe 1158
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QY 1158 tGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrPr 1178
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Db 3253 GGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTTATATATGCCTTACCTGCAGTG 3312
QY 1218 sValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleAr 1238
Db 3313 TGTACTGTGGATTTTCTCTTACAAATACTATGAGAAAAAATATGAGGCGCAGATCAATAAG 3372
QY 1238 gLysAspProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluPr 1258
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Db 4429 ATAGCTTTCTCAAGCAACATTGGAAACAGGTTTTTTGTAGAACTCACTAAAGAACAAAGAGG 4488
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Db 4489 AGGAAGATAAATAGTTGTGGAACCTTAAACAGCACACCTTTGGTGGGACGACCAAGAAG 4548
Qy 1638 spArgValValPhe 1642
Db 4549 ATAGAGTAGTATTT 4562

RESULT 13
US-60-453-135-2441
; Sequence 2441, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2441
; LENGTH: 5595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-135-2441
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Alignment Scores:
Pred. No.: 0 Length: 5595
Score: 7377.00 Matches: 1474
Percent Similarity: 89.67% Conservative: 2
Best Local Similarity: 89.55% Mismatches: 5
Query Match: 87.55% Indels: 167
DB: 102 Gaps: 5

US-10-090-458-5 (1-1642) x US-60-453-135-2441 (1-5595)
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Db 115 ATGTCCTCACTGCAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 174
Qy 21 AanTyrLeuIleLysCysArgThrLysLysSerSerValGlnGlnIleLeuPheProLeu 40
Db 175 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 234
Qy 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 235 TTTTITTTTATTTTGGTTAATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 294
Qy 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 295 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTGGG 354
Qy 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 355 TATACTCCAGTGACTAATATTACAGCAGCATCATGMAGAAAGTGTCTACTGATCATCTA 414
Qy 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 415 CCTGATGTCTAATATTACTGAAGAATATACAAATGAAAGAAAGAAATGTTAATCATCCAGTCTC 474
Qy 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 475 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTTCAAAGACTCCATGTCTCTATGAACCTTCGT 534
Qy 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 535 TTTTITTCCTGATATGATTCAGTATCTTCTATTATATATGATGATTCAGAGCTGGTGTTC 594
Qy 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
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Db 655 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 714
Qy 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 715 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 774
Qy 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db 775 ATTTTAATATACCTAGTTATAGCATTTTCCACCTTTTGGATACTTTTGGCAATTCATATC 834
Qy 241 ValAlaGluLysGluLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 835 GTAGCAGAAAAA----- 846
Qy 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 846 ----- 846
Qy 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerIleValIlePhe 300
Db 846 ----- 846
Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
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Qy 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
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Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 846 ----- 846
Qy 361 ProPheCysHisCysThrPheValIleGlyIleAlaGln-ValMetHisLeuGluAspPh 380
Db 847 -----GAAAGTCATGCATTTAGAAGATTT 870
Qy 380 eAsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 871 TAAFGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAAT 930
Qy 400 eIleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVa 420
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Qy 420 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTr 440
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Qy 440 pSerLysSerLysArgAsnTyrGluGluLeuSerGlyAsnValAsnGlyAsnIleSe 460
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Qy 460 rPheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIl 480
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Qy 500 uSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLy 520
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Qy 520 sSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIl 540
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QY 978 rSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValTh 998
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Db 2773 CTTTGCCATGGAAAAATGCAGAGAAATCAAGAATCAAAAGCTTATCTCAACTTAAACTTTC 2832
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QY 1118 uPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSe 1138
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QY 1298 uTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysValAlaThrLysTy 1318
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Db 846 ----- 846
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Db 846 ----- 846
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Db 847 -----GAAAGTCATGCAATTTAGAACATTT 870
QY 380 eAsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 871 TAATGAAGGTGCTTCATTTTCAAATTTGACTGCAGGCCCATATCTCTAAATTATTACAAT 930
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QY 420 lIleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTr 440
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QY 740 nAspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPh 760
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QY 760 eSerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrTh 780
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QY 780 rLeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSe 800
Db 2071 TTTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAG 2130
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QY 840 pLysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLy 860
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Db 5776 CAATCTTTTAAAGCTGGAAAGAGCTAAACATGCTTTTGCATTGAAGAATATAGCTTT 5835
QY 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620
Db 5836 TCTCAAGCAACATTTGGAACAGGTTTTGTAGAACTCCTAAAGAACACAAGAGGAGGAGAT 5895
QY 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
Db 5896 AATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAACACAAGAGATAGAGTA 5955
QY 1641 ValPhe 1642
Db 5956 GTATTT 5961
RESULT 12
US-60-453-050-2441
; Sequence 2441, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2441
; LENGTH: 5595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-050-2441
Alignment Scores:
Pred. No.: 0 Length: 5595
Score: 7377.00 Matches: 1474
Percent Similarity: 89.67% Conservative: 2
Best Local Similarity: 89.55% Mismatches: 5
Query Match: 87.55% Indels: 167
DB: 102 Gaps: 5
US-10-090-458-5 (1-1642) x US-60-453-050-2441 (1-5595)
QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLys 20
Db 115 ATGTCCACTGCATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG 174
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 175 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTTCCACTA 234
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 235 TTTTTTTATTTTGGTTAATAATTATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 294
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 295 GTGCCATAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGA 354
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 355 TATACTCCAGTGACTAATAATTACAAAGCAGCATCATGMAGAAAGTGTCTACTGATCATCTA 414
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 415 CCGTGTGTCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC 474
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 475 TCTAAGCCGAGCAACTTTGTAGGTGGTTTCAAAGACTCCATGTCTCTATGAACCTTCGT 534
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160

Db 2678 AGTGGTATTGAGAAGACATACAGAAAGAGGGTGAAATGTGGAGGCTTTGAGAAATTTG 2737

QY 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520

Db 2738 TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGAACAGGAAAG 2797

QY 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540

Db 2798 AGTACATTGATGAATATTCTTTGTGGACTCTGCCACCTTCTGATGGTTTGCATCTATA 2857

QY 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560

Db 2858 TATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAATGATTGGCATT 2917

QY 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580

Db 2918 TGTCCACAGTTAGATATACACTTTTGATGTTTGGACAGTAGAAGAAATTTATCAATTTG 2977

QY 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600

Db 2978 GCTTCAATCAAGGGATACCAGCCCAACATATAATACAAGAGTGCAGAGGTTTACTA 3037

QY 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620

Db 3038 GATTTAGACATGCAGACTATCAAGATAACCAAGCTAAATAAATAAGTGGTGGTCAAAA 3097

QY 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640

Db 3098 AGAAAGCTGTATTAGGAATTGCTGTTCTGGGAACCCCAAGATACTGCTGTAGATGAA 3157

QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660

Db 3158 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGA 3217

QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680

Db 3218 AAAGCCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTCITGCA 3277

QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700

Db 3278 GATAGGAAAGCTGTGATATCACAGGAATGCTGAAATGTGTGTTCTTCAATGTTCTCTC 3337

QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720

Db 3338 AAAAGTAAATGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 3397

QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740

Db 3398 GAATCTCTTTCTCACTGGTTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAA 3457

QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760

Db 3458 GACCAACAACCTGTGTATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAGGTTTGTGT 3517

QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780

Db 3518 TCTGCCCTAGACAGTCAATTCAAATTTGGGTGTCAATTTCTTATGGTGTTCATGACGACT 3577

QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800

Db 3578 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATGACCAAGCAGG----- 3630

QY 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820

Db 3630 ----- 3630

QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840

Db 3630 ----- 3630

QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860

Db 3630 ----- 3630

QY 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880

Db 3631 -----TTGCTTCTGCTTTTAATTTTTCACAGTTCAGATTTTATATGTTT 3675

QY 881 LeuValHisHisSerPheLysAsnAlaValPalProIleLysLeuValProAspLeuTyr 900

Db 3676 TTGGTTTCATCACTCTTTTAAAAATGCTGGTTCCTCCATCAAACTTGTTCAGACTTATAT 3735

QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSer 920

Db 3736 TTTCTAAAACCTGGAGACAAACCCACATAAATACAAAACAAGTCTGCTTCTTCAAAATCT 3795

QY 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940

Db 3796 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGACG 3855

QY 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960

Db 3856 ATGATTAAATGACAGTACTATGTATCCGTGGCTCCCATAGTGGGCTTTAAATGTGGTG 3915

QY 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980

Db 3916 CATTCAAGAAAGGACTATGTTTTGCAGCTGTTTTCAACAGTACTATGGTTTATCTTTA 3975

QY 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000

Db 3976 CCTATATTAGTGAATATCATTTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACC 4035

QY 1001 IleGlnIleTrpSerThrProPheGlnGluIleThrAspIleValPheLysIleGlu 1020

Db 4036 ATCCAGATCTGGAGTACCCCATCTTCTCAAGAAATTTACTGATATAGTTTTTAAAAATTGAG 4095

QY 1021 LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040

Db 4096 CTGTATTTTCAAGCAGCTTTTGTCTTGGAAATCATTTTACTGCAATGCCACCTTACTTTGCC 4155

QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060

Db 4156 ATGGAAAATGCAGAGAATCATAGATCAAAAGCTTATACTCACTCAACTTAAACTTTCAGGTCTT 4215

QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIle 1080

Db 4216 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTTTATCAT 4275

QY 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100

Db 4276 CTTATTTTGTGCTAGGAAGCTTATTGGCATTTTCAATATGGATTATATTTTATACTGTA 4335

QY 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120

Db 4336 AAGTTCTTGTGTGGTTTTTTTGCCTTATTGGTTATGTTCCATCAGTTATCTGTTCAC 4395

QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140

Db 4396 TATATTGCTTCTTTCACCTTTTAAAGAAAATTTTAAATACCAAGAAATTTTGGTTCATTTATC 4455

QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160

Db 4456 TATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATAC 4515

QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180

Db 4516 ACAATTGCAACTATTCTTCATTTATGCTTTTGTATCATCATCTCCACTTCTCTA 4575

QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200

Db 4576 GGTTGCCCTGATTTCTTTTCAATAAAGATTCTTTGGAAGAAATGTACGAAAAAATGTGGACACC 4635

QY 1201 TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220

Db 4636 TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATATCGCCTTACCTGCAGTGTGTA 4695

; APPLICANT: JACKSON, Alan A.		
; APPLICANT: JIANG, Xin		
; APPLICANT: JIN, Pei		
; APPLICANT: KABLE, Amy E.		
; APPLICANT: KHARE, Reena		
; APPLICANT: LEE, Soo Y.		
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; APPLICANT: MASON, Patricia M.		
; APPLICANT: MARQUIS, Joseph P.		
; APPLICANT: RAMKUMAR, Jayalaxmi		
; APPLICANT: RICHARDSON, Thomas W.		
; APPLICANT: SWARNAKAR, Anita		
; APPLICANT: TRAN, Uyen K.		
; APPLICANT: CHAWLA, Narinder K.		
; APPLICANT: WILSON, Amy D.		
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS		
; FILE REFERENCE: PF-1435 PCT		
; CURRENT APPLICATION NUMBER: PCT/US03/14026		
; CURRENT FILING DATE: 2003-05-02		
; PRIOR APPLICATION NUMBER: US 60/377,444		
; PRIOR FILING DATE: 2002-05-03		
; PRIOR APPLICATION NUMBER: US 60/377,435		
; PRIOR FILING DATE: 2002-05-03		
; PRIOR APPLICATION NUMBER: US 60/386,497		
; PRIOR FILING DATE: 2002-06-05		
; PRIOR APPLICATION NUMBER: US 60/388,180		
; PRIOR FILING DATE: 2002-06-11		
; NUMBER OF SEQ ID NOS: 132		
; SOFTWARE: PERL Program		
; SEQ ID NO 75		
; LENGTH: 6170		
; TYPE: DNA		
; ORGANISM: Homo sapiens		
; FEATURE:		
; NAME/KEY: misc feature		
; OTHER INFORMATION: Incyte ID No: 7511310CB1		
PCT-US03-14026-75		
Alignment Scores:		
Pred. No.:	0	Length: 6170
Score:	8028.50	Matches: 1573
Percent Similarity:	95.86%	Conservative: 1
Best Local Similarity:	95.80%	Mismatches: 1
Query Match:	95.28%	Indels: 68
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US-10-090-458-5 (1-1642) x PCT-US03-14026-75 (1-6170)		
QY	1	MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLys 20
Db	1238	ATGTCCACTGCAATTAGGAGGTAGGAGTTGGAGACAGACCAGACACTTCTACTGAAG 1297
QY	21	AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db	1298	AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 1357
QY	41	PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db	1358	TTTTTTTATTTGGTTAATATTAAATACCATGATGCATCCAAATAAGAAATATGAAGAA 1417
QY	61	ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db	1418	GTGCCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAATCTAATTCITGGA 1477
QY	81	TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db	1478	TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCACTTA 1537
QY	101	ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db	1538	CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAATGTTAATCCAGTCTC 1597
QY	121	SerLysProSerAsnPheValGlyValPheLysAspSerMetSerTyrGluLeuArg 140
Db	1598	TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAGACTCCATGTCCTATGAACCTTCGT 1657
QY	141	PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db	1658	TTTTTTCTGATATGATCCAGTATCTTCTATTTATATGATTCAGATTCAGAGCTGGCTGTCA 1717
QY	161	LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db	1718	AAATCATGTGAGGCTGCTCAGTACTGGTCTCTCAGTTTCACAGTTTTACAGCATCCATA 1777
QY	181	AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
Db	1778	GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 1837
QY	201	LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db	1838	AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCCCGAGGAGTA 1897
QY	221	IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db	1898	ATTTTAATATACCTAGTTATAGCATTTTTCACCTTTGGATACACTTTTGGCAATTCATATC 1957
QY	241	ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db	1958	GTAGCAGAAAAAGAAAAATAAAAGAAATTTTAAAGATAATGGGACTTTCATGATACT 2017
QY	261	AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db	2018	GCCTTTTGGCTTTCCCTGGGTCTTCTATATACAAAGTTTAATTTTCTTATGTCCTTCTT 2077
QY	281	MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
Db	2078	ATGGCAGTCATTGCGACAGCTTCTTTGTTATTTCCTCAAGTAGCAGCATTTGTGATATTT 2137
QY	301	LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db	2138	CTGCTTTTCTTCTTATGGATTATCATCTGTATTTTGTCTTAAATGCTGACACCTCTT 2197
QY	321	PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db	2198	TTTAAAAAATCAAAACATGTGGAAATAGTTGAATTTTGTGTTACTGTGGCTTTTGGATTT 2257
QY	341	IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db	2258	ATTGGCCTTATGATAATCCTCATAGAAAAGTTTCCCAAAATCGTTAGTGTGGCTTTTCAGT 2317
QY	361	PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db	2318	CCTTTCTGTCACCTGTACTTTTGTGATTGGTATTGCACAGTCATGCATTTAGAGATTTT 2377
QY	381	AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db	2378	AATGAAGGTCTTTCATTTTCAATTTGACTGCAGGCCCATATCTCTAATTATTACAATT 2437
QY	401	IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db	2438	ATCATGCTCACACTTAATAGTATATTCTATGTCCTCTTGGCTGTCTATCTTGTATCAAGTC 2497
QY	421	IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db	2498	ATTCAGGGGGAATTTGGCTTACGGAGATCATCTTTATATATTTTCTGAAGCCTTTCATATTGG 2557
QY	441	SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db	2558	TCAAAGAGCAAAAGAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT 2617
QY	461	PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db	2618	TTTAGTGAAATTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAGCCATAAGAATT 2677
QY	481	SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500

QY	941	MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet	960
DB	2821	ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGGCTTTAAATGTGRTG	2880
QY	961	HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu	980
DB	2881	CATTGAGAAAAGGACTATGTTTTCAGCTGTTTCAACAGTACTATGGTTATCTTTA	2940
QY	981	ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr	1000
DB	2941	CCTATATTAGTGAATATCATTAGTAACCTACTATCTTTATCATTTAAATGTGACTGAAACC	3000
QY	1001	IleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGlu	1020
DB	3001	ATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAAGTACTGATATAGTTTAAATTTGAG	3060
QY	1021	LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla	1040
DB	3061	CTGTATTTCAAGCAGCTTTGCTTGGAAATCATTTGTAATCAATGCAATGCCACCTTACTTTGCC	3120
QY	1041	MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu	1060
DB	3121	ATGGAAAATGCAGAGAAATCAAGATCAAGCTTAYACTCAACTTAACTTCAAGTCTT	3180
QY	1061	LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIle	1080
DB	3181	TTGCCATCTGCATATTGGAATGGACAAGCTGTTGTTGATATCCCTTATTTTATCAT	3240
QY	1081	LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal	1100
DB	3241	CTTATTTTGATGTAGGAAGCTTATGGCATTTTCATATGGATTATATTTTATACTGA	3300
QY	1101	LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr	1120
DB	3301	AAGTTCCTTGCTGGTTTTTGGCTTATTTGTTATGTTCCATCAGTTATTTCTGTTCACT	3360
QY	1121	TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle	1140
DB	3361	TATATTGCTTCTTTCACCTTTAAGAAAATTTTAAATACCAAGAAATTTTGGTCATTATC	3420
QY	1141	TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr	1160
DB	3421	TATTTCTGGCAGCGTTGGCTTGATTTGCAATCACTGAAATAACTTTCTTTTATGGGATAC	3480
QY	1161	ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu	1180
DB	3481	ACAATTGCAACTATTCTTCATATAGCTTTTGTATCATCTCCATCTATCCACTTCTA	3540
QY	1181	GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr	1200
DB	3541	GGTTGCTGATTTCTTTTCAATAAGATTTCTTGGAAAGATGTACGAAAAAATGTGGACACC	3600
QY	1201	TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu	1220
DB	3601	TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCCGCTTACCTGCAGTGTCTACTG	3660
QY	1221	TrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp	1240
DB	3661	TGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGAT	3720
QY	1241	ProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProAsp	1260
DB	3721	CCCTTTTTCAGAAAACCTTTTCAACGAAAGTCTAAAAATAGGAAGCTTCCAGAACCCAGAC	3780
QY	1261	AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly	1280
DB	3781	AATGAGGATGAAGATGAAGATGTCAAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGT	3840
QY	1281	CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp	1300
DB	3841	TGCCAGTGTGTGAGGAGAAACCCTCATTTATGTCAGCAATTTGCATAAAGAAATATGAT	3900
QY	1301	AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer	1320

DB	3901	GACAAAGAAAAGATTTTCTTCTTTCAAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCT	3960
QY	1321	PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer	1340
DB	3961	TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGCGAAAAAGC	4020
QY	1341	ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly	1360
DB	4021	ACAATTATTAAATATTCTGGTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA	4080
QY	1361	AspTyrSerSerGluThrSerGluAspAspAspSerLeuLysCysMetGlyTyrCysPro	1380
DB	4081	GATTATTCTTCAGAGACAAGTGAAGATGATGATTCATCTGAAGTGTATGGTTACTGTCTCT	4140
QY	1381	GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla	1400
DB	4141	CAGATAAACCCCTTTGTGGCCAGATACATACATTCAGGAACATTTTGAATTTATGGAGCT	4200
QY	1401	VallysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu	1420
DB	4201	GTCAAGGAATGAGTCAAGTGACATGAAAGAAAGTCAATAAGTCAATAACACATGCACCT	4260
QY	1421	AspLeuLysGluHisLeuGlnLysThrVallysLysLeuProAlaGlyIleLysArgLys	1440
DB	4261	GATTAAAAAGAACATCTTTCAGAGACTGTAAAGAAACTACCTGCAGGAATCAAAACGAAAG	4320
QY	1441	LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer	1460
DB	4321	TTGTGTTTGTCTTAAGTATGTAGGAATCCTTCAGATTACTTTGCTAGATGAACCATCT	4380
QY	1461	ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys	1480
DB	4381	ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACATGCAATTTAA	4440
QY	1481	AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys	1500
DB	4441	AACAGAAAGCGGGCTGCTATTCTGACCCTCACTATATGGAGGAGGAGGCTGTCTGT	4500
QY	1501	AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu	1520
DB	4501	GATCGAGTAGCTATCATGTTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA	4560
QY	1521	LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn	1540
DB	4561	AAGAGTAAATTTGGAAAAGGCTACTTTTGGAAAATTTAAATTTGAAGGACTGGATAGAAAAC	4620
QY	1541	LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln	1560
DB	4621	CTAGAGTAGACCCGCTTCAAGAGAAAATTCAGTATATTTCCTCCAAATGCAAGCCGTCAG	4680
QY	1561	GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer	1580
DB	4681	GAAAGTTTTTCTTCTATTATTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA	4740
QY	1581	GlnSerPhePheLysLeuGluGlu	1588
DB	4741	CAATCTTTTAAAGCTGGAAGAA	4764

RESULT 11
PCT-US03-14026-75
; Sequence 75, Application PC/TUS0314026
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BECHA, Shanya D.
; APPLICANT: BULLOCH, Sean A.
; APPLICANT: CHANG, Hsin-Ru
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: ISON, Craig H.

Db 601 AAAGCTGTTATTATGGGAGAAACTGCTGTGTAGAAATAGATACTTCCCGAGGAGTA 660
QY 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db 661 ATTTTAATATACCTAGTTATAGCATTTTACCTTTTGGATACCTTTTGGCAATTCATATC 720
QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 721 GTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT 780
QY 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 781 GCCTTTTGGCTTTCCTGGGTTCTTCTATAWACAAGTTTAAATTTTCTTATGTCCTCTCTT 840
QY 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
Db 841 ATGGCAGTCATTGGCAGACTTCTTTGTTATTTCTCAAGTAGCAGCATTTGTGATATTT 900
QY 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 901 CTGCTTTTTCCTTTATGGATTATCATCTGCTATTTTGTGCTTTAATGCTGACACCTCTT 960
QY 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 961 TTTAAAAAATCAAAACATGTGGGAATAGTGAATTTTGTGTTACTGTGGCTTTTGGATTT 1020
QY 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 1021 ATTGGCCTTATGATAATCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 1080
QY 361 PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 1081 CCTTCTGTCTACCTGCTTCTTGTGATTGTTGATGTTGACAGGTCATGCTTTAGAAATTT 1140
QY 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 1141 AATGAAGGTGCTTCAATTTCAAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAAT 1200
QY 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 1201 ATCATGCTCACACTTAATAGTATATTCTATGTCCTCTTGGCTGTCTATCTTGATCAAGTC 1260
QY 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 1261 ATTCAGGGGAATTTGGCTTACGGAGATCATCTTATATTTTCTGAAGCCTTCATATTGG 1320
QY 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db 1321 TCAAAGAGCAAAAGAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT 1380
QY 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db 1381 TTTAGTGAAATATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAACGCCATAAGAAAT 1440
QY 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 1441 AGTGGTATTCAGAAACACATACAGAAAGAGGGTGAAAAATGTGGAGGCTTTGAGAAATTTG 1500
QY 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
Db 1501 TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAAACAGGAAAG 1560
QY 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 1561 AGTACATTGATGAATATTTCTTGTGGACTCTGCCACCTTCTGATGGGTTTGTGATCTATA 1620
QY 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 1621 TATGGACACAGACTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAAATGATTGGCATT 1680
QY 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
Db 1681 TGTCCACAGTTAGATATACACTTTGATGTTTGTGACAGTAGAAGAAAAATTTATCAATTTTG 1740

QY 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 1741 GCTTCAATCAAAAGGATACCAGCCCAATATATAATACAAGAGTGCAGAAGGTTTACTA 1800
QY 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
Db 1801 GATTTAGACATGCAGACTATCAAGATAACCAAGCTAAAAAATAAGTGGTGGTCAAAA 1860
QY 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
Db 1861 AGAAAGCTGTTCATTAGGAATTGCTGTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 1920
QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLysTyrArg 660
Db 1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGA 1980
QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Db 1981 AAAGCCAATCGGTGACAGTGTTCAGTACTCATTTTATGGATGGAAGTGCATTTCTTGCA 2040
QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 2041 GATAGGAAAGCTGTGATATCACAGGAATGCTGAAATGTGTGTTCTTCAATGTTCTCTC 2100
QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 2101 AAAAGTAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 2160
QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
Db 2161 GAATCTCTTCTTCTACTGGTTAAACACATATATCCTGGAGCTACTTTATTACAACAGAA 2220
QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
Db 2221 GACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCAGGTTTGTIT 2280
QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 2281 TCTGCCCTAGACAGTCATTTCAAAATTTGGGTGGCATTTCTTATGGGTTTCCATGACGACT 2340
QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 2341 TTGGAAGACGTTATTTTAAAGCTAGAAATGGAATTCAAAATCTTTTGTGATGAAATGGAA 2400
QY 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 2401 GTATTTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGTGATGAAATGGAA 2460
QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 2461 CAGAGCTTACTTATTTCTTCTGAAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTGG 2520
QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860
Db 2521 AAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTACCTTGAAACGTGAAAGTAAA 2580
QY 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 2581 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2640
QY 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
Db 2641 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATAT 2700
QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSer 920
Db 2701 TTTCTAAAAACCTGGAGACAAACCATATAAATACAAACCAAGCTGCTTCTTCAAAATTTCT 2760
QY 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
Db 2761 GCTGACTCAGATATCAGTGATCTTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGACG 2820

QY 1295 uHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysLysValAl 1315
Db 3919 GCATAAAGAAATATGATGACAAAGAAATTTCTTCTTCAAGAAAGCAAGAAAGTGC 3978
QY 1315 aThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuGlyProAs 1335
Db 3979 AACTAAATACATCTCTTCTGTGTGAAAAAGAGAGATCTTAGGACTATTGGGTCCAA 4038
QY 1335 nGlyAlaGlySerThrIleIleAsnIleLeuValGlyAspIleGluProThrSerG1 1355
Db 4039 TGGTGTGGCAAAAGCACAAATATTATTAATTTCTGTTGGTGATTTGAACCAACTTCAG 4098
QY 1355 yGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLysCy 1375
Db 4099 CCAGGTATTTTAGGAGATTATTTCTTCAGAGACAAGTGAAGATGATTCACCTGAAGTG 4158
QY 1375 sMetGlyTyrCysProGlnIleAsnProLeuTyrProAspThrThrLeuGlnGluHisPh 1395
Db 4159 TATGGTTACTGTCCTCAGATAAACCCCTTTGTGGCCAGATACATTCAGGAAACATTT 4218
QY 1395 eGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerAr 1415
Db 4219 TGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAGAAAGTCATAAGTCG 4278
QY 1415 gIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAl 1435
Db 4279 AATAACACATGCACCTTGATTTTAAAGAACATCTTTCAGAAAGCTGTAAAGAAAGCTACTGC 4338
QY 1435 aGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLe 1455
Db 4339 AGGAATCAAACGAAAGTTGTGTTTCTCTAAGTATGCTAGGAAATCCTCAGATTACTTT 4398
QY 1455 uLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTyrArgAlaI1 1475
Db 4399 GCTAGATGAACCATCTACAGGTATGATGCCAAAGCCAAACAGCACATGTGGCGAAT 4458
QY 1475 eArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluG1 1495
Db 4459 TCGAAGTGCATTTTAAACACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGAGGA 4518
QY 1495 uAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleG1 1515
Db 4519 GGCAGAGTTGTCTGTGATCGAGTAGCTATCATGTTCTGGGCGAGTTAAGATGATCGG 4578
QY 1515 yThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLy 1535
Db 4579 AACAGTACAACATCTAAAGAGTAAATTTGAAAGGCTACTTTTGGAAATTAATTTGAA 4638
QY 1535 sAspTyrIleGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePhePr 1555
Db 4639 GGACTGGATAGAAAACCTAGAGTAGACCGCTTCAAGAGAAATTCAGTATATTTTCCC 4698
QY 1555 oAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAs 1575
Db 4699 AAATGCAAGCCGTCAGGAAAGTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGA 4758
QY 1575 pValGlnSerLeuSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaI1 1595
Db 4759 TGTTCACTCCCTTTTACAATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCAT 4818
QY 1595 eGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysG1 1615
Db 4819 TGAAGATATAGCTTTTCTCAGCAACATTTGGAACAGGTTTGTAGAACTCATAAGAA 4878
QY 1615 uGlnGluGluGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTyrTrpGluArgTh 1635
Db 4879 ACAAGAGGAGGAAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTTGGTGGGAACGAAC 4938
QY 1635 rGlnGluAspArgValValPhe 1642
Db 4939 ACAAGAGATAGAGTAGTATTT 4960

RESULT 10
US-09-971-121-3
; Sequence 3, Application US/09971121
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: Novel Human Transporter Proteins and Polynucleotides Encoding t:
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4785
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-971-121-3
Alignment Scores:
Pred. No.: 0 Length: 4785
Score: 8112.00 Matches: 1583
Percent Similarity: 99.69% Conservative: 0
Best Local Similarity: 99.69% Mismatches: 5
Query Match: 96.27% Indels: 0
DB: 41 Gaps: 0

US-10-090-458-5 (1-1642) x US-09-971-121-3 (1-4785)

QY 1 MetSerThrAlaIleArgGluValGlyValTyrArgGlnThrArgThrLeuLeuLys 20
Db 1 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACAGAACACACTTCTACTGAAG 60
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 61 AATTACTTAATAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA 120
QY 41 PhePheLeuPheTyrLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 121 TTTTCTTATTTTGGTTAATAATTAATAGCATGATGCATCAATAAAGAAATATGAAGAA 180
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 181 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTCTTAATCTAATCTTGA 240
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 241 TATACTCCAGTGACTAATATTACAGCAGCATCATGCAGAAAGTGCTCTACTGATCATCTA 300
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 301 CCTGATGTCATAATTACTGAAGAAATATACAAATGAAAGAAATGTTAATCCAGTCTC 360
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 361 TCTAAGCCGAGCAACTTTGTAGTGTGGTTTTCAAAGACTCCATGCTCTATGAACCTCGT 420
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 421 TTTTCTCTGATATGATTCAGTATCTTCTATTTATATGGAATCAAGAGCTGGCTGTCTCA 480
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 481 AAATCATGTGAGGCTGCTCAGTACTGCTCTCCTCAGGTTTTCACAGTTTACAAAGCATCCATA 540
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTyrLysGluLeuGluSerThr 200
Db 541 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTGGAAAGGAGCTGGAGTCAACT 600
QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220

Db 1730 TGTCCACAGTTAGATATACACTTTGATGTTTTGACAGTAGAAGAAATTTATCAATTTTG 1789
QY 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 1790 GCTTCAATCAAAGGATACCAGCCAAACAATAATACAAAGAGTGAGAGGTTTACTA 1849
QY 601 AspLeuAspMetGlnThrIleLysAspAspGlnAlaLysLysLeuSerGlyGlnLys 620
Db 1850 GATTTAGACATGCAGACTATCGAAGATAACCAAGCTAAAAAATTAAGTGGTGCACAAA 1909
QY 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
Db 1910 AGAAAGCTGTCAATAGGAATGCTGTTCTTGGGAACCCAAAGATACCTGCTAGATGAA 1969
QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLysTyrArg 660
Db 1970 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATGATGGAATCTTTAAATACAGA 2029
QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Db 2030 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGTGACATTTCTTGCA 2089
QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 2090 GATAGGAAGCTGTGATATCACAGGAATGCTGAAATGTTGTTCTTCAATGTTCCCTC 2149
QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 2150 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATACCTGTGCCACA 2209
QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsn 740
Db 2210 GAATCTCTTTCTTCACTGTTTAAACAACATATACCTGGAGCTACTTTATTAACACAGAA 2269
QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
Db 2270 GACCAACAACCTTGTTGATAGCTTGCTTCAAGGACATGGACAAATTTTCAGGTTTGTT 2329
QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 2330 TCTGCCCTAGACAGTCATTCAAATTTGGGTGTCATTTCTTATGGTGTTCATGACGACT 2389
QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 2390 TTGGAAGACGTATTTTAAAGCTAGAAAGTTGAAGCAGAAATTTGACCAAGCAGATTATAG 2449
QY 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 2450 GTATTTTACTCAGCAGCCACTGGAGGAAGAAATGGAATTCCTTATGATGAAATGGAA 2509
QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 2510 CAGAGCTTACTTATTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTTG 2569
QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrValGlnIlePheMetPhe 860
Db 2570 AAACAACAGATGTATACAATAGCAAGTTTCATTTCTTACCTTGAAACGTTGAAAGTAA 2629
QY 861 SerValArgSerValLeuLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 2630 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2689
QY 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
Db 2690 TTGGTTTCATCACTCTTTTAAAAATGCTGGTTCCCATCAAACTTGTTCAGACTTATAT 2749
QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
Db 2750 TTTCTAAACCTGGAGACAAAACCATAAATACAAAACAAAGTCTGCTCTCTTCAAAATCT 2809
QY 921 Ala-----AspSerAspIleSerAspLeuIleSerPhePheThrSerGln 935

Db 2810 GCTGGTGAGAGTGTGTGAAGACTCAGATATACAGTGATCTTATTAGCTTTTTCACAAGCCA 2869
QY 935 nAsnIleMetValThrMetIleAsnAspSerAspTyrValSerValAlaProHisSerAl 955
Db 2870 GAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGC 2929
QY 955 aAlaLeuAsnValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSerTh 975
Db 2930 GGCTTTAAATGTGTGCATTTCAAGAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTAC 2989
QY 975 rMetValTyrSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLe 995
Db 2990 TATGGTTTATTTCTTACCTATATTAGTGAATATCATTTAGTAACCTACTATCTTTATCATTT 3049
QY 995 uAsnValThrGluThrIleGlnIleTrpSerThrProphePheGlnGluIleThrAspIl 1015
Db 3050 AAATGTGACTGAACCATCCAGATCTGGAGTACCCCATTTCTTTCAAGAAATTAAGTAT 3109
QY 1015 eValPheLysIleGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMe 1035
Db 3110 AGTTTTTAAATGAGCTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTACTGCAAT 3169
QY 1035 tProProTyrPheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLe 1055
Db 3170 GCCACCTTACTTTGCCATGGAAATGCAGAGAATCATAA----- 3208
QY 1055 uLysLeuSerGlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIlePr 1075
Db 3209 -----GGTCTTTTGCCATCTGCATATTTGGATTGGACAGCTGTTGTTGATATCCC 3258
QY 1075 oLeuPhePheIleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLe 1095
Db 3259 CTTATTTTATCATTTCTTATTTTGTATGCTAGGAAGCTTTATTGGCATTTTCATTATGGATT 3318
QY 1095 uTyrPheTyrThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProse 1115
Db 3319 ATATTTTATACTGTAAAGTTTCTTGTCTGTTGTTTTCCTTTATTGGTTATGTTTCCATC 3378
QY 1115 rValIleLeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGl 1135
Db 3379 AGTTATTTCTGTTCACTTATATTGCTTCTTTCACCTTTAAGAAAAATTTAAGTACCAAAGA 3438
QY 1135 uPheTrpSerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleTh 1155
Db 3439 ATTTTGGTCATTTATCTATTTCTGTGGCAGCTTGGCTTGTATTGCAATCACTGAAATAAC 3498
QY 1155 rPhePheMetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIlePr 1175
Db 3499 TTTCTTTATGGGATCTCAATTGCAACTATTCTTCAATATATGCTTTTGTATCATCTCC 3558
QY 1175 oIleTyrProLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValAr 1195
Db 3559 AATCTATCCACTTCTAGTTGCTGCTGATTTCTTCAAAAGATTTCTTGAAGAATGTACG 3618
QY 1195 gLysAsnValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerProTy 1215
Db 3619 AAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCCTTA 3678
QY 1215 rLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyAr 1235
Db 3679 CCTGCAGTGTGTACTGTGGATTTTCTCTTACATACTATGAGAAAAAATATGGAGGCAG 3738
QY 1235 gSerIleArgLysAspProphePheArgAsnLeuSerThrLysSerLysAsnArgLysLe 1255
Db 3739 ATCAATAAGAAAAAGATCCCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGCT 3798
QY 1255 uProGluProProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLysVa 1275
Db 3799 TCCAGAACCCACAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGT 3858
QY 1275 lLysGluLeuMetGlyCysGlnCysGlnCysGluGluLysProSerIleMetValSerAsnLe 1295
Db 3859 CAAAGAGCTGATGGGTGCGGTGTTGTTCAGGAGAAACCATCCATTCATTATGTTGTCAGCAATTT 3918

; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PF-1591 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/33087
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 60/419,313
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/421,033
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/421,349
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/423,516
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PERL Program
; SEQ ID NO 82
; LENGTH: 5004
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7523469CB1
PCT-US03-33087-82

Alignment Scores:
Pred. No.: 0 Length: 5004
Score: 8253.50 Matches: 1618
Percent Similarity: 98.60% Conservativeness: 7
Best Local Similarity: 98.18% Mismatches: 7
Query Match: 97.95% Indels: 17
DB: 1 Gaps: 2

US-10-090-458-5 (1-1642) x PCT-US03-33087-82 (1-5004)

QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLys 20
Db 50 ATGTCCACTGCAATTAGGAGGTAGGAGTTGGAGACAGACCAGACACTTCTACTGAAG 109
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 110 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 169
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 170 TTTTITTTTATTTGGTTAATTAATTAAGCATGATGCATCCAAATAGAAATATGAAGAA 229
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 230 GTGCCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAATCTAATTTCTTGA 289
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 290 TATACTCCAGTGACTAATATTAACAAGCAGCATCATGCAGAAAGTGCTACTGATCATCTA 349
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 350 CCTGATGTCATAATTACTGAAGATATATAAATGAAAAAGAAATGTTAAACATCCAGTCTC 409
QY 121 SerLysProSerAsnPheValGlyValPheLysAspSerMetSerTyrGluLeuArg 140
Db 410 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAAGACTCCATGTCCTATGAATTCGT 469
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 470 TTTTTCCTGATATGATATCCAGTATCTTCTATTTATATGATTCAGAGCTGGCTGTCTCA 529
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 530 AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTTCAGATTTTACAAGCATCCATA 589
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
Db 590 GATGCTGCCATTATACAGTTGAAGACCAATCTTCTCTTTTGAAGAGAGCTGGAGTCAACT 649

QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 650 AAAGCTGTTATTATGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 709
QY 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db 710 ATTTTAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACTTTTGGCAATTCATATC 769
QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 770 GTAGCAGAAAAAGAAAAAATAAAAGAAATTTTAAAGATAATGGGACITCATGATACT 829
QY 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 830 GCCTTTTGGCTTTCCCTGGGTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTT 889
QY 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
Db 890 ATGGCAGTCATTGCGACAGCTTCTTTGTTATTTCCTCAAAGTAGCAGCATTTGTGATATTT 949
QY 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 950 CTGCTTTTTCCTTTATGGATTATCATCTGTAATTTTGTGCTTAAATGCTGACACCTCTT 1009
QY 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 1010 TTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTT 1069
QY 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 1070 ATTGGCCTTATGATAATCCTCATAGAAAAGTTTCCCAAATCGTTAGTGGCTTTCCAGT 1129
QY 361 ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 1130 CCTTCTGTCACTGTACTTTTGTGATTGGTATTGCACAGGTCATGCAATTTAGAAAGATTTT 1189
QY 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 1190 AATGAAGGTGCTTCAATTTCAAATTTGACTGCAGGCCCATATCCTCTAATATTATACAATT 1249
QY 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 1250 ATCATGCTCACACTTAATAGTATATTTCTATGTCCTCTTGGCTGTCTATCTTGATCAAGTC 1309
QY 421 IleProGlyGluPheGlyLeuArgArgSerSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 1310 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1369
QY 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db 1370 TCAAAGAGCAAAGAAATATGAGGAGTTATCAGAGGGCAATGTTAATGGAATATCAGT 1429
QY 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db 1430 TTTAGTGAAATTTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAATT 1489
QY 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 1490 AGTGGTATTTCAGAAAGACATACAGAAAGAGGGGTGAAAATGTGGAGGCTTTGAGAAAATTG 1549
QY 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
Db 1550 TCATTTGACATATATGAGGGTCAGATTACTTGCTTACTTTGGCCACAGTGGAAACAGGAAAG 1609
QY 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 1610 AGTACATTGATGAATATCTTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATA 1669
QY 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 1670 TATGGACACAGAGTCTCAGAAAATAGATGAATGTTTGAAGCAAGAAAATGATTGGCATT 1729
QY 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580

QY	1034	aMetProProTyrPheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrG1	1054	QY	1394	sPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSe	1414
Db	3234	AATGCCACCTACTCTGCCATGGAAATGCAGAGAAATCATAA-----	3275	Db	4283	TTTTGAATTTATGGAGCTGTCAAAGGAATGAGTGCAAGTGACATGAAGAAGTCATAAG	4342
QY	1054	nLeuLysLeuSerGlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspI1	1074	QY	1414	rArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPr	1434
Db	3276	-----GGTCTTTGGCCATCTGCATATTGGATTGGACAAGCTGTGTTGATAT	3322	Db	4343	TGGAATAACACATGCACCTGATTTAAAGAACAATCTTCAGAAGACTGTAAAGAAACTACC	4402
QY	1074	eProLeuPhePheIleIleLeuLeuMetLeuGlySerLeuLeuAlaPheHisTyrG1	1094	QY	1434	oAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleTh	1454
Db	3323	CCCTTATTTTATCATCTCTTATTTGATGCTAGGAAGCTTATTGGCAITTCATTATGG	3382	Db	4403	TGCAGGAATCAAACCGAAAGTTGTGTTTGTCTCTAAAGTATGCTAGGGAATCCTCAGATTAC	4462
QY	1094	yLeuTyrPheTyrThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValPr	1114	QY	1454	rLeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAl	1474
Db	3383	ATTATATTTTATACTGTAAAGTTCTTGTGCTGGTTTGTGCTTATTGGTTATGTTCC	3442	Db	4463	TTTGCTAGATGAACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGC	4522
QY	1114	oSerValIleLeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLy	1134	QY	1474	aIleArgThrAlaPheLysAsnArgLysArgAlaIleLeuThrThrHisTyrMetG1	1494
Db	3443	ATCAGTTATCTGTTTCACTTATATTGCTTCTTTCACCTTAAAGAAATTTTAAATACCA	3502	Db	4523	AATTGGAACGTGATTTTAAACAAGAAAGCGGCTGCTATTTCTGACCACTCACTATATGA	4582
QY	1134	sGluPheTrpSerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluI1	1154	QY	1494	uGluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysI1	1514
Db	3503	AGAAATTTGGTCATTTATCTATTCTGTGGCAGCGTTGGTTGTATTGCAATCATGAAT	3562	Db	4583	GGAGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGTGTCTGGCAGTTAAGATGTAT	4642
QY	1154	eThrPhePheMetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleI1	1174	QY	1514	eGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLe	1534
Db	3563	AACCTTCTTTATGGGATACACAATGCAACTATTCTTCAATATGCTTTTGTATCATCAT	3622	Db	4643	CGGAACAGTACAACATCTAAAGAGTAAATTTGGAAGGCTACTTTTGGAAATTAATTT	4702
QY	1174	eProIleTyrProLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnVa	1194	QY	1534	uLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePh	1554
Db	3623	TCCAATCTATCCACTTCTAGGTTGCTGATTTCTTTTCAAAAGATTTCTTGGAGAATGT	3682	Db	4703	GAAGGACTGGATAGAAAACCTAGAAGTAGACCCGCTTCAAAAGAGAAATTCAGTATATT	4762
QY	1194	lArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerPr	1214	QY	1554	eProAsnAlaSerArgGlnGlnSerPheSerSerIleLeuAlaTyrLysIleProLysG1	1574
Db	3683	ACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCC	3742	Db	4763	CCCAATGCAAGCCGTCAGGAAGATTTTCTTCTATTTTGGCTTATAAAATTCCTTAGGA	4822
QY	1214	oTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyG1	1234	QY	1574	uAspValGlnSerLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPheAl	1594
Db	3743	TTACCTGCAGTGTACTGTGGATTTCCTCTTACAATACTATGAGAAAAAATATGGAGG	3802	Db	4823	AGATGTTCACTCCCTTTTCACAATCTTTTAAAGCTGGGAAGAGCTAAACATGCTTTGC	4882
QY	1234	yArgSerIleArgLysAspProphePheArgAsnLeuSerThrLysSerLysAsnArgLy	1254	QY	1594	aIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLy	1614
Db	3803	CAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACCTTTTCAAGGAAGTCTAAAAATAGAA	3862	Db	4883	CATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAA	4942
QY	1254	sLeuProGluProProAspAsnGluAspGluAspValLysAlaGluArgLeuLy	1274	QY	1614	sGluGlnGluGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluAr	1634
Db	3863	GCTTCCAGAACCCAGACACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAA	3922	Db	4943	AGAACAAGAGGAGGAAGATAATAGTTGTGGAACCTTTTAAACAGCACACCTTTGGTGGGAACG	5002
QY	1274	sValLysGluLeuMetGlyCysGlnCysGluGluLysProSerIleMetValSerAs	1294	QY	1634	gThrGlnGluAspArgValPhe 1642	
Db	3923	GGTCAAAGAGCTGATGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGTTGTCAGCAA	3982	Db	5003	AACACAAGAGATAGATAGTATT 5027	
QY	1294	nLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysLysVa	1314				
Db	3983	TTTGCAATAAGAAATATGATGACAAGAAAGATTTTCTTCTTCAAGAAAAAGTAAAGAAAGT	4042				
QY	1314	lAlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyPr	1334				
Db	4043	GGCAACTAAATACATCTCTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCC	4102				
QY	1334	oAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSe	1354				
Db	4103	AAATGGTGTGCAAAAGCACAATTTATTAATATCTGTTGTTGGTGATATTGAACCACTTC	4162				
QY	1354	rGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLy	1374				
Db	4163	AGGCCAGGTATTTTAGGAGATTATTTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAA	4222				
QY	1374	sCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHi	1394				
Db	4223	GTGTATGGGTTACTGCTCAGATAAACCCCTTTGTGGCCAGATACATTCAGGGAACA	4282				

RESULT 9

PCT-US03-33087-82
; Sequence 82, Application PC/TUS0333087
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; Hafalia, April J.A.;
; APPLICANT: KHARE, Reena; LAL, Preeti G.;
; APPLICANT: YUE, Henry; BAUGHN, Mariah R.;
; APPLICANT: THORNTON, Michael B.; LU, Dyung Aina M.;
; APPLICANT: ISON, Craig H.; BECHA, Shanya D.;
; APPLICANT: DING, Li; WARREN, Bridget A.;
; APPLICANT: LEE, Soo Yeun; SWARNAKAR, Anita;
; APPLICANT: ELLIOTT, Vicki S.; RICHARDSON, Thomas W.;
; APPLICANT: MARQUIS, Joseph P.; RAMKUMAR, Jayalaxmi;
; APPLICANT: MURAGE, Jaji; RAUMANN, Brigitte E.;
; APPLICANT: YAO, Monique G.; LU, Yan;
; APPLICANT: GIETZEN, Kimberly J.; YANG, Yonghong G.;
; APPLICANT: CHANG, Hsin-Ru; CHAWLA, Narinder K.;
; APPLICANT: TRAN, Uyen K.; LEE, Sally;
; APPLICANT: YANG, Junming; GANDHI, Ameena R.;
; APPLICANT: TRIBOULEY, Catherine M.; POLICKY, Jennifer L.;
; APPLICANT: RING, Huijun Z.; LEE, Ernestine A.

Db 1014 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTGTCTTAATGCTGACACCTCTT 1073
Qy 321 PheLysLysSerLysHisValGlyIleValGluPheValThrValAlaPheGlyPhe 340
Db 1074 TTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTT 1133
Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 1134 ATTGGCCTTATGATAATCTCATAGAAAAGTTTTCCAAAATCGTTAGTGGCTTTTCAGT 1193
Qy 361 PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 1194 CCTTCTGTCACTGTACTTTTGTGATTGGTATTGCACAGGTCATGCATTAGAAAGATTTT 1253
Qy 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 1254 AATGAAGGTGCTTCATTTCAAAATTTGACTGCAGGCCCATATCCTCTAAATTATACAATT 1313
Qy 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 1314 ATCATGCTCACACTTAATAGTATATCTATGTCTCTGTGGTGTCTATCTGTATCAAGTC 1373
Qy 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 1374 ATTCCAGGGGAATTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1433
Qy 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db 1434 TCAAAAGAGCAAAAGAAATATGAGGAGTTATCAGAGGCAATGTTAATGGAAATATTAGT 1493
Qy 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db 1494 TTTAGTGAAATATTGAGCCAGTTTCTTCAGAAATTTGTAGAAAGAACCCATAAGAATT 1553
Qy 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 1554 AGTGGTATTCAGAGACATACAGAAAGAGGGTGAATGTGGAGGCTTTGAGAAATTTG 1613
Qy 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
Db 1614 TCATTTGACATATATGAGGGTCAGATTACTGCCCTTACTTGGCCACAGTGGAAAG 1673
Qy 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProSerAspGlyPheAlaSerIle 540
Db 1674 AGTACATTGATGAATATTCCTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATA 1733
Qy 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 1734 TATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAATGATGGCATT 1793
Qy 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
Db 1794 TGTCACAGTTAGATATACACTTTGTGATGTTTGGACAGTAGAAGAAATTTATCAATTTG 1853
Qy 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 1854 GCTTCAATCAAAAGGGATACCAGCCAAACAATATAATAACAAGAGTGCAGAAAGTTTACTA 1913
Qy 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
Db 1914 GATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAA 1973
Qy 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
Db 1974 AGAAAGCTGTCAATTAGGAATTTGTGTTCTTGGGAACCCAAAGATACTGTCTAGATGAA 2033
Qy 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660
Db 2034 CCAACAGCTGGAATGGACCCCTGTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA 2093
Qy 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680

Db 2094 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGCATTTCTTGCA 2153
Qy 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 2154 GATAGGAAAGCTGTGATATCAAGGAATGCTGAAATGTGTGGTTCTTCAATGTTCTCTC 2213
Qy 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 2214 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 2273
Qy 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsn 740
Db 2274 GAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTACACAGAA 2333
Qy 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
Db 2334 GACCAACAACCTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCAGGTTTGT 2393
Qy 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 2394 TCTGCCCTAGACAGTCAATCAAAATTTGGGTGTCAATTTCTTATGGTGTTCCTCATGAC 2453
Qy 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 2454 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATGACCAAGCAGATTATAGT 2513
Qy 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 2514 GTATTTACTCAGCAGCCACTGAGGAAGAAATGGATTCAAAATCTTTTGTATGAAATG 2573
Qy 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 2574 CAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTGCTGTAGTGAGCACCATGAGCCT 2633
Qy 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPheThrLeuLysArgGluSerLys 860
Db 2634 AAACAACAGATGTATACATAGCAAAAGTTTCATTTCTTACCTTGAAACGTGAAAGTAA 2693
Qy 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 2694 TCAGTGAGATCAGTGTGTCTGCTTTTAAATTTTTTTTTCACAGTTTCAGATTTTAT 2753
Qy 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
Db 2754 TTGGTTCACTCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCACAGACT 2813
Qy 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
Db 2814 TTTCTAAAAACCTGGAGACAAACCAATATAACAAACAAAGTCTGCTTCTTCAAAATCT 2873
Qy 921 Ala-----AspSerAspIleSerAspLeuIleSerPhePheThrSer 934
Db 2874 GCTGGTGAGAGTGTNNGTGAAGACTCAGATATCAGTGATCTTTATTAGCTTTTTCACA 2933
Qy 935 GlnAsnIleMetValThrMetIleAsnAspSerAspTyrValSerValAlaProHisSer 954
Db 2934 CAGAACATAATGGTGACGATGATTAATGACAGTGACTATGTATCCGTGGCTCCCCATAG 2993
Qy 955 AlaAlaLeuAsnValMetHisSerGluLysAspTyrValPheAlaValPheAsnSer 974
Db 2994 GCGGCTTTAAATGTGATGCAATTCAGAAAAAGGACTATGTTTTCAGCTGTTTTCACAG 3053
Qy 975 ThrMetValTyrSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHis 994
Db 3054 ACTATGGTTTATTTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCAT 3113
Qy 995 LeuAsnValThrGluThrIleGlnIleTrpSerThrProPhePheGlnGluIleThrAsp 1014
Db 3114 TTAAATGTGACTGAAACCATCCAGATCTGGAGTAGCCCATCTTTTCAAGAAATTAAGT 3173
Qy 1015 IleValPheLysIleGluLeuTyrPheGlnAlaAlaLeuLeuGly-IleIleValThrAl 1034
Db 3174 ATAGTTTTTAAAAATTGAGCTGTATTTTCAAGCAGCTTTTGTGTGGAAATCATTTGAACTGC 3233

QY 1394 spheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSe 1414
Db 4170 TTTTGAATTTATGGAGCTGTCAAAGGAATGAGTGCAGTGCATGAAAGAGTCATAAG 4229
QY 1414 rArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPr 1434
Db 4230 TCGAATAACACATGCACCTTGATTTAAAGAAACATCTTCAGAGACTGTAAAGAAACTACC 4289
QY 1434 oAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleTh 1454
Db 4290 TGCAGGAATCAAAACGAAAGTTGTGTTTGTCTTAAGTAATGCTAGGGAATCCTCAGATTAC 4349
QY 1454 rLeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAl 1474
Db 4350 TTTTGCTAGATGAACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGC 4409
QY 1474 aIleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGl 1494
Db 4410 AATTTCGAACCTGCAATTTAAACACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATGGA 4469
QY 1494 uGluAlaGluAlaValCysAspArgValAlaAlaIleMetValSerGlyGlnLeuArgCysIl 1514
Db 4470 GGAGGCAGAGGCTGTCTGTGATCGAGTAGCTATCATGGTGTCTGGCGAGTTAAGATGTAT 4529
QY 1514 eGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLe 1534
Db 4530 CGGAACAGTCAACATCTAAAGAGTAAATTTGGAAAGGCCTCTTTTGGAAATTAAT 4589
QY 1534 uLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePh 1554
Db 4590 GAAGGACTGGATAGAAACCTAGAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTT 4649
QY 1554 eProAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGl 1574
Db 4650 CCCAAATGCAAGCGCTCAGGAAAGTTTCTCTATTGCTTATATAAATTCCTAAGGA 4709
QY 1574 uAspValGlnSerLeuSerGlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAl 1594
Db 4710 AGATGTTTCAGTCCCTTTTCACAACTCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTC 4769
QY 1594 aIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLy 1614
Db 4770 CATTGAAGAAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTGTAGAACTCACTAA 4829
QY 1614 sGluGlnGluGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluAr 1634
Db 4830 AGAACAGAGGAGGAGGAAGATAATAGTTGTGGAACTTTAAACAGCACACTTTTGGTGGGAACG 4889
QY 1634 gThrGlnGluAspArgValValPhe 1642
Db 4890 AACACAAGAAAGATAGTAGTATTT 4914

RESULT 8
US-10-090-458-1
; Sequence 1, Application US/10090458
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090,458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 25,2888,2889
; OTHER INFORMATION: n = A,T,C or G

US-10-090-458-1
Alignment Scores:
Pred. No.: 0 Length: 5463
Score: 8309.00 Matches: 1629
Percent Similarity: 98.85% Conservative: 1
Best Local Similarity: 98.79% Mismatches: 2
Query Match: 98.61% Indels: 18
DB: 44 Gaps: 2
US-10-090-458-5 (1-1642) x US-10-090-458-1 (1-5463)
QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys 20
Db 114 ATGTCCACTGCAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTTACTGAAG 173
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 174 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA 233
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 234 TTTTCTTATTTTGGTTAATATTATATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 293
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 294 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTTCTTAATCTAATCTTGTGA 353
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 354 TATACTCCAGTGACTAATATTACAAGCAGCATCATGTCAGAAAGTGTCTACTGATCATCTA 413
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 414 CCTGATGTCAATAATTACTGAAGAATATACAAATGAAAAGAAATGTTAACAATCCAGTCTC 473
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 474 TCTAAGCCGAGCAACTTTGTAGTGTGGTTTTCAAAAGACTCCATGTCTATGAACCTTCGT 533
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 534 TTTTCTTCTGATATGATTCAGTATCTTCTATTATATGATGATCAAGAGCTGGCTGTTC 593
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 594 AAATCATGTGAGGCTGCTCAGTACTGTCTCAGGTTTTCACAGTTTTCACAGCATCCATA 653
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
Db 654 GATGCTGCCATATATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCACT 713
QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 714 AAAGCTGTTATTATGGGAGAAACTGCTGTGTGTAGAAATAGATACCTTTCCCGAGGAGTA 773
QY 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240
Db 774 ATTTTAATATACCTAGTTATAGCATTTTCACCTTTTGGATACTTTTGGCAATTCATATC 833
QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 834 GTAGCAGAAAAGAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT 893
QY 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 894 GCCTTTTGGCTTTCCTGGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCT 953
QY 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
Db 954 ATGGCAGTCATTCGACAGCTTCTTTGTTATTTCTCTCAAAAGTAGCAGCATTTGTGATATT 1013
QY 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320

Db 1981 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCA 2040
 QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
 Db 2041 GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAATGTGTGGTTCTTCAATGTTCCTC 2100
 QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
 Db 2101 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 2160
 QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
 Db 2161 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAT 2220
 QY 741 AspGlnGlnLeuValTyrSerLeuPropheLysAspMetAspLysPheSerGlyLeuPhe 760
 Db 2221 GACCAACAACCTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCAGGTTTGT 2280
 QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
 Db 2281 TCTGCCCTTAGACAGTCAITCAAAATTTGGGTGTCAATTTCTTATGGTGTTCATGACGACT 2340
 QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
 Db 2341 TTGGAAGACGTAATTTTAAAGCTAGAAGTTGAAGCAGAAATTGACCAAGCAGATTATAGT 2400
 QY 801 ValPheThrGlnGlnProLeuGluGluGluMetAspSerLysSerPheAspGluMetGlu 820
 Db 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAATGGAA 2460
 QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
 Db 2461 CAGAGCTTACTTATTTCTTCTGAAACCAAGGCTGCTCTAGTGAGCACCATGAGCCTTTGG 2520
 QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860
 Db 2521 AAACAACAGATGTATACAAATAGCAAAAGTTTCATTTCTTTTACCTTGAACCTGAAAGTAAA 2580
 QY 861 SerValArgSerValLeuLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
 Db 2581 TCAGTGAGATCAGTGTTGCTTCTGCTTTTAAATTTTTTTCACAGTTTCAGATTTTATGTTT 2640
 QY 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
 Db 2641 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCCAGACTTATAT 2700
 QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
 Db 2701 TTTCTAAACCTGGAGACAAACCCACATAAATACAAACAAAGTCTGCTTCTTCAAAATTTCT 2760
 QY 921 Ala-----AspSerAspIleSerAspLeuIleSerPhePheThrSer 934
 Db 2761 GCTGGTGAGAGTGTNNGTGAAGACTCAGATATCAGTGATCTTTATTAGCTTTTTCACAAAGC 2820
 QY 935 GlnAsnIleMetValThrMetIleAsnAspSerAspTyrValSerValAlaProHisSer 954
 Db 2821 CAGAACATAATGGTGACCATGATTAAATGACAGTGAATATGATATCCCGTGGCTCCCCATAGT 2880
 QY 955 AlaAlaLeuAsnValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSer 974
 Db 2881 GCGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGT 2940
 QY 975 ThrMetValTyrSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHis 994
 Db 2941 ACTATGGTTTATTTCTTACCTATATTAGTGAATATCATTTAGTAACCTACTATCTTTATCAT 3000
 QY 995 LeuAsnValThrGluThrIleGlnIleTrpSerThrProphePheGlnGluIleThrAsp 1014
 Db 3001 TTAAATGTGACTGAAACCATCCAGATCTGGAGTACCCCATTTCTTTCAAGAAATTTACTGAT 3060
 QY 1015 IleValPheLysIleGluLeuTyrPheGlnAlaAlaLeuLeuGly-IleIleValThrAl 1034
 Db 3061 ATAGTTTTTAAATTTGAGCTGTATTTTTCACACAGCTTTTGTCTTGGAAATCATTTGTAACTGC 3120

QY 1034 aMetProProTyrPheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGl 1054
 Db 3121 AATGCCACCCTACTCTGCCATGGAAAATGCAGAGAAATCATAA----- 3162
 QY 1054 nLeuLysLeuSerGlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIl 1074
 Db 3163 -----GGTCTTTTGGCCATCTGCATATTGGATTGGACAAGCTGTTGTGATAT 3209
 QY 1074 eProLeuPhePheIleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGl 1094
 Db 3210 CCCCTTATTTTATCATCTTATTTTGTATGTCTAGGAAGCTTATTGGCATTTTCATTATGG 3269
 QY 1094 yLeuTyrPheTyrThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValPr 1114
 Db 3270 ATTATATTTTATACTGTAAGATTCTTGTCTGTGGTTTTTTTGCCTTATTGGTTATGTTCC 3329
 QY 1114 oSerValIleLeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLy 1134
 Db 3330 ATCAGTTATTTCTGTTCACTTATATTGCTTCTTTTCACTTTTAAAGAAAATTTTAAATACCAA 3389
 QY 1134 sGluPheTrpSerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIl 1154
 Db 3390 AGAATTTTGGTCATTTTATCTATTTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAAT 3449
 QY 1154 eThrPhePheMetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIl 1174
 Db 3450 AACTTCTTTATGGGATACACAATTTGCAACTATTCTTCAATATGCCTTTTGTATCATCAT 3509
 QY 1174 eProIleTyrProLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnVa 1194
 Db 3510 TCCAATCTATCCACTTCTAGGTTGCCTGATTTCTTTTCAATAAGATTTCTTGAAGAATGT 3569
 QY 1194 lArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerPr 1214
 Db 3570 ACGAAAAAATGTGGACACCTATAATCCATGGGATAGGCTTTTCAGTAGCTGTATATCGCC 3629
 QY 1214 oTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGl 1234
 Db 3630 TTACCTGCAGTGTGTACTGTGGATTTCCTCTTACAATACTATGAGAAAAAATATGGAGG 3689
 QY 1234 yArgSerIleArgLysAspProphePheArgAsnLeuSerThrLysSerLysAsnArgLy 1254
 Db 3690 CAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACCTTTCAACGAAGTCTAAAAATAGGAA 3749
 QY 1254 sLeuProGluProProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLy 1274
 Db 3750 GCTTCCAGAACCCACAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAA 3809
 QY 1274 sValLysGluLeuMetGlyCysGlnCysCysGlnGluLysProSerIleMetValSerAs 1294
 Db 3810 GGTCAAAGAGCTGATGGGTTGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAA 3869
 QY 1294 nLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysLysVa 1314
 Db 3870 TTTGCATAAAGAAATATGATGACAAAGAAAGATTTTCTTCTTCAAGAAAAGTAAAGAAAGT 3929
 QY 1314 lAlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyPr 1334
 Db 3930 GGCAACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAGAGATCTTAGGACTATTGGGTCC 3989
 QY 1334 oAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSe 1354
 Db 3990 AAATGGTGTGGCAAAAGCACAATTTATTAATATCTGGTTGGTTGATATTGAACCAACTTC 4049
 QY 1354 rGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLy 1374
 Db 4050 AGGCCAGGTATTTTTAGGAGATTTATTTTCAAGACAAGTGAAGATGATGATGATCACTGAA 4109
 QY 1374 sCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHi 1394
 Db 4110 GTGTATGGGTTACTGTCTCTCAGATAAACCCCTTGTGGCCAGATACATACATTGCAGGAACA 4169

US-10-090-458-3

Alignment Scores:

Pred. No.: 0 Length: 4917
Score: 8309.00 Matches: 1629
Percent Similarity: 98.85% Conservative: 1
Best Local Similarity: 98.79% Mismatches: 2
Query Match: 98.61% Indels: 18
DB: 44 Gaps: 2

US-10-090-458-5 (1-1642) x US-10-090-458-3 (1-4917)

QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys 20
Db 1 ATGTCCACTGCAATTAGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG 60
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnIleLeuPheProLeu 40
Db 61 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGAAATTTCTTTTCCACTA 120
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 121 TTTTITTTTATTTGGTTAATATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 180
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 181 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTGG 240
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 241 TATACTCCAGTGACTAATATTACAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 300
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 301 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAGAAATGTTAAACATCCAGTCTC 360
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 361 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTCAAAGACTCCATGCTCTATGAACCTCGT 420
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 421 TTTTITTTCTGATATGATTCAGATATCTCTATTATATGGAATCAAGAGCTGGCTGTCA 480
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 481 AAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTTCAGATTTTACAGCATCCATA 540
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
Db 541 GATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTGGAAGGAGCTGGAGTCAACT 600
QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 601 AAAGCTGTTATTATGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 660
QY 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240
Db 661 ATTTTAAATATACCTAGTTATAGCATTTTCACCTTTTGGATACTTTTGGCAATTCATATC 720
QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 721 GTAGCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAATGGACTTTCATGATACT 780
QY 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 781 GCCTTTTGGCTTTCTCTGGGTTCTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTT 840
QY 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
Db 841 ATGGCAGTCATTGGCAGACGCTTCTTTGTTATTTCCTCAAGTAGCAGCATTTGTGATATT 900
QY 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320

Db 901 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTCCTTTAATGCTGACACCTCTT 960
QY 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 961 TTTTAAAAAATCAAAACATGTGGATAGTTGAATTTTGTACTGTGGCTTTTGGATT 1020
QY 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 1021 ATTTGGCTTTATGATAATCCTCATAGAAAGTTTCCCAATCGTAGTGTGGCTTTTCAGT 1080
QY 361 PropheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 1081 CCTTTCTGCTACTGTACTTTTGTGATTGGTATTGCACAGGTCATGCAATTAGAAATTT 1140
QY 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 1141 AATGAAGGTGCTTCATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAATT 1200
QY 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 1201 ATCATGCTCACACTTAATAGTATATTCTATGTCTCTTGGCTGTCTATCTTGATCAAGTC 1260
QY 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 1261 ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1320
QY 441 SerLysSerLysArgAsnTyrGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db 1321 TCAAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT 1380
QY 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db 1381 TTTAGTGAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGAAAGAAAGCCATAGAAAT 1440
QY 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 1441 AGTGGTATTCAGAAAGACATACAGAAAGAGGGTGAATTTGAGAGGCTTTGAGAAATTTG 1500
QY 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
Db 1501 TCATTTGACATATATGAGGGTTCAGATTACTGCTTCTTACCTCCACAGTGGAACAGGAAAG 1560
QY 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 1561 AGTACATTGATGAATATTCTTTGTGACTCTGCCACCTCTCTGATGGGTTTGCATCTATA 1620
QY 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 1621 TATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAAATGATTGGCAAT 1680
QY 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
Db 1681 TGTCCACAGTTAGATATACACTTTGATGTTTGTGACAGTAGAAGAAAAATTTATCAATTTTG 1740
QY 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 1741 GCTTCAATCAAAAGGGATACCAGCCCAACAATATAATACAAAGAGTGCAGAAAGTTTACTA 1800
QY 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlnLys 620
Db 1801 GATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAATAAAGTGGTGGTCAAAAA 1860
QY 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
Db 1861 AGAAAGCTGTCATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACCTGCTGCTAGATGAA 1920
QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660
Db 1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA 1980
QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680

QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
Db ATGGAATGACAGAAATCATAGATCAAGCTTAYACTCAACTTAACTTTCAGGCTT 3434
QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValAlaSpilleProLeuPhePheIle 1080
Db TTGCCATCTGCATATTGGATTGGACAAGCTGTGTGTGATATCCCTTATTTTATCAT 3494
QY 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
Db CTTATTTTGATGCTAGGAAGCTTATTGGCAATTCATTATGGATTATATTTTATACTGA 3554
QY 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
Db AAGTTCCITGCTGTGGTTTTTTGGCTTATGGTTATGTTCCATCAGTTATTCTGTTCAC 3614
QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
Db TATATTGCTTCTTCACCTTTAAGAAAAATTTTAAATACCAAGAAATTTTGGTCATTATC 3674
QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
Db TATCTGTGCAGCGTTGGCTTGTATGCAATCACTGAATAAACTTTCTTTATGGGATAC 3734
QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleProIleTyrProLeuLeu 1180
Db ACAATTGCAACTATTCTTCATTATGCCTTTTGTATCATCAATCCAACTATCCACTCTA 3794
QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
Db GGTTGCCTGATTTCTTTCATAAAGATTTCTTGAAGAAATGACGAAAAAATGTGGACACC 3854
QY 1201 TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220
Db TATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCTTACCTGCAGTGTACTG 3914
QY 1221 TrpIlePheLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp 1240
Db TGGATTTCTCTTACAATACTATGAGAAAAAATATGGAGCAGATCAATAAGAAAAGAT 3974
QY 1241 ProPheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
Db CCTTTTTCAGAAACCTTTCAACGAAGCTTAAAAATAGGAAGCTTCCAGAACCCAGAC 4034
QY 1261 AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280
Db AATGAGGATGAAGATGAAGATGCAAGCTGAAAGCTTAAAGGTCAAAGAGCTGATGGT 4094
QY 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
Db TGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGATATGAT 4154
QY 1301 AspLysLysAspPheLeuSerArgLysValLysLysValAlaThrLysTyrIleSer 1320
Db GACAAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 4214
QY 1321 PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340
Db TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGC 4274
QY 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360
Db ACAATTATTAATATTCTGTGTGGTGATATTGAACCAACTTCAGGCCAGGATTTTTAGGA 4334
QY 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380
Db GATTATTCTTCAGAGACAAGTGAAGATGATGATTCATCTGAAAGTGTATGGGTACTGTCCT 4394
QY 1381 GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400
Db CAGATAAACCCCTTTGTGGCCAGATACATACTATGCAGGAACATTTTGAATTTATGGAGCT 4454

QY 1401 ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
Db GTCAAAGGAATGAGTCAAGTGACATGAAAGAAGTCAAGTCGAATAACACATGCACCT 4514
QY 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
Db GATTTAAAGAACATCTTTCAGAAAGACTGTAAAGAACTACCTGCAGGAATCAAACGAAAG 4574
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db TTGTGTTTTTGTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4634
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
Db ACAGGTATGGATCCCAAGCCAAACACACACATGTGGCGAGCAATTCGAACCTGCAATTA 4694
QY 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
Db AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGGAGAGGCAGAGGCTGTCTGT 4754
QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
Db GATCGAGTAGCTATCATGGTGTCTGGCAGTTAAGATGTATCGAAACAGTACAACATCTA 4814
QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540
Db AAGAGTAAATTTGGAAGAGGCTACTTTTGGAAATTTAAATGAAGGACTGGATAGAAAC 4874
QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
Db CTAGAAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAG 4934
QY 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
Db GAAAGTTTTTCTTCTATTGCTTATATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA 4994
QY 1581 GlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600
Db CAATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTT 5054
QY 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620
Db TCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAAGAAACAAGAGGAGGAAGAT 5114
QY 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
Db AATAGTTGTGGAACCTTTAAACAGCACACTTTTGGTGGGAACGAACACAAGAGATAGAGTA 5174
QY 1641 ValPhe 1642
Db 5175 GTATTT 5180

RESULT 7
US-10-090-458-3
; Sequence 3, Application US/10090458
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090,458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4917
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2775, 2776
; OTHER INFORMATION: n = A,T,C or G

Db 1155 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTGTCTTAAATGCTGACACCTCTT 1214
Qy 321 PheLysLysSerLysHisValGlyIleValGluPheValThrValAlaPheGlyPhe 340
Db 1215 TTTAAAAAATCAAAACATGTGGGAATAGTTGAAATTTTGTACTGTGGCTTTTGGATTT 1274
Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 1275 ATTGGCCTTATGATAATCCTCATAGAAAGTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 1334
Qy 361 ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 1335 CCTTCTGTCACTGTACTTTTGTGATTGGTATTGACAGGTCATGCAATTTAGAAATTTT 1394
Qy 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 1395 AATGAAGGTGCTTTCATTTTCAAATTTTGACTGCAGGCCCATATCCTCTAAATTATTACAAT 1454
Qy 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 1455 ATCATGCTCACACTTAATAGTATATTTCTATGTCCCTTGGCTGTCTATCTTGATCAAGTC 1514
Qy 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 1515 ATTCAGGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG 1574
Qy 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db 1575 TCAAGAGCAAAAGAAATTTAGGAGATTATGAGGAGTTATCAGAGGCCAATGTTAATGGAAATATTAGT 1634
Qy 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgile 480
Db 1635 TTTAGTGAAATATTAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAAAGCCATAAGAAATT 1694
Qy 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 1695 AGTGGTATTCAGAAACATACAGAAAGAAAGGGTGAAATGTGGAGGCTTTGAGAAATTTG 1754
Qy 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
Db 1755 TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAAACAGGAAAG 1814
Qy 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 1815 AGTACATTGATGAATATTCTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATA 1874
Qy 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 1875 TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAATAATGATTGGCATT 1934
Qy 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
Db 1935 TGTCCACAGTTAGATATACACTTTGATGTTTTCACAGTAGAAGAAATTTATCAATTTTG 1994
Qy 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 1995 GCTTCAATCAAAGGGATACCAGCCCAATATAATAACAAGAGTGCAGAAGTTTTACTA 2054
Qy 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlnLys 620
Db 2055 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTTAAAAAATTAAGTGGTGGTCAAAA 2114
Qy 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
Db 2115 AGAAGCTGTCTATTAGGAATTGCTGTTCTTGGGAACCAAGATACTGCTGCTAGATGAA 2174
Qy 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660
Db 2175 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA 2234
Qy 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680

Db 2235 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTCTTTGCA 2294
Qy 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 2295 GATAGGAAAAGCTGTGATATCACAAAGGAATGCIGAAATGTGTGTTGTTCTTCAATGTTCCCTC 2354
Qy 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 2355 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 2414
Qy 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsn 740
Db 2415 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATTACAACAGAAT 2474
Qy 741 AspGlnGlnLeuValTyrSerLeuPropheLysAspMetAspLysPheSerGlyLeuPhe 760
Db 2475 GACCAACAACCTTGTGTATAGCTTGCCCTTCAAGGACATGGACAAATTTTTCAGSTTTGTTT 2534
Qy 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 2535 TCTGCCCTAGACAGTCAATCAAATTTGGGTGGCAATTTCTTATGGGTTTCCATGACGACT 2594
Qy 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 2595 TTGGAAGACGATATTTTAAAGCTAGAAGTTGAAGCAGAAATTTGACCAAGCAGATATAGT 2654
Qy 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 2655 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAATCTTTTGTGATAAATGGAA 2714
Qy 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 2715 CAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTGG 2774
Qy 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860
Db 2775 AAACAACAGATGTATACAAATAGCAAAGTTTTCATTTCTTTTACCTTGAAACGTGAAAGTAAA 2834
Qy 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 2835 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2894
Qy 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
Db 2895 TTGTTTCATCACTCTCTTTTAAAAATGCTGTGGTTCCCATCAAACCTTGTTCACAGCTTATAT 2954
Qy 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
Db 2955 TTTTCTAAAAACCTGGAGACAAACCAACATATAAATACAAAAACAAGTCTGCTTCTTCAAAATTCT 3014
Qy 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
Db 3015 GCTGACTCAGATATCAGTGAATCTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGACG 3074
Qy 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960
Db 3075 ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGGGCTTTTAAATGTGRTG 3134
Qy 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
Db 3135 CATTCAAAAAAGGACTATGTTTTCAGCTGTTTTCACAGTACTATGGTATTATCTTTTA 3194
Qy 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
Db 3195 CCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCATTTAAATGTGACTGAAACC 3254
Qy 1001 IleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGlu 1020
Db 3255 ATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTACTGATATAGTTTTTAAAAATTGAG 3314
Qy 1021 LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040
Db 3315 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTACTGTCAATGCCACCTTACTTTGCC 3374

Db 4141 CAGATAAACCCCTTTGTGCCAGATACATTCATTCGAGAACATTTTGAATTTATGGAGCT 4200

QY 1401 VallysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420

Db 4201 GTCAAAGGAATGAGTGAAGTACATGAAAGAACTCATAGTCGAATAACACATGCACCT 4260

QY 1421 AspLeuLysGluHisLeuGlnLysThrVallysLysLeuProAlaGlyIleLysArgLys 1440

Db 4261 GATTTAAAGAACATCTTCAGAAGACTGTAAAGAACTACCTGCAGGAATCAACGAAAG 4320

QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460

Db 4321 TTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4380

QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480

Db 4381 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACTGCATTTAAA 4440

QY 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500

Db 4441 AACAGAAAGCGGCTGCTATCTGACCACTCAGTATATGGAGGAGGCGAGGCTGTCTGT 4500

QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520

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QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540

Db 4561 AAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAAATTTGAAGGACTGGATAGAAAAC 4620

QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560

Db 4621 CTAGAAGTAGACCGCCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAG 4680

QY 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580

Db 4681 GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTCCAGTCCCTTTCA 4740

QY 1581 GlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600

Db 4741 CAATCTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAAATATAGCTTT 4800

QY 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620

Db 4801 TCTCAAGCAACATTTGGAACAGTTTTTGTAGAACTCACTAAAGAACAAAGAGGGAAGAT 4860

QY 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640

Db 4861 AATAGTGTGGAACTTTAAACACACACACTTTTGGTGGGAACGAACACAAAGAGATAGAGTA 4920

QY 1641 ValPhe 1642

Db 4921 GTATTT 4926

RESULT 6

US-09-971-121-5

; Sequence 5, Application US/09971121

; GENERAL INFORMATION:

; APPLICANT: Hu, Yi

; APPLICANT: Nepomnichy, Boris

; TITLE OF INVENTION: Novel Human Transporter Proteins and Polynucleotides Encoding the

; TITLE OF INVENTION: Same

; FILE REFERENCE: LEX-0250-USA

; CURRENT APPLICATION NUMBER: US/09/971,121

; CURRENT FILING DATE: 2001-10-04

; PRIOR APPLICATION NUMBER: US 60/239,629

; PRIOR FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 5262

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-971-121-5

Alignment Scores:

Pred. No.: 0

Score: 8395.00

Percent Similarity: 99.70%

Best Local Similarity: 99.70%

Query Match: 99.63%

DB: 41

Length: 5262

Matches: 1637

Conservative: 0

Mismatches: 5

Indels: 0

Gaps: 0

US-10-090-458-5 (1-1642) x US-09-971-121-5 (1-5262)

QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLys 20

Db 255 ATGTCACCTGCAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 314

QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40

Db 315 AATTACTTAATTAAATGCAAAACCAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA 374

QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60

Db 375 TTTTTTTTATTTTGGTTAATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 434

QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80

Db 435 GTGCTAATATAGAACTCAATCCTATGGACAAGTTACTCTTTCTAATCTAATTTCTTGA 494

QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100

Db 495 TATACTCCAGTGACTAATATTACAAGCAGCATCATGAGAAAGTGTCTACTGATCATCTA 554

QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120

Db 555 CCTGATGTCATAATTACTGAGAATATACAAATGAAAAAGAAATGTTAACATCCAGTCTC 614

QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140

Db 615 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTTCAAAGACTCCATGTCTATGAACCTCGT 674

QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160

Db 675 TTTTTTCTGATATGATTCCAGTATCTTCTATTATATATGATTCAAGAGCTGGCTGTTC 734

QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180

Db 735 AAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTCACAGTTTTACAAGCATCCATA 794

QY 181 AspAlaAlaIleIleGlnLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200

Db 795 GATGCTGCCATTATACAGTTGAAGACCAATGTTCTCTTTTGGAAAGAGCTGGAGTCAACT 854

QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220

Db 855 AAAGCTGTATTATGGGAGAAACTGCTGTGTAGAAATAGATACCTTTTCCCGAGGAGTA 914

QY 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240

Db 915 ATTTTAATATACCTAGTTATAGCATTTTCCACCTTTTGGATACCTTTTGGCAATTCATATC 974

QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260

Db 975 GTAGCAGAAAAAGAAAAATAAAAGAAATTTTAAAGATAAATGGGACTTTCATGATACT 1034

QY 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280

Db 1035 GCCTTTTGGCTTTCTCTGGGTTCTCTATAWACAAGTTTAAATTTTCTTATGTCCCTTCT 1094

QY 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300

Db 1095 ATGGCAGTCATTCGACAGCTTTCTTTGTTATTTCTTCAAGTAGCAGCATTTGTGATATT 1154

QY 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320

QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Dbb 1981 AAAGCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTGCA 2040
QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Dbb 2041 GATAGAAAGCTGTGATATCACAGGAATGCTGAAATGTGTGGTCTTCAATGTCTC 2100
QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Dbb 2101 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGCGCAC 2160
QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsn 740
Dbb 2161 GAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACACAGAAT 2220
QY 741 AspGlnGlnLeuValTyrSerLeuPropheLysAspMetAspLysPheSerGlyLeuPhe 760
Dbb 2221 GACCAACAACTTGTGTATAGCTTGCCTTTCAAGGACATGGACAAATTTTCAGGTTGTT 2280
QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Dbb 2281 TCTGCCCTAGACAGTCAATTCAAATTTGGGTGGCATTTCTATGGGTTTCCATGACGACT 2340
QY 781 LeuGluaspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Dbb 2341 TTGGAAGACGTATTTTAAAGCTAGAAGTTGAAGCAGAAATGACCAAGCAGATTATAGT 2400
QY 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Dbb 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAATGAA 2460
QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Dbb 2461 CAGAGCTTACTTATCTTTCTGAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTGG 2520
QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys 860
Dbb 2521 AAACAACAGATGTATACATAGCAAGTTTCAATTTCTTTTACCTTGAAACGTTGAAGTAA 2580
QY 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Dbb 2581 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTT 2640
QY 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
Dbb 2641 TTGGTTTCACTACTCTTTTAAATATGCTGTGGTTCCCATCAAACTTGTTCACAGACITATAT 2700
QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
Dbb 2701 TTTCTAAACCTGGAGACAAACCATAAATACAAACAAGTCTGCTTCTTCAAAATCTT 2760
QY 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
Dbb 2761 GCTGACTCAGATATCAGTGATCTTTATTAGCTTTTTCACAAAGCCAGAACATATGTTGACG 2820
QY 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960
Dbb 2821 ATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGGGCTTTTAAATGTTGTG 2880
QY 961 HisSerGluLysAspTyrValPheAlaValPheAsnSerThrMetValTyrSerLeu 980
Dbb 2881 CATTTCAGAAAGGACTATGTTTTTGCAGCTGTTTTTCAACAGTACTATGTTTATTTCTTTA 2940
QY 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
Dbb 2941 CCTATATTAGTGAATATCATTAGTAACCTACTATCTTTATCATTTAAATGTGACTGAAAC 3000
QY 1001 IleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGlu 1020
Dbb 3001 ATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAAGTATAGTTTAAATTTGAG 3060
QY 1021 LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040

Dbb 3061 CTGTATTTTCAAGCAGCTTTGCTTGAATCATTTGTTACTGCAATGCCACCTTACTTTGCC 3120
QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
Dbb 3121 ATGGAATAATGCAGAGAAATCAATAAGATCAAAAGCTTAYACTCAACTTAAACTTTCAGGTCTT 3180
QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValAlaAspIleProLeuPhePheIleIle 1080
Dbb 3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTT 3240
QY 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
Dbb 3241 CTTATTTTGTATGCTAGGAAGCTTATTGGCATTTTCATTTATGGATTATATTTTATACGTGA 3300
QY 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
Dbb 3301 AAGTTCCTTGTCTGGTGTGTTTTCCTTATTGGTTATGTTCATCAGTTATTTCTGTTCAC 3360
QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
Dbb 3361 TATATTGCTTCTTTTCCCTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC 3420
QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
Dbb 3421 TATTTCTGTGGCAGCGTTGGCTTGTATTGCAATCATCTTCAATCATCTATCCACTCTA 3480
QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
Dbb 3481 ACAATTGCAACTATTTCTTCAATATGCTTTTGTATCATCATCTCAATCTATCCACTCTA 3540
QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
Dbb 3541 GGTTGCCCTGATTTCTTTTCATAAAGATTTCTTGAAGAAATGTACGAAATAATGTGGACACC 3600
QY 1201 TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220
Dbb 3601 TATAATCCATGGGATAGGCTTTTCAGTAGCTGTTATATCGCTTACCTGCAGTGTGTACTG 3660
QY 1221 TrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp 1240
Dbb 3661 TGGATTTTCTCTTACAATACATATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAAGAT 3720
QY 1241 ProphePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
Dbb 3721 CCCTTTTTCAGAAACCTTTTCAACGAAAGCTTAAAAATAGGAAGCTTCCAGAACCCACACAC 3780
QY 1261 AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280
Dbb 3781 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTTAAAGGTCAAAGAGCTGATGGGT 3840
QY 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
Dbb 3841 TGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAAATATGAT 3900
QY 1301 AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer 1320
Dbb 3901 GACAAGAAAGATTTTCTTCTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 3960
QY 1321 PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340
Dbb 3961 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGC 4020
QY 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360
Dbb 4021 ACAATTATTAATATTCTGTTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTATAGGA 4080
QY 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380
Dbb 4081 GATTATTTCTTCAGACACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTACTGTCTCT 4140
QY 1381 GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400

TYPE: DNA
ORGANISM: homo sapiens
US-09-971-121-1

Alignment Scores:
Pred. No.: 0 Length: 4929
Score: 8395.00 Matches: 1637
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 5
Query Match: 99.63% Indels: 0
DB: 41 Gaps: 0

US-10-090-458-5 (1-1642) x US-09-971-121-1 (1-4929)

QY	1	MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys	20
DB	1	ATGTCACCTGCAATTAGGGAGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG	60
QY	21	AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu	40
DB	61	AATTAATTAATAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA	120
QY	41	PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu	60
DB	121	TTTTTTTATTTTGGTTAATAATTAATAGATGATGATGATGATGATGATGATGATGAT	180
QY	61	ValProAsnIleGluLeuLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly	80
DB	181	GTGCCTAATATAGAACTCAATCTATGGACAAGTTTACTCTTTCTAATCTAATCTTGA	240
QY	81	TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu	100
DB	241	TATACTCCAGTGACTAATATACAGCAGCATCATGAGAGAAAGTGTCTACTGATCATCTA	300
QY	101	ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu	120
DB	301	CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAACATCCAGTCTC	360
QY	121	SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg	140
DB	361	TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTCAGAGACTCCATGTCCTATGAATTCGT	420
QY	141	PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer	160
DB	421	TTTTTTTCTGATATGATTCAGTATCTTCTATTTATATGATGATTCAGAGCTGGTGTCA	480
QY	161	LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle	180
DB	481	AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAGTTTTACAGCATCCATA	540
QY	181	AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr	200
DB	541	GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTGAAGAGGAGCTGGAGTCAACT	600
QY	201	LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal	220
DB	601	AAAGCTGTTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA	660
QY	221	IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle	240
DB	661	ATTTTAATATACCTAGTTATAGCATTTTTCACCTTTTGGATATCTTTTGGCAATTCATATC	720
QY	241	ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr	260
DB	721	GTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTTCATCATACT	780
QY	261	AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu	280
DB	781	GCCTTTTGGCTTCTCTGGGTTCTCTATAWACAAGTTAATTTTCTTATGTCCTCTCT	840
QY	281	MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerIleValIlePhe	300
DB	841	ATGGCAGTCATTCGCAGACGCTTCTTGTATTCTTCTCAAAGTAGCAGCATTTGTGATATT	900

QY	301	LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu	320
DB	901	CTGCTTTTTCCTTTATGGATTATCATCTGATATTTTGTCTTAATGCTGACACCTCTT	960
QY	321	PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe	340
DB	961	TTTTAAAAAATCAAAACATGCGGAATAGTTGAATTTTGTACTGTGGCTTTGGATTT	1020
QY	341	IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer	360
DB	1021	ATTGGCCTTATGATAATCCTCATAGAAAAGTTTCCCAAAATCGTTAGTGTGGCTTTT	1080
QY	361	ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe	380
DB	1081	CTTTCTGTCTACTGTACTTTTCAAAATTTGACTGCAGGCCCATATCCTCTAATTTAT	1140
QY	381	AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle	400
DB	1141	AATGAAGTGTCTTCATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAATTTAT	1200
QY	401	IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal	420
DB	1201	ATCATGCTCACACTTAATAGTATATTTCTATGTCTCTTGGCTGTCTATCTTGATCA	1260
QY	421	IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp	440
DB	1261	ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCAT	1320
QY	441	SerLysSerLysArgAsnTyrGluLeuLeuSerGluGlyAsnValAsnGlyAsnIleSer	460
DB	1321	TCAAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAAT	1380
QY	461	PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle	480
DB	1381	TTTAGTGAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAAAGAGCCATA	1440
QY	481	SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu	500
DB	1441	AGTGTATTTCAGAAAGACATACAGAAAGAGGTGAAATGTGGAGGCTTTGAGAAAT	1500
QY	501	SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys	520
DB	1501	TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAAAC	1560
QY	521	SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle	540
DB	1561	AGTACATGATGAATATTCCTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCT	1620
QY	541	TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle	560
DB	1621	TATGGACACAGAGTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAAATGATTG	1680
QY	561	CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu	580
DB	1681	TGTCCACAGTTAGATATACATTTGATGTTTGTGACAGTAGAAGAAAAATTTATCA	1740
QY	581	AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu	600
DB	1741	GCTTCAATCAAAGGGATACCCAGCCACCAATATAATAACAAGAGTGCAGAGGTTT	1800
QY	601	AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlnLys	620
DB	1801	GATTTAGACATGCAGACTATCAAGATAACCAAGCTAAAAAATAAGTGGTGGTCA	1860
QY	621	ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu	640
DB	1861	AGAAAGCTGTCTATTAGGAATTTCTTCTTGGGAACCCCAAGATACTGCTGCTAG	1920
QY	641	ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLysTyrArg	660
DB	1921	CCAAACAGCTGGAATGGACCCCTCTTCTCGACATATTGTATGGAATCTTTTAA	1980

QY 1021 LeuTyrPheGlnAlaAlaLeuLeuGlyIleValThrAlaMetProProTyrPheAla 1040
DB 4071 CTGTATTTTCAAGCAGCTTTGCTTGGATCATTTGTTACTGCAATGCCACCTTACTTTGCC 4130
QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
DB 4131 ATGGAAAATGAGAGAAATCATAGATCAAGCTTATCTCACTTAAACTTTTCAGGCTTT 4190
QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValAlaAspIleProLeuPhePheIle 1080
DB 4191 TTGCCATCTGCATATTTGGATTGGACCAAGCTTTGTTGATATCCCTTATTTTATCAT 4250
QY 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
DB 4251 CTTATTTTGTATGCTAGGAAGCTTACCTGCACTTTTATTTATGATATATTTTATATCTGA 4310
QY 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
DB 4311 AAGTTCCCTTGTGCTGTTTTCCTTATTTGCTTATGTTTCCATCAGTTATTTCTGTTCACT 4370
QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
DB 4371 TATATTGCTTCTTTCACCTTTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCACTTATC 4430
QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
DB 4431 TATTCTGTGGCAGCGTTGCTTGTATGCAATCACTGAAATTAATTTCTTTTATGGGATAC 4490
QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
DB 4491 ACAATTGCAACTATTTCTTCAATATGCTTGTATGCTTATCAATCACTTCAATCTATCCACTTCTA 4550
QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
DB 4551 GGTTGCCTGATTTCTTTCATAAAGATTTCTTGAAGAAATGACGAAAAAATGTGGACACC 4610
QY 1201 TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220
DB 4611 TATAATCCATGGGATAGGCTTTCAGTAGCTTATATATGCTTATATGCTTACCTGCAGTGTGACTG 4670
QY 1221 TrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGlyArgSerIleArgLysAsp 1240
DB 4671 TGGATTTTCTCTTACAATCACTATGAGAAAAAATATGAGGAGAGATCAATAAGAAAAAGAT 4730
QY 1241 ProphePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
DB 4731 CCCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACAGAC 4790
QY 1261 AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280
DB 4791 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTTAAAGTCAAAGAGCTGATGGGT 4850
QY 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
DB 4851 TGCCAGTGTGTGAGGAGAAACCATCCATTTATGTTGCTCAGCAATTTGCATAAAGAAATATGAT 4910
QY 1301 AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer 1320
DB 4911 GACAAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 4970
QY 1321 PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340
DB 4971 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCCAATGGTGTGGCAAAAGC 5030
QY 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360
DB 5031 ACAATTATTAATATTTCTGTTGGTGTATTTGAACCACTTCCAGGCCAGGTATTTTAGGA 5090
QY 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380
DB 5091 GATTATTTCTTACAGACAAAGTGAAGATGATGATTTCACTGAAGTGTATGGTTACTGTCCT 5150

QY 1381 GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400
DB 5151 CAGATAAACCCCTTTGTGGCCAGATACATCATTTGCAGGAACATTTTGAAATTTATGGAGCT 5210
QY 1401 ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
DB 5211 GTCAAAGGAATGAGTGCAGAGTACATGAAGAAGTCAATAGTCAATACACATGCACCTT 5270
QY 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
DB 5271 GATTTAAAGAAACATCTTTCAGAGACTGTAAAGAACTACTCTGAGGAATCAAACGAAAG 5330
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
DB 5331 TTGTGTTTTCTCTAAGTATGCTAGGCAATCCTCAGATTACTTTGCTAGATGAACCATCT 5390
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
DB 5391 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGCATTTAA 5450
QY 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
DB 5451 AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGGAGAGGCAGAGGCTGCTGT 5510
QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
DB 5511 GATCGAGTAGCTATCATGGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACATCTA 5570
QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLysLeuAspTrpIleGluAsn 1540
DB 5571 AAGAGTAAATTTGAAAGAGGCTACTTTTGGAAATTTAAATTGAAGGACTGGATAGAAAC 5630
QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
DB 5631 CTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAATGCAAGCCGTCAG 5690
QY 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
DB 5691 GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAGATGTTTCAGTCCCTTTCA 5750
QY 1581 GlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600
DB 5751 CAATCTTTTTTAAGCTGGAAGAGCTAAACATGCTTTTGCATTGAAGATATAGCTTT 5810
QY 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620
DB 5811 TCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAAAGAACCAAGAGGAGAGAT 5870
QY 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
DB 5871 AATAGTTGTGAAACTTTTAAACAGCACACTTTGGTGGGAACCAACACAGAGATAGAGTA 5930
QY 1641 ValPhe 1642
DB 5931 GTATTT 5936

RESULT 5
US-09-971-121-1
; Sequence 1, Application US/09971121
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: Novel Human Transporter Proteins and Polynucleotides Encoding th
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4929

Db 1851 ATGGCAGTCATTGCGACAGCTTCTTTGTTATTTCTCCTCAAAGTAGCAGCAATTGTGATATTT 1910
Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 1911 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTCCTTTAATGCTGACACCTCTT 1970
Qy 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 1971 TTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTT 2030
Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 2031 ATTGGCTTATGATAATCCTTCATAGAAAAGTTTCCCAAAATCGTTAGTGTGGCTTTTCAGT 2090
Qy 361 ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 2091 CCTTCTGTCACTGTACTTTTGTGATTGGTATTGCAACAGGTCATGCAATTTAGAAGATTTT 2150
Qy 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 2151 AATGAAGGTGCTTCAATTTTCAAAATTTGACTGCAGGCCCAATATCCTCTAATTATTACAATT 2210
Qy 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 2211 ATCATGCTCACACTTAATAGTATATTTCTATGTCTCTTGGCTGTCTATCTTGATCAAGTC 2270
Qy 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 2271 ATCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCCTTCATATTGG 2330
Qy 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
Db 2331 TCAAAGAGTAAAGAAATTTATGAGGAGTTATCAGAGGCAATGTTAATGGAAATATTAGT 2390
Qy 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db 2391 TTTAGTGAATATTATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAATT 2450
Qy 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 2451 AGTGSTATTCAAGAGACATACAGAAAAGAGGGTGAAAATGTGGAGGCTTTGAGAAAATTTG 2510
Qy 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
Db 2511 TCATTGTACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAAACAGGAAAG 2570
Qy 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 2571 AGTACATTGATGAATATTCTTGTGGACTCTGCCCACTTCTGTATGGGTTTGCACTCTATA 2630
Qy 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 2631 TATGACACAGAGTCTCAGAATAATAGATGAATGTTTGAAGCAAGAAAATGATTGGCATT 2690
Qy 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
Db 2691 TGTCACAGTTAGATATACACTTTGATGTTTTTGACAGTAGAAGAAAATTTATCAATTTTG 2750
Qy 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 2751 GCTTCAATCAAGGGATACCAGCCCAACAATATATAACAAGAAGTGCAGAGGTTTTACTA 2810
Qy 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
Db 2811 GATTTAGACATGCAGACTATCAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 2870
Qy 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
Db 2871 AGAAAGCTGTCTATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGCTAGATGAA 2930
Qy 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660

Db 2931 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA 2990
Qy 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Db 2991 AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTGCA 3050
Qy 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 3051 GATAGGAAAGCTGTGATATCAAGAAGAAATGCTGAAATGTGTGGTCTTCTCAATGTTCCTC 3110
Qy 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 3111 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 3170
Qy 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
Db 3171 GAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAAT 3230
Qy 741 AspGlnGlnLeuValTyrSerLeuPropheLysAspMetAspLysPheSerGlyLeuPhe 760
Db 3231 GACCAACAACCTTGTGTATAGCTTGCCCTTCAAGGACATGACACAAATTTTCAGGTTTGT 3290
Qy 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 3291 TCTGCCCTAGACAGTCATTTCAAAATTTGGGTGTCACTTCTTATGGTGTTCATGACGACT 3350
Qy 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 3351 TTGGAAGACGTAATTTTAAAGTAGAAGTTGAAGCAGAAATGACCAAGCAGATTATAGT 3410
Qy 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 3411 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAATGGAA 3470
Qy 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 3471 CAGAGCTTACTTATTTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTGG 3530
Qy 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPheThrLeuLysArgGluSerLys 860
Db 3531 AAACAACAGATGTATACATAGCAAAAGTTTTCATTTCTTACCTTGAAACGTGAAGTAAA 3590
Qy 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 3591 TCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTTTTTCACAGTTTCAGATTTTATGTTT 3650
Qy 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
Db 3651 TTGGTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCACAGACTTATAT 3710
Qy 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
Db 3711 TTTCTAAAAACCTGGAGACAAACACACATAAATACAAAAAAGTCTGCTTCTTCAAAATCT 3770
Qy 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
Db 3771 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAAGCCAGAACATAATGGTGACG 3830
Qy 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960
Db 3831 ATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGCAGCTTTTAAATGTGATG 3890
Qy 961 HisSerGluLysAspTyrValPheAlaValPheAsnSerThrMetValTyrSerLeu 980
Db 3891 CATTCAGAAAAGGACTATGTGTTTTTGCAGCTGTTTTCAACAGACTACTATGGTATTCTTTA 3950
Qy 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
Db 3951 CCTATATTAGTGAATATCATATTAGTAACACTACTATCTTTATCATTTAAATGTGACTGAACC 4010
Qy 1001 IleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLysIleGlu 1020
Db 4011 ATCCAGATCTGGAGTACCCCATTTCTTTCAAGAAATTACTGATATAGTTTTTAAAAATTGAG 4070

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Db 5498 GATTTAAAGAACATCTTCAGAGACTGTAAAGAACTACCTGCAGGAATCAACGAAAG 5557
Qy 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db 5558 TTGTGTTTGTCTTAAGTATGCTAGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 5617
Qy 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
Db 5618 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGCATTAAA 5677
Qy 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
Db 5678 AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGAGGAGGCGAGGCTGTCTGT 5737
Qy 1501 AspArgValAlaAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
Db 5738 GATCAGTAGCTATCATGTTGCTGGGCAGTTAAGATGATCGGAACAGTACAAACATCTA 5797
Qy 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540
Db 5798 AAGAGTAAATTTGGAAAGGCTACTTTTGGAAATTAATTAAGGACTGGATAGAAAAC 5857
Qy 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
Db 5858 CTAGAAGTAGACCGCCTTCAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAG 5917
Qy 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
Db 5918 GAAAGTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTCA 5977
Qy 1581 GlnSerPhePheLysLeuGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600
Db 5978 CAATCTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTT 6037
Qy 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620
Db 6038 TCTCAAGCAACATTTGGAACAGGTTTGTAGAACTCACTAAGAACAAAGAGGGAAGAT 6097
Qy 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
Db 6098 AATAGTTGTGGAACTTTAAACAGCACACTTTGGTGGGAACGAACACAGAGATAGATA 6157
Qy 1641 ValPhe 1642
Db 6158 GTATTT 6163
RESULT 4
US-10-005-338B-1
; Sequence 1, Application US/10005338B
; GENERAL INFORMATION:
; APPLICANT: DENEFLÉ, Patrice
; APPLICANT: ROSIER-MONTUS, Marie-Francoise
; APPLICANT: PRADES, Catherine
; APPLICANT: ARNOULD-REGUIGNE, Isabelle
; APPLICANT: DUVERGER, Nicolas
; APPLICANT: ALLIKMETS, Rando
; APPLICANT: DEAN, Michael
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENES
; TITLE OF INVENTION: CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
; FILE REFERENCE: ABCA5, 6, 9, 10
; CURRENT APPLICATION NUMBER: US/10/005,338B
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/263,231
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: FR 00403440.1
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6525
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4449
; OTHER INFORMATION: n=unknown, may be a or g or c or t
US-10-005-338B-1
Alignment Scores:
Pred. No.: 0 Length: 6525
Score: 8422.00 Matches: 1641
Percent Similarity: 99.94% Conservative: 0
Best Local Similarity: 99.94% Mismatches: 1
Query Match: 99.95% Indels: 0
DB: 43 Gaps: 0
US-10-090-458-5 (1-1642) x US-10-005-338B-1 (1-6525)
Qy 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys 20
Db 1011 ATGTCACCTGCAATTAGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG 1070
Qy 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 1071 AATTACTTAATTAAATGCAAGAACCAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA 1130
Qy 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 1131 TTTTITTTTATTTTGGTTAATTAATTAGCATGATGATCCAAATAAGAAATATGAAGAA 1190
Qy 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 1191 GTGCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGA 1250
Qy 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 1251 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 1310
Qy 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 1311 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAACATCCAGTCTC 1370
Qy 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 1371 TCTAAGCCGAGCAACTTTGTAGGTGTGTTTTCAAAGACTCCATGTCTCTATGAACCTCGT 1430
Qy 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 1431 TTTTTCCTGATATGATTCAGTATCTTCTATTATATATGGATTCAAGAGCTGGCTGTTC 1490
Qy 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 1491 AAATCATGTGAGGCTGCTCAGTACTGGTCTCCTCAGGTTTCACAGTTTACAAAGCATCCATA 1550
Qy 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
Db 1551 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 1610
Qy 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 1611 AAAGTGTATTATGCGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 1670
Qy 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db 1671 ATTTTAATATACCTAGTTATAGCATTTTTCACCTTTGGATACCTTTTGGCAATTCATATC 1730
Qy 241 ValAlaGluLysGluLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 1731 GTAGCAGAAAGAAAGAAAAATAAAGAAATTTTAAAGATAATGGGACCTCATGATACT 1790
Qy 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 1791 GCCTTTTGGCTTTCTCTGGTCTCTCTATATACAGTTTAAATTTTCTTATGTCCCTTCTT 1850
Qy 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
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QY	701	LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr	720
Db	3338	AAAAGTAAATGGGGATCGCTACCGCTAGCATGTACATAGACAAATATTGTGCCACA	3397
QY	721	GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsn	740
Db	3398	GAATCTCTTTCTTCACCTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAT	3457
QY	741	AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe	760
Db	3458	GACCAACAACCTTGTTGTATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAGGTTTGTIT	3517
QY	761	SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr	780
Db	3518	TCTGCCCTAGACAGTCATCAAAATTTGGGTGTCTATTTCTTATGGTGTTCATGACGACT	3577
QY	781	LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer	800
Db	3578	TTGGAAGACGATATTTTAAAGCTAGAAATTGAAGCAGAAATTGACCAAGCAGATTATAGT	3637
QY	801	ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu	820
Db	3638	GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAATGGAA	3697
QY	821	GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp	840
Db	3698	CAGAGCTTACTTATCTTCTGAAACCAAGGCTTCTAGTGAGCACCATGAGCCTTTTGG	3757
QY	841	LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrValGlnIlePheMetPhe	860
Db	3758	AAACAACAGATGTATACAATAGCAAAAGTTTCATTTCTTTTACCTTGAAACGTGAAAGTAAA	3817
QY	861	SerValArgSerValLeuLeuLeuLeuIlePhePhePheThrValGlnIlePheMetPhe	880
Db	3818	TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTCAGATTTTATGTTT	3877
QY	881	LeuValHisHisSerPheLysAsnAlaValProIleLysLeuValProAspLeuTyr	900
Db	3878	TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCATCAAACTTGTTCAGACTTATAT	3937
QY	901	PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer	920
Db	3938	TTTCTAAAACCTGGAGACAAACACACATAAATACAAAACAAGTCTGCTTCTCAAAATCT	3997
QY	921	AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr	940
Db	3998	GCTGACTCAGATATCAGTGATCTTATAGCTTTTTCACAAGCCAGAACATAATGGTGACG	4057
QY	941	MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet	960
Db	4058	ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGGGCTTTAAATGTGGTG	4117
QY	961	HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu	980
Db	4118	CATTCAGAAAAGGACTATGTTTTCAGCTGTTTTCACAGTACTATGGTTTATCTTTA	4177
QY	981	ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr	1000
Db	4178	CCTATATTAGTAATATCATAGTAACACTATCTTTATCATTTAAATGTGACTGAAACC	4237
QY	1001	IleGlnIleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLysIleGlu	1020
Db	4238	ATCCAGATCTGGAGTACCCCATCTTTCAGAAGAAATTAAGTATAGTTTTTAAATTTGAG	4297
QY	1021	LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla	1040
Db	4298	CTGTATTTTCAAGCAGCCTTGTGGAATCATTTGTACTGCAATGCCACCTTACTTTGCC	4357
QY	1041	MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu	1060
Db	4358	ATGGAATAATGCAGAGAAATCATAGATCAAGCCTTACTCAACTTAAACTTTCAGGTCTT	4417

QY	1061	LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIle	1080
Db	4418	TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTGATATCCCTTATTTTATCAT	4477
QY	1081	LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal	1100
Db	4478	CTTATTTTGTATGCTAGGAAGCTTATTGGCATTTCAATTATGGATTATATTTTATCTGTA	4537
QY	1101	LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr	1120
Db	4538	AAGTCCCTTGCTGTGGTCTTTTTCCTTATTGGTTATGTTCCATCAGTTATCTGTTCACT	4597
QY	1121	TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle	1140
Db	4598	TATATTGCTTCTTTTCACCTTTAAGAAAAATTTTAAATACCAAGAAATTTTGGTCATTATC	4657
QY	1141	TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr	1160
Db	4658	TATTTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAAATTTCTTTATGGGATAC	4717
QY	1161	ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu	1180
Db	4718	ACAATTGCAACTATTCTTCATTTATGCTTTTGTATCATCATTTCCAATCTATCCACTTCTA	4777
QY	1181	GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr	1200
Db	4778	GGTTGCTGATTTCTTTTCATAAAGATTTCTTTGGAAGAAATGTACGAAAAAATGTGGACACC	4837
QY	1201	TyrAsnProTipAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu	1220
Db	4838	TATTAATCCATGGGATAGGCTTTTCAGTAGCTGTTTATATCGCCTTACCTGCAGTGTACTG	4897
QY	1221	TrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp	1240
Db	4898	TGGATTTTCTCTTACAATACTATGAGAAAAAATATGAGGCAGATCAATAAGAAAAAGAT	4957
QY	1241	ProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp	1260
Db	4958	CCCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCACAGAC	5017
QY	1261	AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly	1280
Db	5018	AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGT	5077
QY	1281	CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp	1300
Db	5078	TGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGAAATATGAT	5137
QY	1301	AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer	1320
Db	5138	GACAAGAAAAGATTTTCTTCTTCAAGAAAAGTAAAGAAAGTGGCAACTTAATATCATCTCT	5197
QY	1321	PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer	1340
Db	5198	TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGC	5257
QY	1341	ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly	1360
Db	5258	ACAAATATTAAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA	5317
QY	1361	AspTyrSerSerGluThrSerGluAspAspAspSerLeuLysCysMetGlyTyrCysPro	1380
Db	5318	GATTATTCTTCAGAGACAAGTGAAGATGATGATTCATCACTGAAGTGTATGGGTACTGTCT	5377
QY	1381	GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla	1400
Db	5378	CAGATAAACCCCTTTGTGGCAGATACATCACTTCAGAGAAACATTTTGAATTTATGGAGCT	5437
QY	1401	ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu	1420
Db	5438	GTCAAAGGAATGAGTGCACAGTACATGAAGAAGTCAATGAATGAATGAATGAATGAAT	5497
QY	1421	AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys	1440

Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.94% Mismatches: 0
Query Match: 99.95% Indels: 0
DB: 78 Gaps: 0

US-10-090-458-5 (1-1642) x US-60-223-269-15 (1-6369)

QY	1	MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLys	20
Db	1238	ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACACTTCTACTGAAG	1297
QY	21	AsnTyrLeuIleLysCysArgThrLysLysSerValGlnGluIleLeuPheProLeu	40
Db	1298	AATTACTTAATTAAATGCAGAACCAAAAAGAGTAGTGTTTCAGGAAATTCCTTTTCCACTA	1357
QY	41	PhePheLeuPheTyrLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu	60
Db	1358	TTTTTTTATTGTTTAAATTAATTAATAGCATGATGCATCCAAATAAGAAATATGAAGAA	1417
QY	61	ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly	80
Db	1418	GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATTTCTTGA	1477
QY	81	TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu	100
Db	1478	TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGCTACTGATCATCTA	1537
QY	101	ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu	120
Db	1538	CCTGATGTCATAATTACTGAAGAATATACAAATGAAAAAGAAATGTTAACATCCAGTCTC	1597
QY	121	SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg	140
Db	1598	TCTAAGCCGAGCAACTTTGTAGGTGTGTTTTCAAAGACTCCATGTCCTATGAACCTCGT	1657
QY	141	PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer	160
Db	1658	TTTTTTTCTTGATATGATTCAGTATCTTCTATTATATAGGATTCAGAGCTGGGTGTTCA	1717
QY	161	LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle	180
Db	1718	AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAGTTTACAGGATCCATA	1777
QY	181	AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr	200
Db	1778	GATGCTGCCATTATACAGTTGAACCAATGTTTCTCTTGAAGGAGCTGGAGTCAACT	1837
QY	201	LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal	220
Db	1838	AAAGCTGTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA	1897
QY	221	IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle	240
Db	1898	ATTTTAAATATACCTAGTTATAGCAATTTTCACCTTTTGGATACCTTTTGGCAATTCATATC	1957
QY	241	ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr	260
Db	1958	GTAGCAGAAAAAGAAAAATAAAAGAAATTTTAAAGATAATGGGACTTTCATGATACT	2017
QY	261	AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu	280
Db	2018	GCCTTTTGGCTTTCTCTGGGTTCTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTT	2077
QY	281	MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe	300
Db	2078	ATGGCAGTCATTGGCAGACTTCTTTGTTATTTCCTCAAGTAGCAGCATTTGIGATATT	2137
QY	301	LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu	320
Db	2138	CTGCTTTTCTCTTTATGGATTATCATCTGTATTTTTTGTCTTAAATGCTGACACCTCTT	2197
QY	321	PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe	340

Db	2198	TTTAAAAAATCAAAACATGTGGGAATAGTTGAATTTTTTGTACTGTGGCTTTTGATTT	2257
QY	341	IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer	360
Db	2258	ATTGGCCTTATGATAATCCTCATAGAAAAGTTTCCAAAATCGTTAGTGTGGCTTTTCAGT	2317
QY	361	ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe	380
Db	2318	CCTTTCTGTCACTGTACTTTTGTGATTGGTATTGCACAGGTCATGCATTAGAAAGATTTT	2377
QY	381	AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle	400
Db	2378	AATGAAGGTGCTTCAATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAAT	2437
QY	401	IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal	420
Db	2438	ATCATGCTCACACTTAATAGTATATTTCTATGTCTCTTGGCTGTCTATCTTGTATCAAGTC	2497
QY	421	IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp	440
Db	2498	ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG	2557
QY	441	SerLysSerLysArgAsnTyrGluLeuLeuSerGlyGlyAsnValAsnGlyAsnIleSer	460
Db	2558	TCAAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAATATTAGT	2617
QY	461	PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle	480
Db	2618	TTTAGTGAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGAAAGAGCCATAAGAATT	2677
QY	481	SerGlyIleGlnLysThrTyrArgLysLysGlyGlyAsnValGluAlaLeuArgAsnLeu	500
Db	2678	AGTGGTATTTCAGAAACATACAGAAAGAGGGTGAAATGTGGAGGCTTTGAGAAATTTG	2737
QY	501	SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys	520
Db	2738	TCATTTGACATATATGAGGGTCAGATTACTGCCITACTTGGCCACAGTGGACAGGAAAG	2797
QY	521	SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle	540
Db	2798	AGTACATTGATGAATATTTCTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATA	2857
QY	541	TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle	560
Db	2858	TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATGGCATT	2917
QY	561	CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu	580
Db	2918	TGTCCACAGTTAGATATACACTTTTGATGTTTTTGACAGTAGAAGAAATTTATCAATTTTG	2977
QY	581	AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu	600
Db	2978	GCTTCAATCAAAGGGATACCAAGCAACATATAATAACAAGAGTGCAGAGGTTTACTA	3037
QY	601	AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlnLys	620
Db	3038	GATTTAGACATGCAGACTATCAAAAGATAACCAAGCTAAAAAAATTAAGTGGTGGTCAAAA	3097
QY	621	ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu	640
Db	3098	AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGTAGATGAA	3157
QY	641	ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLysTyrArg	660
Db	3158	CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAAAATACAGA	3217
QY	661	LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla	680
Db	3218	AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTGCA	3277
QY	681	AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu	700
Db	3278	GATAGGAAAGCTGTGATATCACACAGGAATGCTGAAATGTGTGTTCTTCAATGTTCCTC	3337

QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
DB 4778 GGTGCCTGATTTCTTTCAAAAGATTTCTTGGAGAATGTACGAAAAATGTGGACACC 4837
QY 1201 TyrAsnProTyrAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220
DB 4838 TATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTACTG 4897
QY 1221 TrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp 1240
DB 4898 TGGATTTTCTCTTACAATACTATGAGAAAAATATGGAGGCAGATCAATAAGAAAAAGAT 4957
QY 1241 ProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
DB 4958 CCCTTTTTCAGAAACCTTTCAACGAAGCTTAAAAATAGGAAGCTTCCAGAACACCAGAC 5017
QY 1261 AsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280
DB 5018 AATGAGGATGAAGATGAAGATGTCAAGCTGAAAGACTAAAGGTCAAAGAGGTGATGGT 5077
QY 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
DB 5078 TGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGATATGAT 5137
QY 1301 AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer 1320
DB 5138 GACAAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 5197
QY 1321 PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340
DB 5198 TTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTCTGGCAAAAGC 5257
QY 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360
DB 5258 ACAATTATTAATATTCTGGTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 5317
QY 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380
DB 5318 GATTATCTTTCAGAGACAAGTGAAGATGATGATTCAGTGAAGTGTATGGGTACTGTCCT 5377
QY 1381 GlnIleAsnProLeuTyrProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400
DB 5378 CAGATAAAACCCCTTTGTGGCCAGATACATACATTGCAGGAACATTTTGAATTTATGGAGCT 5437
QY 1401 ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
DB 5438 GTCAAAGGAATGAGTGCAGTACATGAAAGAGTCAATGAAGTCAATGAATGAATGAGCT 5497
QY 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
DB 5498 GATTAAAAAGAACATCTTTCAGAGACTGTAAAGAACTACCTGCAGGAATCAACGAAAG 5557
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
DB 5558 TTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 5617
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTyrArgAlaIleArgThrAlaPheLys 1480
DB 5618 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGATTAAA 5677
QY 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
DB 5678 AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGGAGGAGGAGGCTGTCTGT 5737
QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
DB 5738 GATCAGTAGCTATCATGTTGTTGGCAGTTAAGATGTATCGGAACAGTACAACATCTA 5797
QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTyrIleGluAsn 1540
DB 5798 AAGAGTAAATTTGGAAAAGGCTACTTTTGGAAATTAATTAAGGACTGGATAGAAAC 5857
QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560

DB 5858 CTAGAAGTAGACCGCCTTCAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCGTCAG 5917
QY 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
DB 5918 GAAAGTTTTCCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTCA 5977
QY 1581 GlnSerPhePheLysLeuGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600
DB 5978 CAATCTTTTAAAGCTGGAGAGAGCTAAACATGCTTTTGCATTTGAAGAATATAGCTTT 6037
QY 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluAsp 1620
DB 6038 TCTCAAGCAACATTGGAAACAGGTTTTTTGTAGAACTCACTAAAGAACAGAGGAGAT 6097
QY 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTyrTrpGluArgThrGlnGluAspArgVal 1640
DB 6098 AATAGTTGTGGAACCTTTTAAACAGCACACTTTGGTGGGAACGACACACAAGAGATAGAT 6157
QY 1641 ValPhe 1642
DB 6158 GTATT 6163

RESULT 3
US-60-223-269-15
; Sequence 15, Application US/60223269
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Thornton, Michael
; APPLICANT: Ramkumar, Jaya
; APPLICANT: Tang, Y. Tom
; APPLICANT: Azimzai, Yalda
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Yang, Junming
; APPLICANT: Yao, Monique G.
; APPLICANT: Lal, Preeti
; APPLICANT: Walia, Narinder K.
; APPLICANT: Gandhi, Ameena R.
; APPLICANT: Hafalia, April
; APPLICANT: Nguyen, Danniel B.
; APPLICANT: Patterson, Chandra
; APPLICANT: Elliott, Vicki S.
; APPLICANT: Tribouley, Catherine M.
; APPLICANT: Lu, Dyung Aina M.
; APPLICANT: Xu, Yuming
; APPLICANT: Reddy, Roopa
; APPLICANT: Hernandez, Roberto
; APPLICANT: Borowsky, Mark L.
; APPLICANT: Lo, Terence P.
; APPLICANT: Lu, Yan
; APPLICANT: Policky, Jennifer L.
; APPLICANT: Greene, Barrie D.
; APPLICANT: Sanjanwala, Madhu S.
; APPLICANT: Rauman, Brigitte E.
; APPLICANT: Burford, Neil
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0183 P
; CURRENT APPLICATION NUMBER: US/60/223,269
; CURRENT FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 6369
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 2798241CB1
US-60-223-269-15

Alignment Scores: 0 Length: 6369
Pred. No.: 8422.00 Matches: 1641
Score:

Db 2558 TCAAGAGCAAAAGAAATTATGAGGAGCTTATCAGAGGGCAATGTTAATGGAAATATTAGT 2617
QY 461 PheSerGluIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db 2618 TTTAGTGAATATTATGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAGAATT 2677
QY 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 2678 AGTGGTATTGAGAAGACATACAGAAAGAGGGTGAAATGTGGAGGCTTTGAGAAATTTG 2737
QY 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuGlyHisSerGlyThrGlyLys 520
Db 2738 TCATTTGCATATATGAGGGTCAGATTACTGCCCTTACTTGGCCACAGTGGAAACAGGAAAG 2797
QY 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 2798 AGTACATTGATGAATATTCTTTGTGGACTCTGCCACCTTCTGATGGGTTTGCATCTATA 2857
QY 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
Db 2858 TATGGACACAGACTCTCAGAAATAGATGAATGTTTGAAGCAAGAAAATGATTGGCATT 2917
QY 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
Db 2918 TGTCCACAGTTAGATATACACTTTTGATGTTTTGACAGTAGAAGAAAATTTATCAATTTG 2977
QY 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 2978 GCTTCAATCAAAAGGGATACCAGCCACAATATATAACAAGAGTGCAGAAGGTTTTACTA 3037
QY 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
Db 3038 GATTTAGACATGAGACTATCAAGAGATAACCAAGCTAAAGAAATTAAGTGGTGGTCAAAA 3097
QY 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
Db 3098 AGAAAGCTGTCAATTAGGAATGCTGTTCTGGGAACCCCAAGATACTGCTGTAGATCAA 3157
QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLysTyrArg 660
Db 3158 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGA 3217
QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Db 3218 AAAGCCAATCGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTCCTGCA 3277
QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 3278 GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTTGGTCTTCAATGTTCCCTC 3337
QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 3338 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 3397
QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
Db 3398 GAAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAA 3457
QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
Db 3458 GACCAACAACCTTGTGTATAGCTTGCCCTTCAAGGACATGGACAAATTTTCAGGTTTGT 3517
QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 3518 TCTGCCCTAGACAGTCATTCAAATTTGGGTGTCTATTCTTATGGTGTTCATGACGACT 3577
QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 3578 TTGGAAGACGTATTTTAAAGCTAGAACGTGAAGCAGAGAAATTTGACCAAGCAGATTATAG 3637
QY 801 ValPheThrGlnGlnProLeuGluGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 3638 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCCAAAATCTTTTGATGAAATGGAA 3697

QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 3698 CAGAGCTTACTTATTCTTTCTGAAACCAAGGCTTCTCTAGTGAGCACCATTGAGCCTTTGG 3757
QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPheThrLeuLysArgGluSerLys 860
Db 3758 AAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTACCTTGAAACGTGAAAGTAAA 3817
QY 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 3818 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTCACAGTTTCAGATTTTATGTTT 3877
QY 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
Db 3878 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCACAGACTTATAT 3937
QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSer 920
Db 3938 TTTCTAAAAACCTGGAGACAAACCCACATAAATACAAACAAAGTCTGCTTCTTCAAAATCT 3997
QY 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
Db 3998 GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAAGCCAGAACATAATGGTGACG 4057
QY 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960
Db 4058 ATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCATAGTCGGCTTTTAAATGTTGTG 4117
QY 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
Db 4118 CATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGTACTATGGTTTATTCITTA 4177
QY 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
Db 4178 CCTATATTAGTGAATATCATTTAGTAAGTACTATCTTTTATCATTTAAATGTGAAACC 4237
QY 1001 IleGlnIleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLysIleGlu 1020
Db 4238 ATCCAGATCTGGAGTACCCCATCTTCTTCAAGAAATTTACTGATATAGTTTTTAAATTTGAG 4297
QY 1021 LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040
Db 4298 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTACTGCAATGCCACCTTACTTTGCC 4357
QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
Db 4358 ATGGAATAATGCAGAGAAATCATAGATCAAAAGCTTATACTCAACTTAAACTTTCAGGTCTT 4417
QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIle 1080
Db 4418 TTGCCATCTGCATATTGGATTGGACAGCTGTTGTGATATCCCTTATTTTATCATTT 4477
QY 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
Db 4478 CTTATTTTGTGCTAGGAAGCTTATTGGCATTTTCATTATGGATTATATTTTATACTGTA 4537
QY 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
Db 4538 AAGTTCTTGTGCTGGTTTTTTTGGCTTATTTGTTATGTTCCATCAGTTATTTCTGTTCACT 4597
QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
Db 4598 TATATTGCTTCTTTCACCTTTTAAAGAAAATTTTAAATACCAAGAAATTTTGGTCATTTATC 4657
QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
Db 4658 TATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATAC 4717
QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
Db 4718 ACAATTGCAACTATTCTTTCATTATGCTTTTGTATCATCATTCCAATCTATCCACTTCTA 4777

APPLICANT: THORNTON, Michael; RAMKUMAR, Jayalaxmi;
APPLICANT: TANG, Y. Tom; AZIMZAI, Yalda;
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APPLICANT: TRIBOULEY, Catherine M.; LU, Dyung Aina M.;
APPLICANT: XU, Yuming; REDDY, Roopa;
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APPLICANT: LO, Terence P.; LU, Yan;
APPLICANT: POLICKY, Jennifer L.; GREENE, Barrie D.;
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APPLICANT: BURFORD, Neil; ISON, Craig H.;
APPLICANT: LEE, Ernestine A.; DING, Li;
APPLICANT: DAS, Debopriya; KALLICK, Deborah A.;
APPLICANT: KHAN, Farrah A.; SEILHAMER, Jeffrey J.;
TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
FILE REFERENCE: PI-0183 USN
CURRENT APPLICATION NUMBER: US/10/343,903
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: PCT/US01/24217
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/231,434
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/230,067
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/228,140
PRIOR FILING DATE: 2000-08-25
PRIOR APPLICATION NUMBER: 60/226,410
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 60/224,456
PRIOR FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 60/223,269
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PERL program
SEQ ID NO 33
LENGTH: 6369
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 2798241CB1
US-10-343-903-33

Alignment Scores:
Pred. No.: 0 Length: 6369
Score: 8422.00 Matches: 1641
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.94% Mismatches: 0
Query Match: 99.95% Indels: 0
DB: 49 Gaps: 0

US-10-090-458-5 (1-1642) x US-10-343-903-33 (1-6369)
Qy 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLys 20
Db 1238 ATGTCCTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGACATTTCTACTGAAG 1297
Qy 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 1298 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCCTTTTCCACTA 1357
Qy 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 1358 TTTTATTTTGGTTAATTAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 1417
Qy 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 1418 GTGCCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAATCTAATCTTGG 1477
Qy 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100

Db 1478 TATACTCCAGTGACTAATATTACAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 1537
Qy 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 1538 CCTGATGTCATAATTACTGAGAAATATACAAATGAAAAAGAAATGTTAAACATCCAGTCTC 1597
Qy 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 1598 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTTCAAGACATCCATGCTTATGAACTCGT 1657
Qy 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 1658 TTTTTCCTGATATGATTCAGTATCTTCTATTTATATGGAATTCAGAGCTGGCTGTCTCA 1717
Qy 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 1718 AAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTCACAGTTTACAAAGCATCCATA 1777
Qy 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTyrLysGluLeuGluSerThr 200
Db 1778 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTTGAAGAGAGCTGGAGTCAACT 1837
Qy 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 1838 AAAGCTGTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGAGTA 1897
Qy 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db 1898 ATTTTAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACCTTTTGGCAATTCATATC 1957
Qy 241 ValAlaGluLysGluLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 1958 GTAGCAGAAAAAGAAAAATAAAGAAATTTTAAAGATAAATGGGACTTTCATGATACT 2017
Qy 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 2018 GCCTTTGGCTTTCTCTGGGTCTTCTATATACAAAGTTTAATTTTCTTATGTCCTTCTT 2077
Qy 281 MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe 300
Db 2078 ATGGCAGTCATTGGCAGCAGCTTCTTTGTTATTTCCTCAAAGTAGCAGCATTTGATATTT 2137
Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 2138 CTGCTTTTCTTTTATGGAATTATCATCTGTATTTTGTCTTAAATGCTGACACCTCTT 2197
Qy 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
Db 2198 TTTAAAAAATCAAACATGCGGAATAGTTGAATTTTGTACTGTGGCTTTTGGATTT 2257
Qy 341 IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer 360
Db 2258 ATTGGCCTTATGATAATCCTCATAGAAAAGTTTTTCCCAAATCGTTAGTGTGGCTTTTCAGT 2317
Qy 361 ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
Db 2318 CCTTTCTGTCACTGTACTTTTGTGATTGGTATTGACAGGTCATGCATTTTAGAAGATTTT 2377
Qy 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
Db 2378 AATGAAGGTGCTTCAATTTCAAATTTGACTGACGGCCCATATCTCTAATATTACAAT 2437
Qy 401 IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal 420
Db 2438 ATCATGCTCACACTTAATAGTATATTCTATGTCTCTCTGCTGTCTATCTTGTATCAAGTC 2497
Qy 421 IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp 440
Db 2498 ATTCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATGG 2557
Qy 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460

QY 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
Db 2994 CATTGAGAAAGGACTATGTTTTGGCAGCTGTTTTCAACAGTACTATGGTTTATCTTA 3053
QY 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
Db 3054 CCTATATTAGTGAATATCATTTAGTAACTACTATCTTTATCATTTAAATGTGACTGAAACC 3113
QY 1001 IleGlnIleTyrSerThrProPhePheGlnGluIleThrAspIleValPheLysIleGlu 1020
Db 3114 ATCCAGATCTGGAGTACCCCATTTCTTCAAGAAATTAAGTATAGTTTTTAAATGAG 3173
QY 1021 LeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAla 1040
Db 3174 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTGTTACTGCAATGCCACCTTACTTTGCC 3233
QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
Db 3234 ATGGAAATGCGAGAGATCATTAAGATCAAGCTTATACTCAACTTAAACTTTCAGGTCTT 3293
QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIle 1080
Db 3294 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTGATATCCCTTATTTTTTATCATTT 3353
QY 1081 LeuIleLeuMetIleuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
Db 3354 CTTATTTTGATGCTAGGAAGCTTATTGGCATTTCATTATGGATTATATTTTTTATACTGTA 3413
QY 1101 LysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThr 1120
Db 3414 AAGTTCTCTGCTGCTGTTTTTTGCCCTTATTGGTTATGTTCCATCAGTTATTTCTGTTCACT 3473
QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
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QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
Db 3534 TATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTTCTTTATGGGATAC 3593
QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
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QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
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Db 3714 TATAATCCATGGGATAGGCTTTCAGTAGCTGTTATATCGCCTTACCTGCAGTGTGTAAGT 3773
QY 1221 TrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGlyArgSerIleArgLysAsp 1240
Db 3774 TGGATTTTCTCTTACAATACTATAGAAAAAATATGAGGAGATCAATAAGAAAAAGAT 3833
QY 1241 ProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
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QY 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
Db 3954 TGCCAGTGTGTGAGGAGAAACCATCCATTATGTTGTCAGCAATTTGCATAAAGAAATATGAT 4013
QY 1301 AspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyrIleSer 1320
Db 4014 GACAAGAAAGATTTTCTTCTTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATACATCTCT 4073

QY 1321 PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340
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QY 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380
Db 4194 GATTATTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGTGTATGGGTACTGTCTCT 4253
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Db 4254 CAGATAAACCCCTTTGTGGCCAGATACATACATTGCAGGAACATTTTGAATTTATGGAGCT 4313
QY 1401 ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
Db 4314 GTCAAAGGAATGAGTGCAGTGCATGAAAGAGTCAATAGTCGAATAACACATGCACIT 4373
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Db 4374 GATTTAAAGAAACATCTTTCAGAGACTGTAAAGAAACTACCTGCAGGAATCAACCGAAAG 4433
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db 4434 TTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGTAGATGAACCATCT 4493
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
Db 4494 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAATGCAATTTAAA 4553
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QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
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QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540
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QY 1581 GlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600
Db 4854 CAATCTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGGCATTGAAGATATAGCTTT 4913
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QY 1641 ValPhe 1642
Db 5034 GTATTT 5039

RESULT 2
US-10-343-903-33
; Sequence 33, Application US/10343903
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	8426	100.0	5475	44	US-10-090-458-4
2	8422	100.0	6369	49	US-10-343-903-33
3	8422	100.0	6369	78	US-60-223-269-15
4	8422	100.0	6525	43	US-10-005-338B-1
5	8395	99.6	4929	41	US-09-971-121-1
6	8395	99.6	5262	41	US-09-971-121-5
7	8309	98.6	4917	44	US-10-090-458-3
8	8309	98.6	5463	44	US-10-090-458-1
9	8253.5	98.0	5004	1	PCT-US03-33087-82
10	8112	96.3	4785	41	US-09-971-121-3
11	8028.5	95.3	6170	1	PCT-US03-14026-75
12	7377	87.6	5595	102	US-60-453-050-2441
13	7377	87.6	5595	102	US-60-453-135-2441
14	7377	87.6	5595	103	US-60-466-412-2441
15	4930.5	58.5	3347	45	US-10-108-260A-160
16	4847.5	57.5	3268	44	US-10-094-749-984
17	4382.5	52.0	3448	45	US-10-144-771-16659
18	4382.5	52.0	3448	93	US-60-360-207-16659
19	4311	51.2	3368	74	US-60-185-213-1454
20	4272	50.7	2573	78	US-60-226-176-242
21	4272	50.7	2573	79	US-60-233-468-242
22	4272	50.7	2573	88	US-60-313-371-241
23	4265	50.6	2926	74	US-60-185-213-1628
24	4265	50.6	2926	84	US-60-278-232-4057
25	3672	43.6	2987	78	US-60-226-176-241
26	3672	43.6	2987	79	US-60-233-468-241
27	3672	43.6	2987	88	US-60-313-371-241
28	3656	43.4	2988	78	US-60-226-176-237
29	3656	43.4	2988	79	US-60-233-468-237
30	3654	43.4	2109	88	US-60-313-371-237
31	3654	43.4	2109	78	US-60-226-176-240
32	3654	43.4	2109	79	US-60-233-468-240
33	3654	43.4	2109	88	US-60-313-371-240
34	3283.5	39.0	2502	20	US-09-496-914A-3176
35	3283.5	39.0	2502	24	US-09-560-875A-3176
36	3266	38.8	4902	1	PCT-US03-30720-38
37	3259	38.7	5797	1	PCT-US02-33496-1
38	3259	38.7	5926	1	PCT-US03-28227-2563
39	3234	38.4	5445	1	PCT-US03-33087-108
40	3234	38.4	6181	43	US-10-005-338B-4
41	3229	38.3	5722	46	US-10-171-423-3
42	3200.5	38.0	4875	44	US-10-090-454-3
43	3200.5	38.0	5018	44	US-10-090-454-1
44	3197.5	37.9	5981	43	US-10-005-338B-3
45	3195	37.9	5311	1	PCT-US02-41825-88

ALIGNMENTS

RESULT 1
US-10-090-458-4
; Sequence 4, Application US/10090458
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun

; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090,458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 25
; OTHER INFORMATION: n = A,T,C or G
US-10-090-458-4

Alignment Scores:
Pred. No.: 0
Score: 8426.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 44
Length: 5475
Matches: 1642
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-090-458-5 (1-1642) x US-10-090-458-4 (1-5475)
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QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGlnLeuLeuPheProLeu 40
DB 174 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTTCTTTTCCACTA 233
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
DB 234 TTTTGTGTTTGGTTAATTAATAGCATGTGTCATCCAAATAAGAAATATGAGAA 293
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
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QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
DB 354 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 413
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
DB 414 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAGAAATGTTTAAACATCCAGTCTC 473
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
DB 474 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTCAGAGACTCCATGTCTTATGAATTCGT 533
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
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QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
DB 594 AAATCATGTGAGGCTGCTCAGTACTGCTCCTCAGGTTTTCACAGTTTACAGCATCCATA 653
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QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
DB 714 AAAGCTGTATTATGGGAGAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 773
QY 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 12, 2004, 21:29:55 ; Search time 7298 Seconds
(without alignments)
7916.636 Million cell updates/sec

Title: US-10-090-458-5
Perfect score: 8426
Sequence: 1 MSTAIREVGVWRQTRILLK.....CGTLNSTLWERTQEDRVVF 1642

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 37577330 seqs, 17593059518 residues
Total number of hits satisfying chosen parameters: 75154660

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Db GACCTAAGTATATTGATTACCACCATG-----GTATGGTTCCTTCA 3492
QY 1177 TyrProLeuLeuGlyCysLeuIleSerPheIleIleIleSerTrpLysAsnValArgLys 1196
Db TATACCTTGCTTGA---TTTAAACTTTTGGAGTG-----AGA 3531
QY 1197 AsnValAspThrTyrAsnProTrpAspArgLeuSer----- 1208
Db GACGAGGAGCACTACAGAGAATTTCAGAGGCAAAATTTGAATTGAGTGCCACTGATTTT 3591
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QY 1249 LysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspVal 1268
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QY 1269 LysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysPro 1288
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Job time : 1339 secs

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; Publication No. US20020173004A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Le Bihan, Stephane
; APPLICANT: Kulhanek, Barbara
; TITLE OF INVENTION: NOVEL ABCA6 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.404
; CURRENT APPLICATION NUMBER: US/10/090,453A
; NUMBER FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4854
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-090-453A-3

Alignment Scores:
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Score: 3117.00 Matches: 687
Percent Similarity: 61.08% Conservative: 330
Best Local Similarity: 41.26% Mismatches: 554
Query Match: 36.99% Indels: 94
DB: 13 Gaps: 33

US-10-090-458-5 (1-1642) x US-10-090-453A-3 (1-4854)

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Qy 160 -----SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrVal 175
Db 472 GATGGATATGGTGAGTTTTTCATGTACATTGACCAATACTGGAATAGAGGATTTGTGGCT 531
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Db 2645 CAGACAGCT---GTGAGTGACATGGGCTCTGGAGATGCAAGTCTTTGCCATGGCAGG 2701
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Db 2750 TTATTGGTATTGGGAATCGCAATATTCCCTTTGATTGTTGAAAATATAATATATGCTATG 2809
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Db 3041 AAACAAAAGGATTATAGATTTTCAGTTGTGTGTAATACCAAGAGATTCGACTGTTTTCCA 3100
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QY 1022 TyrPheGlnAlaAlaLeuGlyIleIleValThrAlaMetProProTyrPheAlaMet 1041
Db 3215 CCGGATGGTTCTCTTTCTTATTTTGGTCTATGTAGCATTTCTCTTATATACCCATG 3274
QY 1042 GluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeu 1061
Db 3275 GGCAGCATCAGTGATTACAAGAAAAATGCTAAGTCCAGCTATGATTTTCAGGCCTCTAC 3334
QY 1062 ProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeu 1081
Db 3335 ACTTCTGCTTACTGCTGGTGGCAGGCACCTAGTGGACGTCAGCTTCTTCAATTTAATCTC 3394
QY 1082 IleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLys 1101
Db 3395 CTTTAAATG-----TATTTAATTTTCTACATAGAAAAACATGCAGTACCTTCTTATT 3445
QY 1102 PheLeuAlaValPheCysLeuIle-----GlyTyrValProSerValIle 1117
Db 3446 ACAAGCCAAATGTGTTGCTTTTGGTTATAGTTACTCTCTGGTTATGACGCTTCTCTTGT 3505
QY 1118 LeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrp 1137
Db 3506 TTCTTCATATATATGATATCATTTTATTTTCGCAAAAGGAGAAAAAACAGTGGCCTTTGG 3565

QY 1138 SerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePhe 1157
Db 3566 TCATTTTACTTCTTTTTCCTCCACCATCATGTTTTCATCATCTTTAATCAATCATTTT 3625
QY 1158 ---MetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIle 1176
Db 3626 GACCTAAGTATATTGATTACCACCATG-----GTATTGGTTCCTTCA 3667
QY 1177 TyrProLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLys 1196
Db 3668 TATACCTTGTCTGGA---TTTAAAACTTTTGGAAAGTG-----AGA 3706
QY 1197 AsnValAspThrTyrAsnProTrpAspArgLeuSer----- 1208
Db 3707 GACCAGGAGCACTACAGAGAAATTTCCAGAGGCAAATTTTGAATTGAGTGCCACTGATTTT 3766
QY 1209 ValAlaValIleSerProTyrLeuGlnCysValLeuTyrIlePheLeuLeuGlnTyr 1228
Db 3767 CTAGTCTGCTTCATACCTACTTTTCAGACTTTTGCTATTCTGTTTGTCTTAAGATGCATG 3826
QY 1229 GluLysLysTyrGlyArgSerIleArgLysAspProphePheArgAsnLeuSerThr 1248
Db 3827 GAACATAAATGTGGAAGAAAGAAATGCGAAAGATCCTGTTTTCAGA---ATTTCCTCCC 3883
QY 1249 LysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspVal 1268
Db 3884 CAAAGTAGAGATGCTAAG---CCAAATCCAGAGAACCCCATAGATGAAGATATT 3940
QY 1269 LysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysPro 1288
Db 3941 CAAACAGAAAGAAATAAGAACAGCCACTGCTCTGACCCTTCTCAATCTTAGATGAGAAACCT 4000
QY 1289 SerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSer 1308
Db 4001 GTTATAATTGCCAGCTGTCTACACAAAGAATATGCAGGCCAGAGAAAGTTGCTTTTCA 4060
QY 1309 ArgLysValLysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluIle 1328
Db 4061 AAGAGGAAGAAAGAAATAGCAGCAAGAAATATCTCTTTCTGTGTTCAAGAAGTGAAATT 4120
QY 1329 LeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGly 1348
Db 4121 TTGGGATTGTAGGACCCAGTGGTGTCTGGAAAAAGTTTCATCTATTAGATATCTGGG 4180
QY 1349 AspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGlu 1368
Db 4181 ATCACAAGCCAACTGCTGGAGAGGTGGAACCTGAAAGGCTGCAGTTCA----- 4228
QY 1369 AspAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrpProasp 1388
Db 4229 -----GTTTGGGCCACCTGGGGTACTGCCCTCAAGAGAACGCTGTGTGGCCCATG 4279
QY 1389 ThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAsp 1408
Db 4280 CTGACGTTGAGGGAACACCTGGAGGTGTATGCTGCCCTCAAGGGGCTCAGGAAAGCGGAC 4339
QY 1409 MetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLys 1428
Db 4340 GCGAGGCTCGCCATCGCAAGATTAGTGAGTGCTTTCAAACCTGCATGAGCAGCTGAATGTT 4399
QY 1429 ThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeu 1448
Db 4400 CCTGTGCAGAAATTAACAGCAGGAATCAGAGAAAGTTGTGTTTGTGTGAGCCTCCTG 4459
QY 1449 GlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLysAlaLys 1468
Db 4460 GGAAACTCACCTGTCTTGTCTCTGGATGAACCATCTACGGGCATAGACCCACAGGGCAG 4519
QY 1469 GlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaIleLeu 1488
Db 4520 CAGCAAATGTGGCAGGCAATCCAGGCAGTCGTTAAAAACACACAGAGAGAGGTGTCTCCTG 4579
QY 1489 ThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMetValSer 1508

Db 362 AATCTGGGAAGGTAGATAAATTTAATAGCTCTTCTTTAATGGTTGTGTATACACCAATA 421
Qy 85 ThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu-----Pro 101
Db 422 TCTAATTTAACCCAGCAGATAATGAATAAACACGACCTTGCTCCTCTTTTGAAGGAACA 481
Qy 102 AspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSer 121
Db 482 AGTGTCAATGGGCACCAATAAAACACACATGGACGAATACTTCTGGAAAATTTACCA 541
Qy 122 LysProSerAsnPheValGlyValPheLysAspSerMetSerTyrGluLeuArgPhe 141
Db 542 TATGCT-----ATGGGAATCATCTTTAATGAACTTCTCTTATAAGTTAATATTT 592
Qy 142 PheProAspMetIleProValSerSerIleTyrMet---AspSerArgAlaGlyCys--- 159
Db 593 TTCCAGGGATAT-----AACAGTCCACTTTGGAAAGAAAGATTCTCAGCTCATTTGCTGG 646
Qy 160 -----SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrVal 175
Db 647 GATGATATGGTGAGTTTTCATGTACATTGACCAATACTGGAATAGAGGATTTGTGGCT 706
Qy 176 LeuGlnAlaSerIleAspAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLys 195
Db 707 TTACAAACAGCTATTAAATCTGCCATTATAGAAATCACAACCAATCACCCCTGTGATGGAG 766
Qy 196 GluLeuGluSerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThr 215
Db 767 GAGTTGATGTCAGTTACTGCTATAAATACTATGAAGACATFACCTTTTCATAACTAAAAATCTT 826
Qy 216 PheProArgGlyValIleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPhe 235
Db 827 CTTCAAAATGAGATGTTTATTATTATCTTCTGTGCTTCATTTCTCCCACTTCGTATATTT 886
Qy 236 LeuAlaIleHisIleValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMet 255
Db 887 ATATCACTCAATGTAAACAAAGAGAGA---AAAAAGCTAAGAATTGTGATGAAAATGATG 943
Qy 256 GlyLeuHisAspThrAlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePhe 275
Db 944 GGTCCTCCAAGATTTCAGCATTCCTGCTCTCCTGGGCTCTAATCTATGCTGGCTTCATCTTT 1003
Qy 276 LeuMetSerLeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSer 295
Db 1004 ATTATTTCCATATTTCATTACAAATTATCATACATTCACCCAAATTATAGTCAGCTGGC 1063
Qy 296 SerIleValIlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeu 315
Db 1064 TTCATGGTCATATTTATACTCTTTTATATATGGCTATCTTTGGTAGCTTGGTGTTC 1123
Qy 316 MetLeuThrProLeuPheLysSerLysHisValGlyIleValGluPhePheValThr 335
Db 1124 CTGATGAGTGTGCTGTTAAAGAAAGCTGTCTCCACCAATTGGTTGTGTTTCTCCTTACC 1183
Qy 336 ValAlaPheGlyPheIleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeu 355
Db 1184 CTCTTTGGGGATGTCTGGGA---TTCACTGTATTTTATGAACAACTTCCTTCATCTCTG 1240
Qy 356 ValTrpLeuPhe-----SerPropheCysHisCysThrPheValIleGlyIleAla 372
Db 1241 GAGTGGATTTTGAATATTTGTAGCCCTTTT-----GCCTTTACTACTGGAATGATT 1291
Qy 373 GlnValMetHisLeuGluAspPheAsn---GluGlyAlaSerPheSerAsnLeuThrAla 391
Db 1292 CAGATTATCAAACCTG---GATTATAACTTGAATGGTGTAATTTTTCCTGACCCCTTCAGGA 1348
Qy 392 GlyProTyrProLeuIleIleThrIleIleMetLeuThrLeuAsnSerIlePheTyrVal 411
Db 1349 GACTCATATACAATGATAGCAACTTTTCTATGTTGCTTTTGGATGGTCTCATCTACTTG 1408
Qy 412 LeuLeuAlaValTyrLeuAspGlnValIleProGlyGluPheGlyLeuArgArg----- 429

Db 1409 CTATTGGCATTATACTTTTGACAAAAATTTTACCC-----TATGGAGATGAGCGCCATTAT 1462
Qy 430 SerSerLeuTyrPheLeuLysProSerTyrTrpSerLysSerLysArgAsnTyrGluGlu 449
Db 1463 TCTCCTTTATTTTCTTGAATTCATCATCTTGTGTTTCCAACACCAAGGACTAATGCTAAG 1522
Qy 450 LeuSerGluGlyAsnValAsnGlyAsnIleSerPheSerGluIleIleGluProValSer 469
Db 1523 GTTATTGAGAAAGAAATCGATGCTGAGCATCCCTCTGATGATTATTTTGAACCCAGTAGCT 1582
Qy 470 SerGluPheValGlyLysGluAlaIleArgIleSerGlyIleGlnLysThrTrpArgLys 489
Db 1583 CCTGAATTCGAAGGAAAAGAGCCCATCAGAATCAGAAATGTTAAGAAGGAATATAAGGA 1642
Qy 490 LysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIle 509
Db 1643 AAATCTGGAAAAAGTGAAGCATTGAAGGCTTGCTCTTTGACATATATGAAGGTCAAATC 1702
Qy 510 ThrAlaLeuLeuGlyHisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGly 529
Db 1703 ACGGCAATCCTGGGTACACAGTGGAGCTGGCAAATCTTCACTGCTAAATATTTCTTAATGA 1762
Qy 530 LeuCysProProSerAspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAsp 549
Db 1763 TTGTCTGTTCCAACAGAGGATCAGTTACCATCTATAATAAAAAATCTCTCTGAAAATGCAA 1822
Qy 550 GluMetPheGluAlaArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAsp 569
Db 1823 GACTTGGAGGAATCAGAAAGATAAAGTGGCGTCTGCTCTCAATTCATGTTCAATTTGAC 1882
Qy 570 ValLeuThrValGluGluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsn 589
Db 1883 ATACTCACCGTGAAGGAAAACCTCAGCCTGTTTGTCTAAAATAAAGGGATTTCATCTAAAG 1942
Qy 590 AsnIleIleGlnGluValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLysAsp 609
Db 1943 GAAGTGAACAAGAGGTACACGAATATTATTGGAATTGGACATGCAAAACATTCAGAT 2002
Qy 610 AsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaVal 629
Db 2003 AACCTTGCTAAACATTTTAAGTGAAGGACAGAAAAGAAAGCTGACTTTTGGGATTACCATT 2062
Qy 630 LeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSer 649
Db 2063 TTAGGAGATCCTCAAATTTTGTCTTTTAGATGAACCAACTACTGGATTGGATCCCTTTTCC 2122
Qy 650 ArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsnArgValThrValPheSer 669
Db 2123 AGAGATCAAGTGTGGAGCCTCCTGAGAGAGCGTAGAGCAGATCATGTGATCCTTTTCAGT 2182
Qy 670 ThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGly 689
Db 2183 ACCCAGTCCATGGATGAGGCTGACATCCTGGCTGATAGAAAAGTGCATCATGTCGAATGGG 2242
Qy 690 MetLeuLysCysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArg 709
Db 2243 AGACTGAAGTGTGCAGGTTCTTCTATGTTTGTGAAAAAGAGGTGGGTCTTGGATATCAC 2302
Qy 710 LeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeuSerSerLeuValLysGln 729
Db 2303 CTAAGTTTACATAGGAATGAAATATGTAAACCCAGAACAAATAACATCCTTTCATTACTCAT 2362
Qy 730 HistleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeuPro 749
Db 2363 CACATCCCCGATGCTAAATTAAAAACAGAAAACAAAGAAAGCTTGTATATATACITTGCCA 2422
Qy 750 PheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeuAspSerHisSerAsnLeu 769
Db 2423 CTGGAAGGACAAATACATTTCCAGATCTTTTTCAGTGATCTGGATAAGTGTCTTGACCAG 2482
Qy 770 GlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLysLeuGlu 789
Db 2483 GGAGTGACAGGTTATGACATTTCCATGTCAACTCTAAATGAAGTCTTTTATGAAGAACTGGAA 2542

Db 3642 GGCACCATGTTA-----ATACCTCCCTTCACATGATGGCTCT 3680

Qy 1183 LeuIleSerPheIleLysIleSer-----TrrLysAsnValArgLysAsn 1197

Db 3681 CTATTCAATTTTCTGAGATTCTCTGATTCCATGGATTACTTAGGAGTTCAGAACTCT 3740

Qy 1198 ValAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGln 1217

Db 3741 GAAATGTATAC-----CTGGCACTGTAAATACCTTACCTTCAT 3779

Qy 1218 CysValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIle 1237

Db 3780 TTTCTCATTTTCTTTTCATTTCTGCGATGCGCTAGAAATGAACTGCAGGAAGAACTAATG 3839

Qy 1238 ArgLysAspPropPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGlu 1257

Db 3840 AGAAAGGATCCTGTGTTTCA--ATTCTCCAAGAAGC---AACGCTATTTTTCCAAC 3893

Qy 1258 ProProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGlu 1277

Db 3894 CCAGAAGAGCCTGAAGGAGAGGAGGAAGATATCCAGATGGAAGAATGAGAACAGTGAAT 3953

Qy 1278 LeuMetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLys 1297

Db 3954 GCTATGGCTGTGCGAGACTTTTGATGAGACACCCGTCATCATTCGACGCTGTCTACGGAAG 4013

Qy 1298 GluTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLys 1317

Db 4014 GAATATGCAGGCACAAAGAAAAAATGCTTTTCTAAAAGGAAGAAACAATTGCCACAAGA 4073

Qy 1318 TyriIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAla 1337

Db 4074 AATGCTCTTTTGTGTTAAAAAAGGTGAAGTTATAGGACTGTTAGGACACAATGGAGCT 4133

Qy 1338 GlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnVal 1357

Db 4134 GGTAAAAGTACAACACTATTAAAGATGATAACTGGAGACACAAACCAACTGCAGACAGGTG 4193

Qy 1358 PheLeuGlyAspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGly 1377

Db 4194 ATTTTG-----AAAGGGAGCGGTGGAGGGAAACCCCTGGGCTTCTCTGGGG 4238

Qy 1378 TyrCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIle 1397

Db 4239 TACTGCCTCAGGAGAAATCGCTGTGGCCCAACCTGACAGTGAGGACACCTGGAGGTG 4298

Qy 1398 TyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThr 1417

Db 4299 TACGCTCCGTGAAGGTCTCAGGAAGGGGACCGCAATGATCGCCATCACACGCTTAGTG 4358

Qy 1418 HisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIle 1437

Db 4359 GATCGCTCAAGCTGCAGGACCACTGAAGGCTCCCGTGAAGACCTTGTTCAGAGGAATA 4418

Qy 1438 LysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAsp 1457

Db 4419 AAGCGAAAGCTGCGCTTTGTGCTGAGCATCCTGGGGAAACCCGTCAGTGGTGTCTTGGAT 4478

Qy 1458 GluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThr 1477

Db 4479 GAGCCGTCGACCCGGGATGGACCCCGAGGGGCAGCAGCAAAATGTGGCAGGTGATCGGGCC 4538

Qy 1478 AlaPheLysAsnArgLysArgAlaIleLeuThrThrHisTyrMetGluGluAlaGlu 1497

Db 4539 ACCTTTAGAAAACACGGAGAGGGGCGCCCTCCTGACCCACCCACTACATGGCAGAGGCTGAG 4598

Qy 1498 AlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrVal 1517

Db 4599 GCGGTGTGTGACCGAGTGGCCATCATGTGTGTCAGGAAGGCTGAGATGTATGGTTCATC 4658

Qy 1518 GlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrp 1537

Db 4659 CAACACCTGAAAAGCAAAATTTGGCAAAAGACTACCTGCTGAGATGAAGTGAAG----- 4712

Qy 1538 IleGluAsnLeu---GluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsn 1556

Db 4713 -----AACCTGGCACAAATGGAGCCCTCCATGCAGAGATCCTGAGGCTTTTCCCCCAG 4766

Qy 1557 AlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspVal 1576

Db 4767 GCTGCTCAGCAGGAAAGGTCTCTCCCTGATGGTCTATAAGTTGCCCTGTGAGGATGTG 4826

Qy 1577 GlnSerLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPheAlaIleGlu 1596

Db 4827 CGACCTTTATCACAGGCTTCTTCAAATTAGATAGATTAAACAGAGATTTCGACCTGGAG 4886

Qy 1597 GluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGln 1616

Db 4887 GAGTACAGCCTCTCACAGTCTACCTGGAGCAGGTTTCTTGAGCTCTCCAAGGAGCAG 4946

Qy 1617 Glu-----GluGluAsp 1620

Db 4947 GAGCTGGGTGATCTTGAAGAGGAC 4970

RESULT 14

US-10-005-338B-2

Sequence 2, Application US/10005338B

Publication No. US20030044895A1

GENERAL INFORMATION:

APPLICANT: DENEFELE, Patrice

APPLICANT: ROSIER-MONTUS, Marie-Francoise

APPLICANT: PRADES, Catherine

APPLICANT: ARNOULD-REGUIGNE, Isabelle

APPLICANT: DUVERGER, Nicolas

APPLICANT: ALLIKMETS, Rando

APPLICANT: DEAN, Michael

TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENE

TITLE OF INVENTION: CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF

FILE REFERENCE: ABCA5, 6, 9, 10

CURRENT APPLICATION NUMBER: US/10/005,338B

CURRENT FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: US 60/263,231

PRIOR FILING DATE: 2001-01-23

PRIOR APPLICATION NUMBER: FR 00403440.1

PRIOR FILING DATE: 2000-12-07

NUMBER OF SEQ ID NOS: 217

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 5296

TYPE: DNA

ORGANISM: Homo sapiens

US-10-005-338B-2

Alignment Scores:

Pred. No.: 9.46e-246 Length: 5296

Score: 3124.00 Matches: 688

Percent Similarity: 61.14% Conservative: 330

Best Local Similarity: 41.32% Mismatches: 553

Query Match: 37.08% Indels: 94

DB: 14 Gaps: 33

US-10-090-458-5 (1-1642) x US-10-005-338B-2 (1-5296)

Qy 5 IleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLysAsnTyrLeuIle 24

Db 182 ATGAACAGAAAGCGTGTATCAGCAACCAAGCACTTCTGTGCAAGAATTTCTTAAG 241

Qy 25 LysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeuPhePheLeuPhe 44

Db 242 AAATGGAGGATGAAAGAGAGAGCTTATTGGAATGGGGCTCTCAATACTTCTAGGACTG 301

Qy 45 TrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGluValProAsnIle 64

Db 302 TGTATTGCTCTGTTTCCAGTCCATGAGAAATGTCCAGTTTCTTGGAAATGGCTCCTCAG 361

Qy 65 GluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProVal 84

Db 4749 CTGAGGCTTTTCCCCCAGGCTGCTCAGCAGGAAGGTTCTCCTCCCTGATGGTCTATAAG 4808
QY 1571 IleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeuGluAlaLys 1590
Db 4809 TTGCCCTGTGAGGATGTGCGACCTTATCAGAGCTTTCTCAAAATTAGAGATAGTAA 4868
QY 1591 HisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheVal 1610
Db 4869 CAGAGTTTCGACCTGGAGGAGTACAGCTCTCACAGTCTACCTGGAGCAGGTTTCTCTG 4928
QY 1611 GluLeuThrLysGluGlnGlu-----GluGluAsp 1620
Db 4929 GAGCTCTCCAAGGAGCAGGAGCTGGGTGATCTTGAAGAGGAC 4970

RESULT 13
US-10-005-338B-3
; Sequence 3, Application US/10005338B
; Publication No. US20030044895A1
; GENERAL INFORMATION:
; APPLICANT: DENEFE, Patrice
; APPLICANT: ROSIER-MONTUS, Marie-Francoise
; APPLICANT: PRADES, Catherine
; APPLICANT: ARNOULD-REGUIGNE, Isabelle
; APPLICANT: DUVERGER, Nicolas
; APPLICANT: ALLIKMETS, Rando
; APPLICANT: DEAN, Michael
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENES
; TITLE OF INVENTION: CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF
; FILE REFERENCE: ABCA5, 6, 9, 10
; CURRENT APPLICATION NUMBER: US/10/005,338B
; PRIOR FILING DATE: 2001-12-07
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: FR 00403440.1
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 5981
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-005-338B-3

Alignment Scores:
Pred. No.: 1.05e-251 Length: 5981
Score: 3197.50 Matches: 690
Percent Similarity: 61.35% Conservative: 321
Best Local Similarity: 41.87% Mismatches: 562
Query Match: 37.95% Indels: 75
DB: 14 Gaps: 27

US-10-090-458-5 (1-1642) x US-10-005-338B-3 (1-5981)
QY 6 ArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLeuLysAsnTyrLeuIleLys 25
Db 153 AGACGCATGAGCGTGGGTGAGCAACATGGGCTCTTCTCTGCAAGAACTGTCTCAAAAAA 212
QY 26 CysArgThrLysLysSerSerValGlnGluIleLeuPhePro---LeuPhePheLeuPhe 44
Db 213 TGGAGAAATGAAAAGACAGACCTTGTGGAATGGCTCTTTTCATTTCTTCTGGTACTGTT 272
QY 45 TrpLeuIleLeuLeuSerMetMetHisProAsnLysLysTyrGluGluValProAsnIle 64
Db 273 CTGTACCTATTTTCTCCAAATTTACATCAAGTTTCATGACACTCTCAAAATGTCTTCAATG 332
QY 65 GluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProVal 84
Db 333 GATCTGGGACGTGTAGATAGTTTAAATGATATACTAATATGTTATGTCATTTGCACCTGAA 392
QY 85 ThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeuProAspValIle 104
Db 393 TCCAAAACACTACCCCAAGAGATAATGAACAAAGTGGCTTCAGCCCCCATTCCTAAAGGAAGA 452

QY 105 IleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLysProSer 124
Db 453 ACAATCATGGGTGGCTGATGAAAAAAGCATGATGAATGGATTTGAACATATTCAATA 512
QY 125 AsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArgPhe---PhePro 143
Db 513 GACGCACTGAGAGTCATCTTTACTGATACCTTCTCCTACCATTTGAAGTTTCTTGGGGA 572
QY 144 AspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCys----- 159
Db 573 CATAGAATCCCATGATGAAGAGCACAGAGACCATTCAGTCACTGTCAAGCAGTGAAT 632
QY 160 ---SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAla 178
Db 633 GAAAAAATGAAGTGTGAAGGTTGAGAGTTCTGGAGAAAGGCTTTGTAGCTTTTCAAGCT 692
QY 179 SerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGlu 198
Db 693 GCCATTAAATGCTGCTATCATAGAAATCGCAACAAATCATTCAGTGTGGAACAGCTGATG 752
QY 199 SerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArg 218
Db 753 TCAGTTACTGGTGTACATATGAAGATATTACCTTTTGTGGCCCAAGGAGGAGTTGCCAACT 812
QY 219 GlyValIleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIle 238
Db 813 GATTTTTCATTTCTTTTGCATATTCTTTTCTACATTTATATCTACTATGTATCAGTC 872
QY 239 HisIleValAlaGluLysGluLysIleLysGluPheLeuLysIleMetGlyLeuHis 258
Db 873 AATGTTACACAAGAAAGACAA---TACATTACGTTCATTGTGATGACAATGATGGGACTCCGA 929
QY 259 AspThrAlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSer 278
Db 930 GAGTCAGCATTTGGCTTTCTCTGGGTTTGATGTATGCTGGCTTCATCTTATCATGGCC 989
QY 279 LeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerIleVal 298
Db 990 ACTTTAATGGCTCTTATTGTAAATCTGCACAAATGTGCTGCTGACTGGTTTGTGATG 1049
QY 299 IlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThr 318
Db 1050 GTCTTCACCTCTTTCTCTCTATGGCTGTCTTTGTGATAACTTTAGCTTTCCTGATGAGT 1109
QY 319 ProLeuPheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPhe 338
Db 1110 GTGTTGATAAAGAAACCTTTCCTTACGGGCTTGGTTGTGTTCTCCTTATTGTCTTTGG 1169
QY 339 GlyPheIleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrp--- 357
Db 1170 GGGATCCTGGGATTTCCCA---GCATTGTATACACATCTTCTGCACTTTTGGAAATGGACT 1226
QY 358 -----LeuPheSerProPheCysHisCysThrPheValIleGlyIleAlaGlnValMet 375
Db 1227 TTGTGCTCTTCTAGCCCCCTTT-----GCCTTCACTGTTGGGATGGCCAGCTTATA 1277
QY 376 HisLeuGlu---AspPheAsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyr 394
Db 1278 CATTTGGACTATGATGTGAATTTCTAATGCCCACTTGGATTCT---TCACAAAAATCCATAC 1334
QY 395 ProLeuIleIleThrIleIleMetLeuThrLeuAsnSerIlePheThrValLeuLeuAla 414
Db 1335 CTCATAATAGCTACTCTTTTCATGTTGGTTTGTGACACCCCTCTGTTATTGTTGATGACA 1394
QY 415 ValTyrLeuAspGlnValIleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPhe 434
Db 1395 TTATATTTTGACAAAAATTTTGCCCGCTGAATATGGACATCGATGTTCTCCCTTGTTTTTC 1454
QY 435 LeuLysProSerTyrTrpSerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsn 454
Db 1455 CTGAAATCCTGTTTGTGTTTCAACACGGAAGGGCTAATCATGTGGTCTCTTGAGAAATGAA 1514

Db 513 GACGAGTGAGAGTCATCTTTACTGATACCTTCTCTACCATTTGAAGTTTCTTTGGGA 572
Qy 144 AspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCys----- 159
Db 573 CATAGAAATCCCATGATGAAGAGCACAGAGACCATTTCAGCTCAGTGTCAAGCAGTGAAT 632
Qy 160 ---SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAla 178
Db 633 GAAAAAATGAAGTGTGAAGGTTTCAGAGTTCTGGGAGAAAGGCTTTGTAGCTTTTCAAGCT 692
Qy 179 SerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGlu 198
Db 693 GCCATTAATGCTGCTATCATAGAAATCGCAACAATCATTCAGTGATGGAACAGCTGATG 752
Qy 199 SerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArg 218
Db 753 TCAGTTACTGGTGTACATATGAAGATATTACCTTTTGTGCCCCAAGGAGGAGTTGCAACT 812
Qy 219 GlyValIleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIle 238
Db 813 GATTTTTCATTTTCTTTTGCATATTCTTTTCTACATTTATATATACTATGATCAGTC 872
Qy 239 HisIleValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHis 258
Db 873 AATGTACACAAGAAAGACAA--TACATTACGTCAATGATGACAATGATGGACTCCGA 929
Qy 259 AspThrAlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSer 278
Db 930 GAGTCAGCATTTCTGGCTTTCTCGGGGTTTGTATGATGCTGGCTTCATCCTTATCATGGCC 989
Qy 279 LeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerIleVal 298
Db 990 ACTTTAATGGCTCTTATTGTAAAAATCTGCACAAATGTCGTCCTGACTGGTTTGTGATG 1049
Qy 299 IlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThr 318
Db 1050 GTCTTCACCCCTCTTTCTCTCTATGGCCTGTCTTTGATAAATTTAGCTTTTCTCGATGAGT 1109
Qy 319 ProLeuPheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPhe 338
Db 1110 GTGTTGATAAAGAAACCTTTCCTTACGGGCTTGGTGTGTTTCTCCTTATTGCTTTTGG 1169
Qy 339 GlyPheIleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrp--- 357
Db 1170 GGGATCCTGGGATTCCCA---GCATTGTATACACGCTCTCCTGCAATTTTGGAAATGGACT 1226
Qy 358 -----LeuPheSerPropheCysHisCysThrPheValIleGlyIleAlaGlnValMet 375
Db 1227 TTGTGTCTTCTTAGCCCCCTT-----GCCTTCACTGTGGGATGGCCAGCTTATA 1277
Qy 376 HisLeuGlu---AspPheAsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyr 394
Db 1278 CATTTGGACTATGATGTGAATTCTAATGCCCACTTGGATCT--TCACAAAATCCATAC 1334
Qy 395 ProLeuIleIleThrIleIleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAla 414
Db 1335 CTCATAATAGCTACTCTTTTTCATGTTGGTTTTTGGACACCCCTTCTGTATTTGGTATTGACA 1394
Qy 415 ValTyrLeuAspGlnValIleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPhe 434
Db 1395 TTATATTTTGACAAAATTTTGGCCGCTGAATATGGACATCGATGTTCTCCCTTGTTTTTC 1454
Qy 435 LeuLysProSerTyrTrpSerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsn 454
Db 1455 CTGAAATCCTGTTTTTGGTTTCAACACGGGAAGGCTAATCATGTGCTTCCAGAAATGAA 1514
Qy 455 ValAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPheValGly 474
Db 1515 ACAGATCTGATCCTACACCTAATGACTGTTTTGAACACAGTGTCTCCAGAAATCTGTGGG 1574
Qy 475 LysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyLeuAsnVal 494

Db 1575 AAAGAAGCCCATCAGAATCAAAAAATCTTAAAAAAGAATATGCAGGGAAGTGTGAGAGTA 1634
Qy 495 GluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGly 514
Db 1635 GAAGCTTTGAAAGGTGTGGTGTTTTGACATATATGAAGGCCAGATCACTGCCCTCCTTGGT 1694
Qy 515 HiserGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSer 534
Db 1695 CACAGTGGAGCTGGAANAACCTCCCTGTTTAAACATTTCTTAGTGGTGTGCAATCCAACA 1754
Qy 535 AspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAla 554
Db 1755 TCAGGTTCACTCACTGTCTATAATCACACACTTTCAAGAATGGCTGATATAGAAAAATATC 1814
Qy 555 ArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGlu 574
Db 1815 AGCAAGTTCAGTGGATTTTGTCCACAATCCAATGTGCAATTTGGATTTCTCACTGTGAAA 1874
Qy 575 GluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGlu 594
Db 1875 GAAAACCTCAGGCTGTTTGTCTAAAAATAAAGGGATTTTGCACATGAAGTGAGAGAAAGAG 1934
Qy 595 ValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLys 614
Db 1935 GTACAACGAGTTGTACAGGAATTAGAAATGGAATAATTTCAAGACATCCTTGTCTCAAAAC 1994
Qy 615 LeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLys 634
Db 1995 TTAAGTGGTGACAAATAAGGAACTAACTTTTGGGATTTGCCATTTTAGGAGATCCTCAA 2054
Qy 635 IleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleValTrp 654
Db 2055 GTTTTGTCTATTGGATGAACCGACTGCTGGATTGGATCCTCTTTCAAGGCCCGAATATGG 2114
Qy 655 AsnLeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPheMetAsp 674
Db 2115 AATCTCCTGAAAGAGGGGAATCAGACAGAGTAATTTCTTTCAGCACCCAGTTTATAGAT 2174
Qy 675 GluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLysCysVal 694
Db 2175 GAGCTGACATTTCTGGCGGACAGGAAGGTGTTTCATATCCAATGGGAAGCTGAAGTGTGCA 2234
Qy 695 GlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIle 714
Db 2235 GGCTCTTCTCTGTTCTTAAAGAAGAAATGGGGCATAGGCTACCATTTTAAGTTTGCATCTG 2294
Qy 715 AspLysTyrCysAlaThrGluSerLeuSerSerLeuValLysGlnHisIleProGlyAla 734
Db 2295 AATGAAAGGTGTGATCCAGAGAGTATAACATCACTGTTAAGCAGCACATCTCTGATGCC 2354
Qy 735 ThrLeuLeuGlnAsnAspGlnGlnLeuValTyrSerLeuProPheLysAspMetAsp 754
Db 2355 AAATTGACAGCACAAAGTGAAGAAAAAATTGTATATATTTTGCCTTTTGGAAAGGACAAAC 2414
Qy 755 LysPheSerGlyLeuPheSerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyr 774
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Qy 775 GlyValSerMetThrThrLeuGluAspValPheLeuLysLeuGluValGluAlaGluIle 794
Db 2475 GGTGTTTCCATAACAACCTTTGAATGAGGTGTTTCTGAAATTAGAAGGAAAAATCAACTATT 2534
Qy 795 AspGlnAlaAspTyrSerValPheThrGlnGlnProLeuGluGluMetAspSerLys 814
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Qy 815 SerPheAspGluMetGluGlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuVal 834
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Qy 835 SerThrMetSerLeuTrpLysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThr 854
Db 2652 AGTGGCGTGGCGCTCTGGAGGCAGCAGGTCTGTGCAATAGCAAAAGTTTCGCTTCTCTAAAG 2711

Db 3538 CTATTCATTTTTTCTGAGATT----- 3558
Qy 1203 ProTrpAspArgLeuSer-----ValAlaVal 1211
Db 3559 CCTCCTGATTCATGGATTCCCTTAGGAGCTTCAGAAATCTGATACTGCACACTG 3618
Qy 1212 IleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLys 1231
Db 3619 CTGATCCCTTACCTTTCATTTTCTCATTTTCTTTTCTGCGATCGCTAGAAATGAAC 3678
Qy 1232 TyrGlyGlyArgSerIleArgLysAspProPhePheArgAsnLeuSerThrLysSerLys 1251
Db 3679 TGCAGGAAGAAACTAATAGAAAGGATCCTGTGTTTCAGA--ATTCTCCAAGAAGC--- 3732
Qy 1252 AsnArgLysLeuProGluProProAspAsnGluAspGluAspGluAspValLysAlaGlu 1271
Db 3733 AACGCTATTTTCCAAACCCAGAGAGCCTGAAGGAGAGGAGAGATATCCAGATGGAA 3792
Qy 1272 ArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysProSerIleMet 1291
Db 3793 AGAATGAGAACAGATGAATGCTATGGCTGTGCGAGACTTGTATGAGACACCCGTCATCAT 3852
Qy 1292 ValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArgLysVal 1311
Db 3853 GCAGCTGTCTACGGAAGGAATATGCAGGCCAAAGAAAAATTGCTTTTCTAAAAGGAAG 3912
Qy 1312 LysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeu 1331
Db 3913 AAAACAATTGCCACAAGAAATGTCTCTTTTGTGTAAAAAAGGTGAAGTATAGGACTG 3972
Qy 1332 LeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGlu 1351
Db 3973 TTAGGACACAATGGGGCTGGTAAAGTACAACCTATTAAAGATGATACTGGAGACACAAA 4032
Qy 1352 ProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAspAsp 1371
Db 4033 CCAACTGCAGGACAGGTGATTTTG-----AAAGGGAGCGGTGGAGGGAA 4077
Qy 1372 SerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeu 1391
Db 4078 CCCCTGGGCTTCCTGGGTACTGCCCTCAGGAGATGCGCTGTGGCCCAACCTGCACAGTG 4137
Qy 1392 GlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGlu 1411
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Qy 1412 ValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLys 1431
Db 4198 GCCATCACACGGTTAGTGATGCGCTCAAGCTGCAGGACCAGCTGAAGGCTCCCGTGAAG 4257
Qy 1432 LysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnPro 1451
Db 4258 ACCTTGTCAGAGGGAATAAAGCGAAAGCTGTGCTTGTGCTGAGCATCCTGGGAAACCCG 4317
Qy 1452 GlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMet 1471
Db 4318 TCAGTGGTGTCTTCTGGATGAGCCGTCGACCCGGATGACCCCGAGGGSCAGCAGCAATG 4377
Qy 1472 TrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThrThrHis 1491
Db 4378 TGGCAGGTGATTCCGGGCCACCTTTAGAAACACGAGAGGGGCGCCCTCTGACCCACCAC 4437
Qy 1492 TyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeu 1511
Db 4438 TACATGGCAGAGGCTGAGCGGTGTGTACCCAGTGGCCATCATGTGTGTGAGGAAGGCTG 4497
Qy 1512 ArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGlu 1531
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Qy 1532 IleLysLeuLysAspTrpIleGluAsnLeu---GluValAspArgLeuGlnArgGluIle 1550
Db 4558 ATGAAGCTGAAG-----AACCTGGCACAAATGGAGCCCTCCATGCAGAGATC 4605

Qy 1551 GlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerSerIleLeuAlaTyrLys 1570
Db 4606 CTGAGGCTTTTCCCCAGGCTGCTCAGCAGGAAAGGTTTCTCTCCCTGATGGTCTATAAG 4665
Qy 1571 IleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeuGluGluAlaLys 1590
Db 4666 TTGCCTGTGTGAGGATGTGCGACCTTTATCACAGGCTTTCTTCAAATTAGAGATAGTAAA 4725
Qy 1591 HisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheVal 1610
Db 4726 CAGAGTTTCGACCTGGAGGAGTACAGCCTCTCACAGTCTACCTGGAGCAGGTTTCTCTG 4785
Qy 1611 GluLeuThrLysGluGlnGlu-----GluGluAsp 1620
Db 4786 GAGCTCTCCAAGGAGCAGGAGCTGGGTGATCTTTGAAGAGGAC 4827

RESULT 12

US-10-090-454-1
; Sequence 1, Application US/10090454
; Publication No. US20020123106A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Le Bihan, Stephane
; APPLICANT: Nathwani, Parimal S.
; APPLICANT: Connop, Bruce P.
; TITLE OF INVENTION: NOVEL ABCA9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.405
; CURRENT APPLICATION NUMBER: US/10/090,454
; -CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5018
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-090-454-1

Alignment Scores:
Pred. No.: 4.56e-252 Length: 5018
Score: 3200.50 Matches: 690
Percent Similarity: 61.00% Conservative: 319
Best Local Similarity: 41.72% Mismatches: 558
Query Match: 37.98% Indels: 87
DB: 13 Gaps: 27

US-10-090-458-5 (1-1642) x US-10-090-454-1 (1-5018)

Qy 6 ArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLysAsnTyrLeuIleLys 25
Db 153 AGACGCATGAGCGTGGGTGAGCAACATCGGCTCTTCTGCAAGAACTGCTCAAAA 212
Qy 26 CysArgThrLysLysSerSerValGlnGluIleLeuPhePro---LeuPheLeuPhe 44
Db 213 TGGAGAATGAAAAGACAGACCTTGTGGAAATGGCTCTTTTCATTTCTTGGTACTGTTT 272
Qy 45 TrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGluValProAsnIle 64
Db 273 CTGTACCTATTTTCTCCAATTTACATCAAGTTCATGACACTCCTCAATGTCTTCAATG 332
Qy 65 GluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProVal 84
Db 333 GATCTGGGACGTGTAGATAGTTTTTAATGATACTAATATGTTATTGCAATTCACCTGAA 392
Qy 85 ThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeuProAspValIle 104
Db 393 TCCAAAACACTACCCACAGAGATAATGAACAAAGTGGCTTCAGCCCCATTCCTAAAGGAAGA 452
Qy 105 IleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLysProSer 124
Db 453 ACAATCATGGGTGGCTGATGATGAAAAAGCATGGATGAATGGATTGAACTATTCAATA 512
Qy 125 AsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArgPhe---PhePro 143

QY 475 LysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnVal 494
Dbb 1432 AAAGAACCATCAGAATCAAAATCTTAAAGAAAGATATGCAGGGAAGTGTGAGAGATGTA 1491
QY 495 GluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGly 514
Dbb 1492 GAAGCTTTGAAAGGTGTGGTGTGTGACATATATGAAGGCCAGATCCTGCCCTCTTGGT 1551
QY 515 HisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSer 534
Dbb 1552 CACAGTGGAGCTGGAAAACTCCCTGTAAACATTTCTAGTGGTGTGTGACITCCAACA 1611
QY 535 AspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAla 554
Dbb 1612 TCAGGTTCACTGCTCTATAATCACACACTTTCAAGAAATGGCTGATATAGAAAAATATC 1671
QY 555 ArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGlu 574
Dbb 1672 AGCAAGTTCACCTGGATTTTGTCCCAATCCAAATGTGCAATTTGGATTTCTCCTGTGAAA 1731
QY 575 GluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGlu 594
Dbb 1732 GAAACCTCAGGCTGTTTGTCTAAATAAAGGATTTTGCACATGAAGTGGAGAAAGAG 1791
QY 595 ValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLys 614
Dbb 1792 GTACAAACGAGTTGTACAGGAATTAGAAATGGAATAATTCAAGACATCCTTGTCTCAAAAC 1851
QY 615 LeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLys 634
Dbb 1852 TTAAGTGGTGGACAAAATAGGAATACTAACTTTTGGGATTTGCCATTTTAGGAGATCCTCAA 1911
QY 635 IleLeuLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleValTyr 654
Dbb 1912 GTTTTGTCTATGGATGAACCGACTGCTGGATTTGGATTTGGATTTTCAAGGCACCGAATATGG 1971
QY 655 AsnLeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPheMetAsp 674
Dbb 1972 AATCTCTGAAAGAGGGGAAATCAGACAGAGTAAATCTCTTCAGCACCCAGTTTATAGAT 2031
QY 675 GluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLysCysVal 694
Dbb 2032 GAGGCTGACATTTCTGGCGACAGGAAGGTGTTTCATATCCAATGGGAAGCTGAAGTGTGCA 2091
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QY 715 AspLysTyrCysAlaThrGluSerLeuSerSerLeuValLysGlnHisIleProGlyAla 734
Dbb 2152 AATGAAAGGTGTGATCCAGAGAGTATAACATCCTGTTTAAAGCAGCACATCTCTGATGCC 2211
QY 735 ThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeuProPheLysAspMetAsp 754
Dbb 2212 AAATTGACAGACACAAAGTGAAGAAAACTTGATATATTTTGCCTTTGGAAAGGACAAAC 2271
QY 755 LysPheSerGlyLeuPheSerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyr 774
Dbb 2272 AAATTTCCAGAACTTTACAGGGATCTTGATAGATGTTCTTAACCAAGGCATTTGAGGATTAT 2331
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QY 815 SerPheAspGluMetGluGlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuVal 834
Dbb 2452 AGCCTTGTGAGCTGGAACAAGTTTGTCTCTCTCCACGAAACAAGGAAAAACA---ATC 2508
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Dbb 2509 AGTGGCTGGCGCTCTGGAGGCAGCAGGTCTGTGTGCAATAGCAAAAGTTGCTTCTCTAAAG 2568
QY 855 LeuLysArgGluSerLysSerValArgSerValLeuLeuLeuLeuLeuIlePhePheThr 874
Dbb 2569 TTAAGAAAGAAAGAAAGCGCTGTGGACTATATATTGCTTTTGGTATTAGCTTTATC 2628
QY 875 ValGlnIlePheMetPheLeuValHisHisSerPheLysAsnAlaValValProIleLys 894
Dbb 2629 CCTCAACTTTTGGAAACATCTATCTACGAGTCATATCAGAAAAAGT---TACCCGTGGGAA 2685
QY 895 LeuValProAspLeuTyrPheLeuLysProGlyAspLysProHisLysTyrLysThrSer 914
Dbb 2686 CTGTCTCCAAAATACATACTTCTCTCACAGGACAAACACACAGGATCCTCTGACCCAT 2745
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Dbb 2746 TTACTGTTCATCAATAAGACAGGGTCAACCATTTGATAACTTTTACATTTCACTGAGCGCA 2805
QY 935 GlnAsnIleMetValThrMet-----IleAsnAspSerAspTyrValSer 949
Dbb 2806 CAGAACATAGCTATAGAAGTGGATGCCCTTTTGGAACTAGAAATGGCACAGATGACCCATCT 2865
QY 950 ValAlaProHisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyrValPheAla 969
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Dbb 2917 ATAGCATGTAATACAAACCGCTGAATTTCTTCTGTCTCTCTGATGTCTTAGCAAT 2976
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Dbb 2977 GGACTACTTGGAAATTTTAATTCTGTGAGAACACATTCAGACTGACAGAAAGCACATTTT 3036
QY 1010 GlnGluIleThrAspIleVal-----PheLysIleGluLeuTyrPheGlnAlaLeu 1027
Dbb 3037 GAAGAGCATATGGATTATGAGTATGGTACCGAAGTAACACCTTCTTCTGGATACCGATG 3096
QY 1028 LeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsnAlaGluAsnHis 1047
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QY 1048 LysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAlaTyrTrpIle 1067
Dbb 3145 AAAAAAAGCTCATTTCCAGCTACGGATTTTCAGGCCCTCTACCCCTTCTGCATACTGGT 3204
QY 1068 GlyGlnAlaValValAspIleProLeuPhePheIleIleLeuIleLeuMetLeuGlySer 1087
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QY 1088 LeuLeuAlaPheHisTyrGly-----LeuTyrPheTyrThrValLysPheLeuAla 1104
Dbb 3259 ATAATGGATTATATTTTAGCCAGAGGAGATTATATATTATTAATTCAAAAACCTGTTAATT 3318
QY 1105 ValValPheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSer 1124
Dbb 3319 CAAATCCTGTGTAGTATTGGCTATGTCTCATCTCTTGTTTTCTTGACATATGTGATTCA 3378
QY 1125 PheThrPheLysLysIleLeuAsnThrLysGluPheThrPheIleTyrSerValAla 1144
Dbb 3379 TTCAATTTTCGCAATGGGAGAAAAAATAGTGGCATTGTCATTTTCTTCTTCTTAATTGTG 3438
QY 1145 AlaLeuAlaCysIleAlaIleThrGluIleThr-----PhePheMetGlyTyrThrIle 1162
Dbb 3439 GTCATCTTCTCGATAGTTGCTACTGATCTAAATGAATATGGATTTCTAGGGCTATTTTTT 3498
QY 1163 AlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeuGlyCys 1182
Dbb 3499 GGCACCATGTTA-----ATACCTCCCTTTCACATTGATTTGGCTCT 3537
QY 1183 LeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThrTyrAsn 1202

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Db 5230 CACACAGAGATTTTGAAGCTTTTCCACACAGGCTGGCTGGCAGGAAAGATATCTCTCTTTA 5289
Qy 1567 LeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeu 1586
Db 5290 ATGGCGTATAAGTTACCTGTGGAGGATGTCACCCCTCTATCTCGGGCCTTTTCAAGTTA 5349
Qy 1587 GluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGlu 1606
Db 5350 GAGGCGATGAACAGACACCTTCAACCTGGAGGAATACAGCCTCTCTCAGGCTACCTTGGAG 5409
Qy 1607 GlnValPheValGluLeuThrLysGluGlnGluAspAsnSerCysGlyThrLeu 1626
Db 5410 CAGGTATTCTTAGAACTCTGTAAAGAGCAG--GAGCTGGGAAATGTTGATGATAAAATT 5466
Qy 1627 AsnSerThrLeuTrpTrpGlu---ArgThrGlnGluAsp 1638
Db 5467 GATACAAACAGTTGAATGGAAACTTCTCCACAGGAAGAC 5505

RESULT 11
US-10-090-454-3
; Sequence 3, Application US/10090454
; Publication No. US20020123106A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Ie Bihan, Stephane
; APPLICANT: Nathwani, Parimal S.
; APPLICANT: Connop, Bruce P.
; TITLE OF INVENTION: NOVEL ABCA9 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.405
; CURRENT APPLICATION NUMBER: US/10/090,454
; CURRENT FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4875
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-090-454-3

Alignment Scores:
Pred. No.: 4,37e-252 Length: 4875
Score: 3200.50 Matches: 690
Percent Similarity: 61.00% Conservative: 319
Best Local Similarity: 41.72% Mismatches: 558
Query Match: 37.98% Indels: 87
DB: 13 Gaps: 27

US-10-090-458-5 (1-1642) x US-10-090-454-3 (1-4875)
Qy 6 ArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLysAsnTyrLeuIleLys 25
Db 10 AGACGCATGACGCTGGTGCAGCAACATGGGCTCTCTCTGCAAGAACTCTCAAAAAA 69
Qy 26 CysArgThrLysLysSerSerValGlnGluIleLeuPhePro--LeuPhePheLeuPhe 44
Db 70 TGGAGAATGAAAGACAGACACCTTGTGGAAATGGCTCTTTTCATTTCTTCTGGTACTGTT 129
Qy 45 TrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGluValProAsnIle 64
Db 130 CTGTACCTATTTTCTCCAAATTACATCAAGTTCATGACACCTCCTCAATGTCTTCAATG 189
Qy 65 GluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProVal 84
Db 190 GATCTGGGACGTGTAGATAGTTTAAATGATACTAATATGTTATTGTCATTGCACCTGAA 249
Qy 85 ThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeuProAspValIle 104
Db 250 TCCAAAACTACCCCAAGAGATAATGAACAAAGTGGCTTCAGCCCCATTCCTAAAGGAAGA 309
Qy 105 IleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLysProSer 124
Db 310 ACAATCATGGGCTGGCTGATGAAAAAAGCATGGATGAATTGGATTGAACTATTCAATA 369
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Qy 125 AsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArgPhe---PhePro 143
Db 370 GACGAGTGAGAGTCATCTTTACTGATACCTTCTCCTACCATTTTGAAGTTTTCTTGGGA 429
Qy 144 AspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCys----- 159
Db 430 CATAGAATCCCATGATGAAGAGCACAGAGACCATTGAGCTCACTGTCAAGCAGTGAAT 489
Qy 160 ---SerLysSerCysGluAlaIleGlnTyrTrpSerSerGlyPheThrValLeuGlnAla 178
Db 490 GAAAAAATGAAGTGTGAAGGTTGAGAGTTCTGGGAGAAAGGCTTTGTAGCTTTTCAAGCT 549
Qy 179 SerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGlu 198
Db 550 GCCATTAAATGCTGCTATCATAGAAATCGCAACAATCATTCAGTGATGGAACAGCTGATG 609
Qy 199 SerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArg 218
Db 610 TCAGTTACTGGTGATACATAGAGATATTACCTTTTGTGCCCCAAGGAGGAGTTGCAACT 669
Qy 219 GlyValIleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIle 238
Db 670 GATTTTTCATTTTCTTTTGCATTATTTCTTTTCTACATTATATATACTATGATCAGTC 729
Qy 239 HisIleValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHis 258
Db 730 AATGTTACACAAGAAAGACAA--TACATTACGTCATGATGACAAATGATGGGACTCGGA 786
Qy 259 AspThrAlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSer 278
Db 787 GAGTCAGCATTTCTGGCTTCTGGGTTTGATGTATGCTGGCTTCATCCTTATCATGGCC 846
Qy 279 LeuLeuMetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleVal 298
Db 847 ACTTTAATGGCTCTTATTGTAATAATCTGCACAATGTCGTCCTGACTGGTTTGTGATG 906
Qy 299 IlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThr 318
Db 907 GTCTTCACCCCTCTTTCTCTCTATGGCCTGTCTTGATAACTTTAGCTTTCTCGATGAGT 966
Qy 319 ProLeuPheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPhe 338
Db 967 GTGTTGATAAAGAAACCTTTCCTTACGGGCTTGGTGTGTCTCTCCTTATTGTCTTTGG 1026
Qy 339 GlyPheIleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrp--- 357
Db 1027 GGGATCCTGGGATTTCCCA---GCATTGTATACACGCTCTCTGCACTTTTGGAAATGGACT 1083
Qy 358 -----LeuPheSerPropheCysHisCysThrPheValIleGlyIleAlaGlnValMet 375
Db 1084 TTGTGTCTTCTTAGCCCCCTTT-----GCCTTCACTGTGGGATGGCCAGCTTATA 1134
Qy 376 HisLeuGlu---AspPheAsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyr 394
Db 1135 CATTTGGACTATGATGTGAATTTCTAATGCCCACTTGGATTCT---TCACAAAAATCCATAC 1191
Qy 395 ProLeuIleIleThrIleIleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAla 414
Db 1192 CTCATAATAGCTACTCTCTTTTCATGTTGGTTTTTGACACCCCTTCTGTATTGTTGATTGACA 1251
Qy 415 ValTyrLeuAspGlnValIleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPhe 434
Db 1252 TTATATTTTGACAAAATTTGCGCGCTGAATATGACATCGATGTTCTCCCTTGTTTTTC 1311
Qy 435 LeuLysProSerTyrTrpSerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsn 454
Db 1312 CTGAAATCCTGTTTTTGGTTTCAACACGGAAGGCTAATCATGTGTGCTCTGAGAATGAA 1371
Qy 455 ValAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPheValGly 474
Db 1372 ACAGATTCTGATCCTACCTAATGACTGTTTTTGAACCAAGTGTCTCTCCAGAAATTTCTGGG 1431
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QY	848	AlaLysPheHisPhePheThrLeuLysArgGluSerLysSerValArgSerValLeuLeu	867
DB	3157	GCAACACTTCGCTCTTAAAGTTAAGCGGTGAAAGGAGAGCTCTTTTGTGTTGTACTA	3216
QY	868	LeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHisHisSerPheLys	887
DB	3217	GTACTTGGAATTGCTTTT--ATCCCATCATCTAGAGAAAGATAATGTATATAAAGTAACT	3273
QY	888	AsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLysProGlyAspLys	907
DB	3274	CGTGAAACTCATTTGTTGGGAGTTTTCACCCAGCATGTATTTCTCTTCTCTGGAACAAATC	3333
QY	908	ProHisLysTyrLysThrSerLeuLeuGlnAsnSerAlaAspSerAspIleSerAsp	927
DB	3334	CCGAAGACGCCTCTTACCAGCCTGTTAATCGTTAATAATACAGGATCAATAATTTGAAGAC	3393
QY	928	LeuIleSerPhePheThrSerGlnAsnIleMetValThrMet	942
DB	3394	CTCGTGCAATTCAGTGAAGTGTACAGGATATAGTTTGGAAATAGATGACTTTAGAAACAGA	3453
QY	943	AsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMetHisSer	962
DB	3454	AATGGCTCAGATGATCCCTCC-----TACAATGGAGCCATCATAGTGTCTGGTGAC	3504
QY	963	GluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeuProIle	982
DB	3505	CAGAAGGATTACAGATTTCTGTGCGTGTAAATACCAAGAAATTTGAATTTGTTTCTCTGTT	3564
QY	983	LeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThrIleGln	1002
DB	3565	CTTATGGGAATTGTAGCAATGCCCTTATGGGAATTTTAACTTCACGGAGCTTATTCAA	3624
QY	1003	IleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLysIleGluLeuTyr	1022
DB	3625	ACGGAGAGCACTTCATTTCTCGTGAT-----GACATAGTCTGGATCTTGGTTTATA	3678
QY	1023	PheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGlu	1042
DB	3679	GATGGGTCCATATTTTGTGTTGATCACAACACTCGCTTCTCCTTTTATCGGCATGAGC	3738
QY	1043	AsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuPro	1062
DB	3739	AGCATCAGCGATTATAAAAAAATGTTCAATCCAGTTATGGATTTCAGGCCTCTGGCCT	3798
QY	1063	SerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeuIle	1082
DB	3799	TCAGCATACTGGTGTGGACAGGCTCTGGTGGACATTCATTTATCTTCTTGATT-----	3852
QY	1083	LeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPhe	1102
DB	3853	-----CTCTTTTCAATACATATTAATTTACTACTTTCATATTTCTGGGATTCT	3897
QY	1103	-----LeuAlaValValPheCysLeuIleGlyTyrValProSer	1115
DB	3898	CAGCTTTTCATGGGAACATCATGTTTGTGGTGTATGCATAATTTGGTTGTGCAGTTTCT	3957
QY	1116	ValIleLeuPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGlu	1135
DB	3958	CTTATATTCCTCACATATGTGCTTTCATTCATCTTCGCAAGTGGAGAAAAATAATGGC	4017
QY	1136	PheTrpSerPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThr	1155
DB	4018	TTTTGGTCTTTTGGCTTTTATT--ATCTTAATATGTGTATCCACAATATATGGTATCA	4074
QY	1156	PhePheMetGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIle	1174
DB	4075	-----ACTCAATATGAAAAAACTCAACTTAATTTTGTGCATGATTTTCATA	4119
QY	1175	ProIleTyrProLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnVal	1194
DB	4120	CCTTCCCTTCACTTGTGGGGTATGTATGTTTATGATCCAGCTCGACTT-----	4170

QY	1195	ArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSer	-----	1200
DB	4171	ATGAGAAACTTGGACAGTCTGGAC	-----AATAGAATAAATGAAGTCAATAAAACCATT	4224
QY	1209	---ValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyr		1227
DB	4225	CTTTTAAACAACCTTAATACCATACCTTCAGAGTGTATTATTTCCCTTTTGTGCATAAAGGTGT		4284
QY	1228	TyrGluLysLysTyrGlyArgSerIleArgLysAspProphePheArgAsnLeuSer		1247
DB	4285	CTGGAAATGAAGTATGGAATGAAATAATGAATAAAGACCCAGTTTTTCAGA--ATCTCT		4341
QY	1248	ThrLysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspGluAsp		1267
DB	4342	CCACGGAGTAGAGAAACTCAT--CCCAATCCGGAAGAGCCCGAAGAAGAAGATGAAGAT		4398
QY	1268	ValLysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLys		1287
DB	4399	GTTCAAGCTGAAAGAGTCCAAGCAGCAAAATGCACTCACTGCTCCAACTTGGAGGAGGAA		4458
QY	1288	ProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeu		1307
DB	4459	CCAGTCATAACTCAAGCTGTTTACACAAGGAATATATGAGACAAAGAAAAGTTGCTTT		4518
QY	1308	SerArgLysValLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGlu		1327
DB	4519	TCAACAAGAAAGAGAAATAGCCATCAGAAATGTTTCCTTTTGTGTTAAAAAAGTGAA		4578
QY	1328	IleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuVal		1347
DB	4579	GTTTTGGGATTACTAGGACACAATGGAGCTGCTAAAGTACTTCCATTAAAAATGATAACT		4638
QY	1348	GlyAspIleGluProThrSerGlyGlnValPheLeu--GlyAspTyrSerSerGluThr		1366
DB	4639	GGGTGCACAAAGCAACTGCAGGAGTGTGTGTTTACAAGGCAGCAGCATCAGTAAGG		4698
QY	1367	SerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrp		1386
DB	4699	CAACAGCATGACAAAGAGCACTTGGAGTGTATGAGCTGCCCTCAGGAGAACTCACTGTGG		4758
QY	1387	ProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAla		1406
DB	4759	CCCAAGCTTACAATGAAAGAGCACTTGGAGTGTATGAGCTGTGAAAGGACTGGGCAAA		4818
QY	1407	SerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeu		1426
DB	4819	GAAGATGCTGCTCTCAGTATTTACGATTGTGTGAAGCTCTTAAGCTCCAGGAACAACTT		4878
QY	1427	GlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSer		1446
DB	4879	AAGGCTCCTGTGAAAACTCTATCAGAGGGAATAAAGAGAAAGCTGTGCTTTGTGCTGAGC		4938
QY	1447	MetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLys		1466
DB	4939	ATCTTGGGGAACCCATCAGTGGTGTCTTCTAGATGAGCCGTTTACCCGGATGGACCCCGAG		4998
QY	1467	AlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAla		1486
DB	4999	GGGCAGCAGCAAAATGTGCAGATACTTTCAGGCTACCGTTAAAAACAAGGAGGGGCACC		5058
QY	1487	IleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMet		1506
DB	5059	CTCTTGACCAACCCATTACATGTCAGAGGCTGAGGCTGTGTGTGACCGTATGGCCATGATG		5118
QY	1507	ValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLys		1526
DB	5119	GTGTGAGGAACGCTAAGGTGATTGGTTCCATTCAACATCTGAAAAACAAGTTTGGTAGA		5178
QY	1527	GlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeu		1546
DB	5179	GATTATTACTAGAAATAAAAAATGAAA-----GAACCTACCCAGGTGGAAGCTCTC		5229
QY	1547	GlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerIle		1566

Db 973 TACCATGAATGGTGGAGTTATATTAGTGATACTTTCTCATATCGCTGAAGTTTAAT 1032
QY 142 PheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCys----- 159
Db 1033 TGGGGATATAGAAATCCAGTTATAAAGGAGCAGCTCTGAATACACAGAACACTGTTGGGCC 1092
QY 160 -----SerLysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeu 176
Db 1093 ATGCATGGTGAATTTTTTTGTACTTTGGCAAAGTACTGGCTAAAGGGTTTGTAGCTTTT 1152
QY 177 GlnAlaSerIleAspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGlu 196
Db 1153 CAAGCTGCAATTAATGCTGCAATATAGAAAGTCACAAATAATCAATCTCTGAATGGAGGAG 1212
QY 197 LeuGluSerThrLysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPhe 216
Db 1213 TTGACATCAGTTATTGGGAATAAATATG-----AAGATACACACCTTTC 1254
QY 217 ---ProArgGlyValIleLeu-----IleTyrLeuValIleAlaPheSer 230
Db 1255 ATTTCTAAGGGAGAAATATGAATGAATGGTTTCATTTTACTTGTCTTAGTTCTTCTCT 1314
QY 231 ProPheGlyTyrPheLeuAlaIleHisIleValAlaGluLysGluLysLysIleLysGlu 250
Db 1315 TCCTTTATATACTTTTGCAATCAATAAAT--GTTGCAAGGGAAGAGAAATTTAAGAAA 1371
QY 251 PheLeuLysIleMetGlyLeuHisAspThrAlaPheTrpLeuSerTrpValLeuLeuTyr 270
Db 1372 CTGATGACAGTAATGGGTCTCCGAGAGTCAGCATTTCTGGCTCTCTCTGGNGATGACATAC 1431
QY 271 ThrSerLeuIlePheLeuMetSerLeuLeuMetAlaValIleAlaThrAlaSerLeuLeu 290
Db 1432 ATTTGCTTCATCTTCATTATGTCATTTTATGGCTCTGGTCTATAACATCAATCTCAATT 1491
QY 291 PheProGlnSerSerSerIleValIlePheLeuLeuPhePheLeuTyrGlyLeuSerSer 310
Db 1492 GTATTTCATACTGGCTTCATGGTGATATTACACTCTATAGCTTATATGGCCTTCTTTG 1551
QY 311 ValPhePheAlaLeuMetLeuThrProLeuPheLysLysSerLysHisValGlyIleVal 330
Db 1552 ATAGCATGGCTTTCTCATGAGTGTGTTTAAATAAGGAACCTATGCTCGCTGGTTGGCT 1611
QY 331 GluPhePheValThrValAlaPheGlyPheIleGlyLeuMetIleIleLeuIleGluSer 350
Db 1612 GGATTTCTCTTCACTGATTTTGGGGATGCTGCGGA---TTCACTGTGTTATACAGACAA 1668
QY 351 PheProLysSerLeuValTrp-----LeuPheSerProPheCysHisCysThrPhe 367
Db 1669 CTTCTTTATCTTTGGGATGGGTATTAAAGTCTTCTTAGCCCTTTT-----GCCTTC 1719
QY 368 ValIleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSerPheSer 387
Db 1720 ACTGCTGGAATGGCCAGGTTACACACCTGGATAATTAAGTGGTGTATTATTTTCCT 1779
QY 388 AsnLeuThrAlaGlyProTyrProLeuIleIleThrIleIleMetLeuThrLeuAsnSer 407
Db 1780 GATCCCTCTGGGATTCATACAAAATGATAGCCACTTTTTCATTTTGGCATTGTGATACT 1839
QY 408 IlePheTyrValLeuLeuAlaValTyrLeuAspGlnValIleProGlyGluPheGlyLeu 427
Db 1840 CTTTCTCTATTTGATATTCACATTATATTTTGAGCGAGTTTACCTGTATAAAGATGGCCAT 1899
QY 428 ArgArgSerSerLeuTyrPheLeuLysProSerTyrTrpSerLysSerLysArgAsnTyr 447
Db 1900 GGGGATTCCTCATTTATTTTCTTAAGTCTCTCATTTTGGTCCAAACATCAAAATACTCAT 1959
QY 448 GluGluLeuSerGluGlyAsnValAsnGlyAsnIleSerPheSerGluIleIleGluPro 467
Db 1960 CATGAATCTTTGAGAATGAATAAATCCTTGAGCATTCCTCTGATGATTTCTTTTGAACCG 2019
QY 468 ValSerSerGluPheValGlyLysGluAlaIleArgIleSerGlyIleGlnLysThrTyr 487

Db 2020 GTGTCTCCAGAATTCATGGAAAAAGAACCCATAAGAAATCAGAAATGTTTATAAAGAATAT 2079
QY 488 ArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeuSerPheAspIleTyrGluGly 507
Db 2080 AATGGAAGACTGGAAAAAGTAGAAGCATTTGCAAGGCATATTTTTTGACATATATCAAGGA 2139
QY 508 GlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLysSerThrLeuMetAsnIleLeu 527
Db 2140 CAGATCACTGCAATACTTTGGGCATAAATGGAGCTGGTAAATCAACACTGTCTAAACATTTCT 2199
QY 528 CysGlyLeuCysProProSerAspGlyPheAlaSerIleTyrGlyHisArgValSerGlu 547
Db 2200 AGTGGATTGTCTGTTTCTACAGAAGGATCAGCCACTATTTATAATACTCAACTCTCTGAA 2259
QY 548 IleAspGluMetPheGluAlaArgLysMetIleGlyIleCysProGlnLeuAspIleHis 567
Db 2260 ATAACGTGACATGGAAGAAATTAGAAAAGAAATATTGGATTTTGTCCACAGTTCAATTTTCAA 2319
QY 568 PheAspValLeuThrValGluGluAsnLeuSerIleLeuAlaSerIleLysGlyIlePro 587
Db 2320 TTTGACTTCTCTACTGTGTAGAGAAAAACCTCAGGGTATTTGCTAAAAATAAAGGATTCAG 2379
QY 588 AlaAsnAsnIleIleGlnGluValGlnLysValLeuLeuAspLeuAspMetGlnThrIle 607
Db 2380 CCAAGGAAGTGGAAACAAGAGTAAAGAAATATATAATGGAATTAGACATGCAAAAGCAT 2439
QY 608 LysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIle 627
Db 2440 CAAGACATTATTGCTAAAAAATTAAAGTGGTGGGCAGAGAGAAACTTAACACTAGGATT 2499
QY 628 AlaValLeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAlaGlyMetAspPro 647
Db 2500 GCCATCTTAGGAGATCCTCAGGTTTTGCTGTAGATGAACCAACTGCTGGATTGGATCCC 2559
QY 648 CysSerArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsnArgValThrVal 667
Db 2560 TTTTCAAGACACCGAGTGTGGAGCCTCCTGAAGGAGCATAAAGTAGACCGACTTATCCTC 2619
QY 668 PheSerThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSer 687
Db 2620 TTCAGTACCCCAATTCATGGATGAGGCTGACATCTTGGCTGATAGGAAAGTATTCTGTCT 2679
QY 688 GlnGlyMetLeuLysCysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGly 707
Db 2680 AATGGGAAGTTGAAATGTGAGGATCATCTTTGTTCTGAAGCGAAAGTGGGTATTTGGA 2739
QY 708 TyrArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeuSerSerLeuVal 727
Db 2740 TATCATTTAAGTTTACACAGGAATGAAATGTGTGACACAGAAAAAATCACATCCCTTATT 2799
QY 728 LysGlnHisIleProGlyAlaThrLeuLeuGlnAsnAspGlnGlnLeuValTyrSer 747
Db 2800 AAGCAGCACATTCCTGATGCCCAAGTTAAACAACAGAAAGTAGAAGAAAACTTGATATAGT 2859
QY 748 LeuProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeuAspSerHisSer 767
Db 2860 TTGCCCTTTGGAAAAAACGAACAATTTCCAGATCTTTACAGTGACCTTGATAGTGTCTCT 2919
QY 768 AsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLys 787
Db 2920 GACCAGGSCATAAGGAATTTATGCTGTTTTCAGTGACATCTCTGAATGAAGTATTTCTGAAC 2979
QY 788 LeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThrGlnGlnProLeu 807
Db 2980 CTAGAAGGAAAAATCAGCAATTGTGAACCAAGATTTTGACATTTGGGAAACAAGAGAAAAATA 3039
QY 808 GluGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeuLeuIleLeuSer 827
Db 3040 CATGTGACAAGAAATACTGGAGATGAGTCTGAAATGGAACAGGTTCTTTGTTCTCTCTCT 3099
QY 828 GluThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGlnMetTyrThrIle 847
Db 3100 GAAACAAGAAAGGCT---GTCAGTAGTGCAGCTCTCTGGAGACGACACAAATCTATGCAGTG 3156

Db 1686 TCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCAGACAAATGAGGATGAAGATGAA 1745

QY 1267 AspVallysAlaGluArgLeuLysVallysGluLeuMetGlyCysGlnCysCysGluGlu 1286

Db 1746 GATGTCAAAGCTGAAGACTAAAGGTCAAAGAGCTGATGGTTGCCAGTGTTGTGAGGAG 1805

QY 1287 LysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeu 1306

Db 1806 AAACCATCCATTATGGTCAGCAATTTGCATAAAGAATATGATGACAAAGAAATTTTCTT 1865

QY 1307 LeuSerArgLysVallysLysValAlaThrLysTyrIleSerPheCysValLysLysGly 1326

Db 1866 CTTTCAAGAAAAGTAAAGAAAGTGGCAACTAAATACATCTCTTCTGTGTGAAAAAGGA 1925

QY 1327 GluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeu 1346

Db 1926 GAGATCTTAGGACTATGGTCCAAATGGTGTGGCAAAAGCACAAATTATTAATATCTG 1985

QY 1347 ValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThr 1366

Db 1986 GTTGGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGAGATTATCTTCAGAGACA 2045

QY 1367 SerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTip 1386

Db 2046 AGTGAAGATGATGGTTCACTGAAGTGATGGTTACTGTCTCCTCAGATAAACCTTTGTGG 2105

QY 1387 ProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAla 1406

Db 2106 CCAGATACTACATTGCAGGAACATTTTGAAATTTATGGAGCTGTCAAAGGAATGAGTGA 2165

QY 1407 SerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeu 1426

Db 2166 AGTGACATGAAGAAGTCAATAGTCGAATAACACATGGACTTGATTTTAAAGAACATCTT 2225

QY 1427 GlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSer 1446

Db 2226 CAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAACGAAAGTTGTGTTTGTCTCTAAGT 2285

QY 1447 MetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLys 1466

Db 2286 ATGTAGGGAAATCCTCAGATTACTTTTGCTAGATGAACCATCTACAGGTATGGATCCCAA 2345

QY 1467 AlaLysGlnHisMetTyrArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAla 1486

Db 2346 GCCAAACAGCACATGTGGCGAGCAATTCGAACCTGCATTTAAAAACAGAAACGGGCTGCT 2405

QY 1487 IleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMet 1506

Db 2406 ATCTGACCACCTCACTATATGAGGAGGCGAGAGGCTGTCTGTGATCGAGTAGCTATCATG 2465

QY 1507 ValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLys 1526

Db 2466 GTGTCTGGGCAGTTAAGATGTATCGGAACAGTACAACTCTAAAGAGTAGATTGGAAAA 2525

QY 1527 GlyTyrPheLeuGluIleLysLeuLysAspTyrIleGluAsnLeuGluValAspArgLeu 1546

Db 2526 GGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAAACCTAGAAAGTAGACCGCCTT 2585

QY 1547 GlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerSerIle 1566

Db 2586 CAAAGAGAAATTCAGTATATTTCCCAAATGCAAGCCGTCAGGAAAGTTTTTCTCTATT 2645

QY 1567 LeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePheLysLeu 1586

Db 2646 TTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTTCAAAATCTTTTTTAAGCTG 2705

QY 1587 GluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGlu 1606

Db 2706 GAAGAAGCTAAACATGCTTTTGCCATTGAAGAATATAGCTTTTCTCAGGCAACATTGGAA 2765

QY 1607 GlnValPheValGluLeuThrLysGlnGluGluAspAsnSerCysGlyThrLeu 1626

Db 2766 CAGGTTTTTTAGAACTCACTAAAGAACACAGAGGAGGAAGATAATAGTTGTGGAACCTTA 2825

QY 1627 AsnSerThrLeuTipTyrGluArgThrGlnGluAspArgValValPhe 1642

Db 2826 AACAGCACACTTTGGTGGGAACGAACAACAAGAAGATAGAGTAGATTATTT 2873

RESULT 10

US-10-005-338B-4

; Sequence 4, Application US/10005338B

; Publication No. US20030044895A1

; GENERAL INFORMATION:

; APPLICANT: DENEFE, Patrice

; APPLICANT: ROSIER-MONTUS, Marie-Francoise

; APPLICANT: PRADES, Catherine

; APPLICANT: ARNOULD-REGUIGNE, Isabelle

; APPLICANT: DUVERGER, Nicolas

; APPLICANT: ALLIKMETS, Rando

; APPLICANT: DEAN, Michael

; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENE

; FILE REFERENCE: ABCA5, 6, 9, 10

; CURRENT APPLICATION NUMBER: US/10/005,338B

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: US 60/263,231

; PRIOR FILING DATE: 2001-01-23

; PRIOR APPLICATION NUMBER: FR 00403440.1

; PRIOR FILING DATE: 2000-12-07

; NUMBER OF SEQ ID NOS: 217

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 6181

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 1420

; OTHER INFORMATION: n=unknown, may be a o r g o r c o r t

US-10-005-338B-4

Alignment Scores:

Pred. No.: 1.11e-254 Length: 6181

Score: 3234.00 Matches: 714

Percent Similarity: 61.39% Conservative: 313

Best Local Similarity: 42.68% Mismatches: 561

Query Match: 38.38% Indels: 86

DB: 14 Gaps: 30

US-10-090-458-5 (1-1642) x US-10-005-338B-4 (1-6181)

QY 6 ArgGluValGlyValTyrArgGlnThrArgThrLeuLeuLysAsnTyrLeuIleLys 25

Db 624 AAAGAGATAAGCGTCGTCACAAATTCAGGCTCTCTGTACAAGAAATTTCTTAAAAA 683

QY 26 CysArgThrLysLysSerSerValGlnGluIleLeuPheProLeuPhePheLeuTip 45

Db 684 TGGAGATAAAAGAG--AGTTATTGGAATGGACAATAACATTGTTTCTAGGGCTATAT 741

QY 46 LeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluValProAsnIleGlu 65

Db 742 TTGTGCATCTTTTCGGAACACTTCAGAGCTACCCGTTTCTCTGAACACCTCCTAAAGTC 801

QY 66 LeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGlyTyrThrProValThr 85

Db 802 CTGGGAAGCGTGGATCAGTTTAAATGACTCTGGCCCTGGTAGTGGCATATACACCGTCAGT 861

QY 86 AsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu-----ProAsp 102

Db 862 AACATAACAAAGGATAATGAATAAGATGGCCTTGGCTTCCTTTATGAAAGGAGAGACA 921

QY 103 ValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeuSerLys 122

Db 922 GTCATTTGGGACACCAGAT-----GAAGAGACCATGGATATAGAACTTCCCAAAAAA 972

QY 123 ProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArgPhe--- 141

; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 984
; LENGTH: 3268
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-984

Alignment Scores:
Pred. No.: 0 Length: 3268
Score: 4847.50 Matches: 941
Percent Similarity: 98.64% Conservative: 2
Best Local Similarity: 98.43% Mismatches: 2
Query Match: 57.53% Indels: 11
DB: 15 Gaps: 1

US-10-090-458-5 (1-1642) x US-10-094-749-984 (1-3268)

QY 698 MetPheLeuLysSerLysTyrGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyr 717
Db 6 ATGTTCTCTCAAAAGTAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATAT 65
QY 718 CysAlaThrGluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeu 737
Db 66 TGTGCCACAGATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTA 125
QY 738 GlnGlnAsnAspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSer 757
Db 126 CAACAGAAATGACCAACAACTGTGTATAGCTTGCCCTTCAAGGACATGGACAAAATTTCA 185
QY 758 Gly-----LeuPheSerAlaLeuAspSerHis 766
Db 186 GGAATTGCTTGATAGACAAAAGGATGTTATTGATGTTTGTCTTCTGCCCTAGACAGTCAT 245
QY 767 SerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeu 786
Db 246 TCAAAATTTGGTGTCATTTCTTATGGTGTTCCTCATGACGACTTTGGAGACGTAATTTTA 305
QY 787 LysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThrGlnGlnPro 806
Db 306 AAGCTAGAAGTTGAAGCAGAAAATTGACCAAGCAGATTATAGTGATTTTACTCAGAGCCA 365
QY 807 LeuGluGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeuLeuIleLeu 826
Db 366 CTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAACAGAGCTTACTTATCTT 425
QY 827 SerGluThrLysAlaSerLeuValSerThrMetSerLeuTyrLysGlnGlnMetTyrThr 846
Db 426 TCTGAAACCAAGGCTTCTCTAGTGAGCACCATGAGCCTTTGGAACAACAGATGTATACA 485
QY 847 IleAlaLysPheHisPhePheThrLeuLysArgGluSerLysSerValArgSerValLeu 866
Db 486 ATAGCAAGATTTCATTTCTTTACCTTGAAACGTAAGTAATCATAGTGAGATCAGTGTG 545
QY 867 LeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHisSerPhe 886
Db 546 CTTCTGCTTTTAAATTTTTTTCACAGTTCAGATTTTATGTTTTTGGTTTCATCTCTTT 605
QY 887 LysAsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLysProGlyAsp 906

Db 606 AAAAATGCTGTGTTCCCATCAAACTTGTCCAGACTTATATTTCTTAAACCTGGAGAC 665
QY 907 LysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAspIleSer 926
Db 666 AAACCAATATAAACAACAAGTCTGCTTCTTCAAAATTCCTGCTGACTCAGATATCAGT 725
QY 927 AspLeuIleSerPhePheThrSerGlnAsnIleMetValThrMetIleAsnAspSerAsp 946
Db 726 GATCTTATTAGCTTTTTCACAAGCCAGAACATAATGGTGACGATGATTAATGACAGTGAC 785
QY 947 TyrValSerValAlaProHisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyr 966
Db 786 TATGATCCGTGGCTCCCATAGTGGCGCTTAAATGTGATGCATTCAGAAAAGGACTAT 845
QY 967 ValPheAlaAlaValPheAsnSerThrMetValTyrSerLeuProIleLeuValAsnIle 986
Db 846 GTTTTTCAGAGCTGTTTCAACAGTACTATGGTTTATCTTTTACCTATATTAGTGAATATC 905
QY 987 IleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThrIleGlnIleTyrSerThr 1006
Db 906 ATTAGTAACACTACTATCTTTATCATTTTAAATGTGACTGAAACCATCCAGATCTGGAGTACC 965
QY 1007 PropPheGlnGluIleThrAspIleValPheLysIleGluLeuTyrPheGlnAlaAla 1026
Db 966 CCATTCTTTCAAGAAATTAATCTGATATAGTTTTTAAATTTGAGCTGTATTTTCAAGCAGCT 1025
QY 1027 LeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsnAlaGluAsn 1046
Db 1026 TTGCTTGGAAATCAATTGTTACTGCAATGCCACTTACTTTGCCATGGAAAATGCAGAGAAT 1085
QY 1047 HisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAlaTyrTyr 1066
Db 1086 CATAAGATCAAAGCTTATACTCAACTTAAACTTTTCAAGTCTTTTGGCATCTGCATATTGG 1145
QY 1067 IleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeuIleLeuMetLeuGly 1086
Db 1146 ATGGACAAGCTGTTGTTGATATCCCTTATTTTATCATTCTTATTTTGATGCTAGGA 1205
QY 1087 SerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPheLeuAlaValVal 1106
Db 1206 AGCTTACTGGCATTTTCAATATGGATTATATTTTATATACTGTAAAGTTCCTGTGTGGTT 1265
QY 1107 PheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSerPheThr 1126
Db 1266 TTTTGCTTATTGTTGTTATGTTCCATCAGTTATTCTGTTCACTTATATTGCTTCTTTTACC 1325
QY 1127 PheLysLysIleLeuAsnThrLysGluPheTyrPheIleTyrSerValAlaAlaLeu 1146
Db 1326 TTTAAGAAAATTTTAAATACCAAGAAATTTTGTGTCATTTATCTATTCTGTGGCAGCGTTG 1385
QY 1147 AlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyrThrIleAlaThrIleLeu 1166
Db 1386 GCTGTATTGCAATCACTGAAATAACTTTCTTTTATGGGATACACAAATTGCAACTATTCTT 1445
QY 1167 HisTyrAlaPheCysIleIleIleProIleTyrProLeuLeuGlyCysLeuIleSerPhe 1186
Db 1446 CATTATGCCCTTTTGTATCATCATTTCCAATCTATCCACTTCTAGGTTGCCCTGATTCTTTC 1505
QY 1187 IleLysIleSerTyrLysAsnValArgLysAsnValAspThrTyrAsnProTyrAspArg 1206
Db 1506 ATAAAGATTCTTGGAGAAATGTACGAAAAAATGTGGACACCTATAATCCATGGGATAGG 1565
QY 1207 LeuSerValAlaValIleSerProTyrLeuGlnCysValLeuTyrIlePheLeuLeuGln 1226
Db 1566 CTTTCAGTAGCTGTTTATATCGCCTCACCTGCAGTGTGTACTGTGGATTTTCTCTTACAA 1625
QY 1227 TyrTyrGluLysLysTyrGlyGlyArgSerIleArgLysAspPropPhePheArgAsnLeu 1246
Db 1626 TACTATGAGAAAAAATAIGAGGCGCAGATCAATAAGAAAAAGATCCCTTTTTCAGAAAACCTT 1685
QY 1247 SerThrLysSerLysAsnArgLysLeuProGluProAspAsnGluAspGluAspGlu 1266

1018 sileGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleValThrAlaMetProProTy 1038
1082 AATTGAGCTGTATTTCAAGCAGCTTTGCTTGAATCATTTACTGCAATGCCACCTTA 1141
1038 rPheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSe 1058
1142 CTTTGCCATGGAAATGCAGAGATCATAA----- 1171
1058 rGlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePh 1078
1172 -GGTCTTTTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTT 1230
1078 eIleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTy 1098
1231 TATCATTTCTTATTTTGTGCTAGGAAGCTTACTGCATTTTCAATTATGGATTATATTTTA 1290
1098 rThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLe 1118
1291 TACTGTAAAGTTCCCTTGTGCTGTTTTCCTTATTTGGTTATGTTCCATCAGTTATTCT 1350
1118 uPheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSe 1138
1351 GTTCACCTTATATTGCTTCTTCACCTTTAAGAAATTTAAATACCAAAAGAAATTTTGGTC 1410
1138 rPheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMe 1158
1411 ATTTATCTATTCTGTGGCAGCGTTGGCTTGTATTGCAATCACTGAAATAACTTCTTTAT 1470
1158 tGlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrPr 1178
1471 GGGATACACAATTGCAACTATTCTTCATTTATGCTTTTGTATCATCATTTCCCAATCTATCC 1530
1178 oLeuLeuGlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnVa 1198
1531 ACTTCTAGTTGCCTGATTCTTTCATATAAAATTTCTTGAAGAATGTACGAAAAAATGT 1590
1198 lAspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCy 1218
1591 GGACACCTATAATCCATGGGATAGCTTTCAGTAGCTGTATATCGCCTTACCTGCAGTG 1650
1218 sValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyGlyArgSerIleAr 1238
1651 TGTACTGTGGATTTCTCTTACATACTACTATGAGAAAAATATGGAGGCAGATCAATAAG 1710
1238 gLysAspProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluPr 1258
1711 AAAAGATCCCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAAC 1770
1258 oProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLe 1278
1771 ACCAGACAATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGCTAAAGGTCAAAGAGCT 1830
1278 uMetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGl 1298
1831 GATGGGTTGCCAGTGTTGTGAGGAGAAACCATCCATTATGTCAGCAATTTGCATAAAGA 1890
1298 uTyrAspAspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTy 1318
1891 ATATGATGACAAGAAAGATTTTCTTCTTCAAGAAAAAGTAAAGAAAGTGGCAACTAAATA 1950
1318 rIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGl 1338
1951 CATCTCTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGG 2010
1338 yLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPh 1358
2011 CAAAAGCACAAATTATTAATATTCTGTGTGGTGATATTGAACCAACTCAGGCCAGGTATT 2070
1358 eLeuGlyAspTyrSerSerGluThrSerGluAspAspAspSerLeuLysCysMetGlyTy 1378
2071 TTAGGAGATTATTCTTCAGAGACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTTA 2130

1378 rCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTy 1398
2131 CTGTCTCTCAGATAAACCCCTTTGTGGCCAGATACTACATTTGCAGGAACATTTTGAAATTTA 2190
1398 rGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHi 1418
2191 TGGAGCTGTCAAAGGAATGAGTGCAGTGCATGAAAGAGTCAATAGTCGAATAACACA 2250
1418 sAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLy 1438
2251 TGCACCTTGATTTAAAAAGAACATCTTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAA 2310
1438 sArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGl 1458
2311 ACGAAAGTTGTGTTTGTCTTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGA 2370
1458 uProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAl 1478
2371 ACCATCTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAACCTGC 2430
1478 aPheLysAsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAl 1498
2431 ATTTAAAAACAGAAAGCGGCTGCTATTCTGACCACCTCACTATATGGAGAGGCAGAGGC 2490
1498 aValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGl 1518
2491 TGTCTGTGATCGAGTAGCTATCATGTGTCTGTCGTCGAGTTAAGATGTATCGAAACAGTACA 2550
1518 nHisLeuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIl 1538
2551 ACATCTAAAGAGTAAATTTGGAAGAGGCTACTTTTTTGGAAATTAATTTGAAGACTGGAT 2610
1538 eGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlase 1558
2611 AGAAACCTAGAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAG 2670
1558 rArgGlnGluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSe 1578
2671 CCGTCAGGAAAGTTTTTCTTCTATTTTGGCTCATATAAATTCCTAAGGAAGATGTTCAATC 2730
1578 rLeuSerGlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTy 1598
2731 CCTTTCACAAATCTTTTTTAAGTGGAAAGCTAAACATGCTTTTGCCATTGAAGAATA 2790
1598 rSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGl 1618
2791 TAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTTGTAGAACTCACTAAAGAACAGAGGA 2850
1618 uGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAs 1638
2851 GGAAGATAATAGTTGTGGAACCTTTAAACAGCACACCTTTGGTGGGAACGACACAGAAGA 2910
1638 pArgValValPhe 1642
2911 TAGAGTAGTATTT 2923

RESULT 9

US-10-094-749-984
; Sequence 984, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO

Db 4081 GATTATTCTTCAGAGACAAGTGAAGATGATGATTCACCTGAAGTGTATGGTTACTGTCTCT 4140
QY 1381 GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400
Db 4141 CAGATAAACCCCTTTGTGGCCAGATACACATTCAGAGAACATTTTGAAATTTATGGAGCT 4200
QY 1401 VallysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
Db 4201 GTCAAAGGAATGATGTCGAAGTGACATGAAGAAGAGTCATAAGTCGATAAACACATGCACCT 4260
QY 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
Db 4261 GATTTAAAGAACAATCTTCAGAAGACTGTAAAGAAACTACCTGCAGGAATCAAAACGAAAG 4320
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db 4321 TTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTTGTAGATGAACCATCT 4380
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
Db 4381 ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTCGAAGTGCATTTTAA 4440
QY 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
Db 4441 AACAGAAAGCGGGCTGCTATTCTGACCACTCACTATATATGGAGGAGGCAGAGGCTGTCTGT 4500
QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
Db 4501 GATCGAGTAGCTATCATGTGTCTGTGGCAGTTAAGATGTATCGGAACAGTACAAACATCTA 4560
QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540
Db 4561 AAGAGTAAATTTGGAAGAGCTACTTTTGGAAATTAATTTGAAGGACTGGATAGAAAAC 4620
QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
Db 4621 CTAGAAGTAGACCGCCCTTCAAAGAGAAATTCAGTATATTTTCCCAAATGCAAGCCGTCAG 4680
QY 1561 GluSerPheSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
Db 4681 GAAAGTTTTTCTTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA 4740
QY 1581 GlnSerPhePheLysLeuGluGlu 1588
Db 4741 CAATCTTTTTTAAGCTGGAGAA 4764

RESULT 8
US-10-108-260A-160
; Sequence 160, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 160
; LENGTH: 3347
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-160

Alignment Scores:
Pred. No.: 0 Length: 3347
Score: 4930.50 Matches: 966
Percent Similarity: 98.17% Conservative: 1
Best Local Similarity: 98.07% Mismatches: 2
Query Match: 58.52% Indels: 17
DB: 15 Gaps: 2

US-10-090-458-5 (1-1642) x US-10-108-260A-160 (1-3347)
QY 664 ArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLys 683
Db 2 CGGGTGACAGTGITCAGTACTCATTTTCATGGATGAAGCTGACATTTCTGCAGATAGGAAA 61
QY 684 AlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeuLysSerLys 703
Db 62 GCTGTGATATCAACAGGAATGCTGAAATGTGTGGTTCTTCAATGTTCTCTCAAAAGTAAA 121
QY 704 TrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeu 723
Db 122 TGGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACAGAAATCTCTT 181
QY 724 SerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGln 743
Db 182 TCTTCACTGGTTAAACAAACATATATACCTGGAGTACTTTATTACACAGAAATGACCAACAA 241
QY 744 LeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeu 763
Db 242 CTGTGTATAGCTTGCTTCAAGGACATGGACAAATTTTTCAGGTTTGTCTTCTGCCCTA 301
QY 764 AspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAsp 783
Db 302 GACAGTCATTCAAATTTGGGTGTCTATTTCTTATGTGTGTTTCCATGACGACTTTGGAGAC 361
QY 784 ValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThr 803
Db 362 GTATTTTAAAGCTAGAACTGAAGCAGAAATTTGACCAAGCAGATTATAGTGTATTTACT 421
QY 804 GlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeu 823
Db 422 CAGAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTGATGAAATGGAACAGAGCTTA 481
QY 824 LeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGln 843
Db 482 CTATTTCTTTCTGAAACCCAGGCTTCTCTAGTGAGCACCATGAGCCTTTTGGAAACAAACAG 541
QY 844 MetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLysSerValArg 863
Db 542 ATGTATACATAGCAAAAGTTTCATTTCTTTACCTTGAAACGTTGAAAGTAAATCAGTGAGA 601
QY 864 SerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHis 883
Db 602 TCAGTGTGCTTCTGCTTTTAAATTTTTTTCACAGTTTCAGATTTTATGTTTTTGGTTTCAT 661
QY 884 HisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLys 903
Db 662 CACTCTTTTAAAAATGCTGTGGTTCCCATCAAACTTGTTCAGACTTATATATTTTCTAAAA 721
QY 904 ProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAla----- 921
Db 722 CCTGGAGACAAACCACATATAATAACAAACAAAGTCTGCTTCTTCAAAATTTCTGCTGTGAG 781
QY 922 -----AspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMe 938
Db 782 AGTGTGTGAAGACTCAGATATCTGTGATCTTTATTAGCTTTTTCACAGCCAGAACATAAT 841
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Db 842 GGTGACGATGATTAAATGACAGTACTATGTATCCGTGGCTCCCCATAGTGGGCTTTAAA 901
QY 958 nValMetHisSerGluLysAspTyrValPheAlaValPheAsnSerThrMetValTy 978
Db 902 TGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTTCAACAGTACTATGTTTAA 961
QY 978 rSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValTh 998
Db 962 TTCTTTACCTATATTAGTGAATATCATATTAGTAACACTACTATCTTTATCATTTAAATGTGAC 1021
QY 998 rGluThrIleGlnIleTrpSerThrProphePheGlnGluIleThrAspIleValPheLy 1018
Db 1022 TGAAACCATCCAGATCTGGAGTACCCCATCTTTTCAAGAAATTTACTGATATAGTTTTTAA 1081

QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660
Dd 1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTAAATACAGA 1980
QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Dd 1981 AAAGCCAATCGGGTGACAGCTGTTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCA 2040
QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Dd 2041 GATAGGAAGCTGTGATATACAAAGGAATGCTGAAATGTGTGTTCTTCAATGTTTCTC 2100
QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Dd 2101 AAAAGTAAATGGGGATCGGCTACCGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 2160
QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
Dd 2161 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTTATACACAGAAT 2220
QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
Dd 2221 GACCAACAACCTTGIGTATAGCTGCTTTCCTTCAAGGACATGGACAAATTTTCAGGTTTGT 2280
QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Dd 2281 TCTGCCCTAGACAGTCATTCAAATTTGGGTGGCATTTCTTATGGGTTTCCATGACGACT 2340
QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
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QY 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Dd 2401 GTATTTACTCAGCAGCCACTGAGGAAGAAATGGAATCAAAATCTTTTGATGAAATGGAA 2460
QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Dd 2461 CAGAGCTTACTTATTTCTTTCTGAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTGG 2520
QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrValGlnIlePheMetPhe 860
Dd 2521 AAACACAGATGTATACATAGCAAGTTTTCATTTCTTTACCTTGAACGTAAGTAA 2580
QY 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Dd 2581 TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTTTTTCAGATTCAGATTTTATGTT 2640
QY 881 LeuValHisHisSerPheLysAsnAlaValProLysLeuValProAspLeuTyr 900
Dd 2641 TTGGTTTCATCACTCTTTTAAATGCTGTGGTTCCCATCAACTTGTTCAGACTTATAT 2700
QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSer 920
Dd 2701 TTTTCTAAACCTGGAGACAAACACATAAATACAAACAAGTCTGCTTCTTCAAAATCT 2760
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QY 941 MetIleAsnAspSerAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 960
Dd 2821 ATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGGCTTTTAAATGTGRTG 2880
QY 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
Dd 2881 CATTCAAAAAGGACTATGTTTTTGCAGCTGTTTTTCAACAGTACTATGGTTTATCTTTA 2940
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Dd 3061 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCATTTACTTGCAATGCCACCTTACTTTGCC 3120
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Dd 3361 TATATTGCTTCTTTCACCTTAAAGAAATTTTAAATACCAAGAAATTTTGGTCATTTATC 3420
QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
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Db 3114 TTTAAATGTGACTGAACCATCCAGATCTGGAGTACCCCATCTTTCAAGAAATTAATCTGAT 3173
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QY 1074 eProLeuPhePheIleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGl 1094
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QY 1094 yLeuTyrPheTyrThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValPr 1114
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Db 3743 TTACCTGCAGTGTGTAAGTGTGATTTTCTCTTACATACTATGAGAAAAATATGGAGG 3802
QY 1234 yArgSerIleArgLysAspProphePheArgAenLeuSerThrLysSerLysAenArgLy 1254
Db 3803 CAGATCAATAAGAAAGATCCCTTTTTCAGAAAACTTTCAACGAAGTCTAAAAATAGGAA 3862
QY 1254 sLeuProGluProProAspAenGluAspGluAspGluAspValLysAlaGluArgLeuLy 1274
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Db 3983 TTTGCATAAAGAATATGATGACAAGAAAGATTTTCTTCTTTCAAGAAAAAGTAAAGAAAGT 4042
QY 1314 lAlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyPr 1334
Db 4043 GGCAACTAAATACATCTCTTCTGTGTGAAAAAAGAGAGATCTTAGGACTATTGGGTCC 4102
QY 1334 oAenGlyAlaGlyLysSerThrIleIleAenIleLeuValGlyAspIleGluProThrSe 1354
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QY 1374 sCysMetGlyTyrCysProGlnIleAenProLeuTrpProAspThrThrLeuGlnGluHi 1394
Db 4223 GTGTATGGGTACTGTCCTCAGATAAACCCCTTTTGTGCCAGATACATACATTCAGGAACA 4282
QY 1394 sPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSe 1414
Db 4283 TTTTGAAATTTATGGAGCTGTCAAAGGAATGAGTGCAGATGACATGAAAGAAAGTCATAAG 4342
QY 1414 rArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPr 1434
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Db 4403 TGCAGGAATCAAAACGAAAGTTGTGTTTTGCTCTAAGTATGCTAGGGAATCCTCAGATTAC 4462
QY 1454 rLeuLeuAspGluProSerThrThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAl 1474
Db 4463 TTTGCTAGATGAACCATCTACAGGTATGGATCCCAAGCCCAACACGACATGTGGCGAGC 4522
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QY 1534 uLysAspTrpIleGluAenLeuGluValAlaAspArgLeuGlnArgGluIleGlnTyrIlePh 1554
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QY 1594 aIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLy 1614
Db 4883 CATTGAAGAATATAGCTTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACCTCACTAA 4942
QY 1614 sGluGlnGluGluAspAenSerCysGlyThrLeuAenSerThrLeuTrpTrpGluAr 1634
Db 4943 AGAACAAAGAGGAGGAGAGATAATAGTTGTGGAACCTTTAAACAGCACACTTTGTTGGGAACG 5002
QY 1634 qThrGlnGluAspArgValValPhe 1642
Db 5003 AACACAAGAGATAGATAGTATTT 5027

RESULT 7

US-09-971-121-3
; Sequence 3, Application US/09971121
; Patent No. US20020111477A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: No. US20020111477A1el Human Transporter Proteins and Polynucleot
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629

Db 894 GCCTTTGGCTTCTCTGGGTTCTCTATATACAAGTTTAAATTTTCTTATGTCCTTCTT 953
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Qy 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 1014 CTGCTTTTTCCTTTATGGATTATCATCTGTATTTTTCCTCAAAGTAGCAGCATTT 1073
Qy 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
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Qy 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle 480
Db 1494 TTTAGTGAATATTGTAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAAAT 1553
Qy 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 1554 AGTGGTATTCAAGAAGACATACAGAAAGAAGGGTGAAATGTGGAGGCTTTGAGAAATTG 1613
Qy 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
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Qy 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 1674 AGTACATTGATGAATATTCTTTGTGGACTCTGCCACCTTTCIGATGGGTTTGCATCTATA 1733
Qy 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
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Qy 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
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Db 1854 GCTTCAATCAAAAGGGATACCAGCCACAATATAATAACAAGAGTCAGAAGGTTTACTA 1913
Qy 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
Db 1914 GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA 1973
Qy 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640

Db 1974 AGAAAGCTGTCTATTAGGAATTGCTGTTCTTGGGAACCCAAAGATACTGCTGTAGTGAA 2033
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Db 2034 CCAACAGCTGGAATGGACCCCTGTCTCGACATATTGTATGGAATCTTTTAAAATACAGA 2093
Qy 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Db 2094 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTTTCCA 2153
Qy 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 2154 GATAGGAAAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGGTTCTTCAATGTTCTC 2213
Qy 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 2214 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAAATATTGTGCCACA 2273
Qy 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
Db 2274 GAATCTCTTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAT 2333
Qy 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
Db 2334 GACCAACAACCTTGTATAGCTTGCCTTTCAGGACATGGACAAAATTTTCAGGTTTGT 2393
Qy 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 2394 TCTGCCCTAGACAGTCATTTCAAATTTGGGTGTCAATTTCTTATGTGTTCATGACGACT 2453
Qy 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 2454 TTGGAAGACGTATTTTAAAGCTAGAAATTGAAGCAGAAATTTGCCAAGCAGATTATAGT 2513
Qy 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 2514 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAATCTTTGATGAAATGGAA 2573
Qy 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 2574 CAGAGCTTACTTATTCTTTCTGAAACCAGGCTGCTCTAGTGAGCACCATGAGCCTTTGG 2633
Qy 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPheThrLeuLysArgGluSerLys 860
Db 2634 AAACAACAGATGTATACAATAGCAAAGTTTCATTTCTTACCCTTGAAACGTTGAAAGTAAA 2693
Qy 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 2694 TCAGTGAGATCAGTGTGCTTCTGCTTTTAATTTTTCACAGTTCAGATTTTATATGTTT 2753
Qy 881 LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr 900
Db 2754 TTGGTTTCATCACTCTTTTAAAAATGCTGTGGTTCCCATCAAACCTGTTCCAGACTTATAT 2813
Qy 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSer 920
Db 2814 TTTCTAAAACCTGGAGACAAAACCAATAAATAACAAAACAAGTCTGCTTCTTCAAAATTC 2873
Qy 921 Ala-----AspSerAspIleSerAspLeuIleSerPhePheThrSer 934
Db 2874 GCTGGTGAGAGTGTFNNGTGAAGACTCAGATATCAGTGATCTTATTAGCTTTTTCACAAGC 2933
Qy 935 GlnAsnIleMetValThrMetIleAsnAspSerAspTyrValSerValAlaProHisSer 954
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Qy 955 AlaAlaLeuAsnValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSer 974
Db 2994 GCGGCTTTAAATGTGATGCATTCAGAAAAGGACTATGTTTTTGCAGCTGTTTTCAACAGT 3053
Qy 975 ThrMetValTyrSerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHis 994
Db 3054 ACTATGGTTTATTCTTTTACCTATATTAGTGAATATCATTAGTAACACTACTATCTTTATCAT 3113

Db	4050	AGCCAGGTATTTT	AGGAGATTATCT	TCAGAGACAAGTGAAGATGATTCAC	TGAA	4109
QY	1374	sCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHi				1394
Db	4110	GTGTATGGGTTACT	GTCTCAGATAAACCC	TTTGTGGCCAGATACATACATTCAGGAACA		4169
QY	1394	sPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSe				1414
Db	4170	TTTTGAAATTTAT	GGAGCTGTCAAAGGAATGAGTGAAGTACATGAAGAAGATCATAAG			4229
QY	1414	rArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuPr				1434
Db	4230	TCGAAATAACACAT	GCACITGATTTAAAGAACAATCTTCAGAAAGACTGTAAAGAAACTACC			4289
QY	1434	oAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleH				1454
Db	4290	TGCAGGAATCAAACG	AAAGTGTGTTTGTCTCTAAGTATGCTAGGGAATCCTCAGATTAC			4349
QY	1454	rLeuLeuAspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAl				1474
Db	4350	TTTTGTAGATGAACCAT	CTACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGC			4409
QY	1474	alleArgThrAlaPheLysAsnArgLysArgAlaIleLeuThrThrHisTyrMetGl				1494
Db	4410	AATTCGAAC	TGCACTTAAACACAGAAAGCGGGTGTCTATTCTGCACCACTCACTATATGA			4469
QY	1494	uGluAlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIl				1514
Db	4470	GGAGCAGAGGCTGTCT	GTGATCGAGTAGCTATCATGGTGTCTGGCAGATTAAAGATGTAT			4529
QY	1514	eGlyThrValGlnHisIleuLysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLe				1534
Db	4530	CGGAACAGTACAACAT	CTAAAGAGTAAATTTTGGAAAAGGCTACTTTTGGAAAATTTAAATT			4589
QY	1534	uLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePh				1554
Db	4590	GAAGGACTGGATAGAAAC	CTAGAACTAGAACCGCCTTCAAAGAGAAATTCAGTATATTTT			4649
QY	1554	eProAsnAlaSerArgGlnGluSerPheSerIleLeuAlaTyrLysIleProLysGl				1574
Db	4650	CCCAAAATGCAAGCCGT	CAAGAAAGTTTTTCTCTATATTTGGCTTATAAAATTCCTAAAGCA			4709
QY	1574	uAspValGlnSerLeuSerGlnSerPhePheLysLeuGluAlaLysHisAlaPheAl				1594
Db	4710	AGATGTTTCAGTCCCT	TTTTCACAAATCTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGC			4769
QY	1594	alleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnValPheValGluLeuThrLy				1614
Db	4770	CATTGAAGAAATATAGC	TTTTCTCAAGCAACATTTGGAACAGGTTTTTGTAGAACTCACTAA			4829
QY	1614	sGluGlnGluGluAspAsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluAr				1634
Db	4830	AGAACAGAGGAGGAGAGATAATAGTT	TGTGGAACCTTTAAACAGCACACATTTGGTGGGAACG			4889
QY	1634	gThrGlnGluAspArgValValPhe				1642
Db	4890	AAACAAGAAGATAGAGTAGTATTT				4914

RESULT 6

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US-10-090-458-1
; Sequence 1, Application US/10090458
; Publication No. US20020123107A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090,458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0

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 QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
 Db 1981 AAAGCCAATCGGGTGACAGTGTTTCAGTACTCATTTTCATGGATGAAGCTGACATTTCTTGCA 2040
 QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
 Db 2041 GATAGGAAAGCTGTGATATCACAGGAATGCTGAAATGTGTGGTTCTTCAATGTTCCCTC 2100
 QY 701 LysSerLysTirGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
 Db 2101 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTTGTGCCACA 2160
 QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsn 740
 Db 2161 GAATCTCTTTCTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTAACAAGAAAT 2220
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 QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
 Db 2281 TCTGCCCTAGACAGTCATTTCAAATTTGGGTGTCAATTTCTTATGGTGTTCATGACGACT 2340
 QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
 Db 2341 TTGGAAGACGATATTTTAAAGCTAGAAATGGAAGCAGAAATTTGATGAAATGGAA 2400
 QY 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
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 QY 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
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QY 995 LeuAsnValThrGluThrIleGlnIleTirPheSerThrProphePheGlnGluIleThrAsp 1014
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 Db 3163 -----GGTCTTTTGGCCATCTGCATATTTGGATTGGACAAGCTTGTGTTGATAT 3209
 QY 1074 eProLeuPhePheIleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrG1 1094
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 QY 1254 sLeuProGluProProAspAsnGluAspGluAspGluuAspValLysAlaGluArgLeuLy 1274
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 QY 1274 sValLysGluLeuMetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAs 1294
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 Db 3870 TTTTGCAATAAAGATATATGATGACAAAGAAAGATTTTCTTCTTCAAGAAAGTAAAGAAAGT 3929
 QY 1314 lAlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyPr 1334
 Db 3930 GGCACTAAATACATCTCTTTCTGTGTGAAAAAAGGAGAGATCTTAGGACTATTGGGTCC 3989
 QY 1334 oAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSe 1354
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; LENGTH: 4917
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2775, 2776
; OTHER INFORMATION: n = A,T,C or G
US-10-090-458-3
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Alignment Scores:
Pred. No.: 0 Length: 4917
Score: 8309.00 Matches: 1629
Percent Similarity: 98.85% Conservative: 1
Best Local Similarity: 98.79% Mismatches: 2
Query Match: 98.61% Indels: 18
DB: 13 Gaps: 2
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US-10-090-458-5 (1-1642) x US-10-090-458-3 (1-4917)

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QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerValGlnGluIleLeuPheProLeu 40
Db 61 AATTACTTAATAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAAATCTTTTTCCACTA 120
QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 121 TTTTTTTTATTTGGTTAATATTAAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA 180
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 181 GTGCCATAATAGAACTCAATCCCTATGGACAAAGTTTACTCTTTCTAATCTAATCTTGG 240
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
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QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
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QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 361 TCTAAGCCGAGCAACTTTGTAGGTGTGTTTTCAAGACTCCATGTCCTATGAACCTCGT 420
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 421 TTTTTTCTGTATGATGATCCAGTATCTTCTATTATATGGATTCAAGAGCTGGCTGTTC 480
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 481 AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTTCACAGTTTTACAAGCATCCATA 540
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Db 541 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTTGAAGGAGCTGGAGTCACT 600
QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 601 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATAACCTTTCCCGAGAGTA 660
QY 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240
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QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 721 GTAGCAGAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTTCATGATACT 780
QY 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
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Db 841 ATGGCAGTCATTGCGACAGCTCTCTTTGTTATTATTCCTCAAAAGTAGCAGCATTGTGATTT 900
QY 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
Db 901 CTGCTTTTTTTCCTTTATGGATTATCATCTGTATTTTTTGTCTTAATGCTGACACCTCTT 960
QY 321 PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe 340
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QY 381 AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle 400
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Db 1381 TTTAGTGAAATATTGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAAGAGCCATAAGAATT 1440
QY 481 SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu 500
Db 1441 AGTGGTATTCAGAAAGACATACAGAAAGAGGTGAAATGTGGAGGCTTTTGAGAAATTG 1500
QY 501 SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys 520
Db 1501 TCATTTGACATATATGAGGTCAGATTACTGCCCTTACTTTGGCCACAGTGGAAACAGGAAAG 1560
QY 521 SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle 540
Db 1561 AGTACATTGATGAATATTCTTTGTGGACTCTGCCACCTCTCTGATGGGTTTGTCACTATA 1620
QY 541 TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle 560
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QY 561 CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu 580
Db 1681 TGTCCACAGTTAGATATACACTTTGATGTTTGTGACAGTAGAAGAAAAATTTATCAATTTTG 1740
QY 581 AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu 600
Db 1741 GCTTCAATCAAAAGGGATACCAGCCCAACAATATAATACAGAGTGACAGAGGTTTACTA 1800
QY 601 AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys 620
Db 1801 GATTTAGACATGCAGACTATCAAGATAACCAAGCTAAAAAATAAGTGGTGGTCAAAAA 1860
QY 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
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Db 3315 CTGTATTTTCAAGCAGCTTTGCTTGAATCATTTGTTACTGCAATGCCACCTTACTTTGCC 3374
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QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValAlaAspIleProLeuPhePheIleIle 1080
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QY 1121 TyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIle 1140
Db 3615 TATATTGCTTCTTTCACCTTTAAGAAATTTTAAATACCAAGAAATTTTGGTCAATTTATC 3674
QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
Db 3675 TATTCTGTGGCAGCGTTGGCTTGATTGCAATCACTGAAATAAACTTTCTTTATGGGATAC 3734
QY 1161 ThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleIleProIleTyrProLeuLeu 1180
Db 3735 ACAATTGCAACTATTCTTCATTATGCTTTTGTATCATCATTTCCAATCTCACTTCTA 3794
QY 1181 GlyCysLeuIleSerPheIleLysIleSerTrpLysAsnValArgLysAsnValAspThr 1200
Db 3795 GGTGCTGATTTCTTTCAATAAGATTTCTTGAAGAATGTACGAAAAAATGTGGACACC 3854
QY 1201 TyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCysValLeu 1220
Db 3855 TATAATCCATGGGATAGGCTTTCAGTAGCTGTATATCGCCTTACCTGCGAGTGTACTG 3914
QY 1221 TrpIlePheLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArgLysAsp 1240
Db 3915 TGGATTTTCTCTTACAATACTATGAGAAAAAATATGGAGGCAGATCAATAAGAAAAGAT 3974
QY 1241 ProphePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluProProAsp 1260
Db 3975 CCTTTTTCAGAAACCTTTCAACGAAGTCTAAAAATAGGAAGCTTCCAGAACCCAGAC 4034
QY 1261 AsnGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeuMetGly 1280
Db 4035 AATGAGGATGAAGATGAAGATGTCAAAGCTGAAAGACTAAAGGTCAAAGAGCTGATGGGT 4094
QY 1281 CysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAsp 1300
Db 4095 TGCCAGTGTGTGAGGAGAAACCATCCATTATGGTCAGCAATTTGCATAAAGATATGAT 4154
QY 1301 AspLysLysAspPheLeuLeuSerArgLysValLysValAlaThrLysTyrIleSer 1320
Db 4155 GACAAGAAAGATTTTCTTTTCAAGAAAAGTAAAGAAAGTGGCACTAAATACATCTCT 4214
QY 1321 PheCysValLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340
Db 4215 TTCTGTGTGAAAAAAGAGAGAGATCTTAGGACTATTGGGTCCAAATGGTGTGGCAAAAGC 4274
QY 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360
Db 4275 ACAATTATTAAATATTCTGGTTGGTGTGATATTGAACCAACTTCAGGCCAGGTATTTTAGGA 4334
QY 1361 AspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysPro 1380

Db 4335 GATTATTCTTTCAGAGACAAGTGAAGATGATGATTCACTGAAGTGTATGGGTACTGTCTCT 4394
QY 1381 GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400
Db 4395 CAGATAAAACCCCTTTGTGGCAGATACTACTATTGCAGAAACATTTTGAATTTATGGAGCT 4454
QY 1401 ValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
Db 4455 GTCAAAAGGAATGAGTGAAGTGAACATGAAAGAAAGTCAATAAGTCGAATAACACATGCACCT 4514
QY 1421 AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
Db 4515 GATTAAAAAGAACATCTTCAGAAAGACTGTAAAGAAACTACCTGCAGGAATCAAAACGAAAG 4574
QY 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db 4575 TTGTGTTTTCCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4634
QY 1461 ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
Db 4635 ACAGGTATGGATCCCAAAGCCAAACAGCACATGTGGCGAGCAATTTCGAACATGCATTAAA 4694
QY 1481 AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
Db 4695 AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATATGGAGGAGGCAGAGCTGTCTGT 4754
QY 1501 AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
Db 4755 GATCGAGTAGCTATCATGTGTCTGGGCAGTTAAGATGTATCGGAACAGTACACATCTA 4814
QY 1521 LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540
Db 4815 AAGAGTAAATTTGAAAAAGGCTACTTTTGTGAATAATAATTGAAGGACTGGATAGAAAAC 4874
QY 1541 LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
Db 4875 CTAGAAGTAGACCGCCCTTCAAAGAGAAATTCAGTATATATTTCCCAAATGCAAGCCGTCAG 4934
QY 1561 GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
Db 4935 GAAAGTTTTTCTTCTATTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTTCA 4994
QY 1581 GlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600
Db 4995 CAATCTTTTTTAAAGCTGGAAGAAAGCTAAACATGCTTTTGCATTGAAGAATATAGCTTT 5054
QY 1601 SerGlnAlaThrLeuGlnGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620
Db 5055 TCTCAAGCAACACATTGGAACAGGTTTTTGTAGAACTCACTAAAGAACACAGAGGAGGAAGAT 5114
QY 1621 AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
Db 5115 AATAGTTGTGGAACCTTAAACAGCACACTTTTGTGGGGAACGAAACACAAAGAAGATAGAGTA 5174
QY 1641 ValPhe 1642
Db 5175 GTATTT 5180

RESULT 5

US-10-090-458-3
; Sequence 3, Application US/10090458
; Publication No. US20020123107A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090,458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3

QY	281	MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe	300
DB	1095	ATGGCAGTCATTGGACAGCTCTTTTGTATTCTCTCAAAGTAGCAGCATTTGTGATATTT	1154
QY	301	LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu	320
DB	1155	CTGCTTTTTTTCCTTTATGGATTATCATCTGTATTTTTTTTGGCTTTAATGCTGACACCTCTT	1214
QY	321	PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe	340
DB	1215	TTTAAAAAATCAAAACATGTGGGAATAGTTGAAATTTTTTTGTTACTGTGGCTTTTGGATTT	1274
QY	341	IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer	360
DB	1275	ATTGGCCTTATGATAATCCTCATAGAAAGTTTTTCCAAATCGTTAGTGTGGCTTTTTCAGT	1334
QY	361	ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe	380
DB	1335	CCTTTCTGTCACTGTACTTTTGTGATTGGTATTGGACAGGTCATGCATTAGAAAGATTTT	1394
QY	381	AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle	400
DB	1395	AATGAAGGTGCTTCAATTTCAAATTTGACTGCAGGCCCATATCCTCTAATTATTACAATT	1454
QY	401	IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal	420
DB	1455	ATCATGCTCACACTTAATAGTATATTCTATGTCTCTTGGCTGTCTATCTTGTATCAAGTC	1514
QY	421	IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp	440
DB	1515	ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG	1574
QY	441	SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer	460
DB	1575	TCAAAGAGCAAAAGAAATTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT	1634
QY	461	PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle	480
DB	1635	TTTAGTGAAATTATTGAGCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAATT	1694
QY	481	SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu	500
DB	1695	AGTGGTATTCAGAAAGACATACAGAAAGAGGGTGAAATGTGGAGGCTTTGAGAAATTTG	1754
QY	501	SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys	520
DB	1755	TCATTTGACATATATGAGGGTCAGATTACTGCCTTACTTGGCCACAGTGGAACAGGAAAG	1814
QY	521	SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle	540
DB	1815	AGTACATTGATGAATATTCTTTGTGGACTCTGCCCACTTCTGATGGGTTTGCATCTATA	1874
QY	541	TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle	560
DB	1875	TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAATGATTGGCATT	1934
QY	561	CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu	580
DB	1935	TGTCCACAGTTAGATATACACTTTGATGTTTTTGACAGTAGAAGAAAATTTATCAATTTTG	1994
QY	581	AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu	600
DB	1995	GCATTCAATCAAAGGGATACCAGCCACCAATATATACAGAAGTGCAGAAGGTTTTTACTA	2054
QY	601	AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLys	620
DB	2055	GATTTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAA	2114
QY	621	ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu	640
DB	2115	AGAAAGCTGTCAATTAGGAATTGCTGTTCTTGGGAACCCCAAGATACTGCTGCTAGATGAA	2174

QY	641	ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg	660
DB	2175	CCAAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGA	2234
QY	661	LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla	680
DB	2235	AAAGCCAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTCTTGCA	2294
QY	681	AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu	700
DB	2295	GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGGTTCCTTCAATGTTCCCTC	2354
QY	701	LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr	720
DB	2355	AAAGTAAATGGGGATCGGCTACCGCCCTGAGCATGTACATAGACAAATATTGTGCCACA	2414
QY	721	GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsn	740
DB	2415	GAATCTCTTTCTTCAGTGGTTAAACAACATATACCTGGAGCTACTTTATTACAACAGAAT	2474
QY	741	AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe	760
DB	2475	GACCAACAACCTTGTTATAGCTTGCCCTTTCAGGACATGGACAAATTTTCAGGTTTGT	2534
QY	761	SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr	780
DB	2535	TCTGCCCTAGACAGTCATTCAAATTTGGGTGGCATTTCTTATGGGGTTCCTCATGACGACT	2594
QY	781	LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer	800
DB	2595	TTGGAAGACGTAATTTTAAAGCTAGAAAGTTGAAGCAGAAATTGACCAACAGCATTATAGT	2654
QY	801	ValPheThrGlnGlnProLeuGluGluGluMetAspSerLysSerPheAspGluMetGlu	820
DB	2655	GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAAATCTTTTGATGAAATGGAA	2714
QY	821	GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp	840
DB	2715	CAGAGCTTACTTATTCTTCTGAAAACCAAGGCTKCTCTAGTGAGCCATGAGCCCTTTGG	2774
QY	841	LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrLeuLysArgGluSerLys	860
DB	2775	AAACAACAGATGTATACAATAGCAAAAGTTTTCATTTCTTTACCTTGAAACGCGAAAGTAAA	2834
QY	861	SerValArgSerValLeuLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe	880
DB	2835	TCAGTGAGATCAGTGTGCTTCTGCTTTTAAATTTTTTTCACAGTTTCAGATTTTATGTTT	2894
QY	881	LeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAspLeuTyr	900
DB	2895	TTGTTTCATCACTCTTTTAAAAATGCTGTGGTCCCATCAAACTTGTTCAGACTTATAT	2954
QY	901	PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer	920
DB	2955	TTTTTAAACCTGGAGACAAACCACATAAATACAAAAAAGTCTGCTTCTTCAAAAATCT	3014
QY	921	AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr	940
DB	3015	GCTGACTCAGATATCAGTGATCTTATTAGCTTTTTTCAAGCCAGAACATAATGCTGACG	3074
QY	941	MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet	960
DB	3075	ATGATTAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGGCTTTAAATGTTGRTG	3134
QY	961	HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu	980
DB	3135	CATTGAGAAAAGGACTATGTTTTTGCAGCTGTTTTTCAACAGTACTATGTTTTATTCTTTA	3194
QY	981	ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr	1000
DB	3195	CCTATATTAGTGAATATCAATTAGTAACACTACTATCTTTATCATTTAAATGTGACTGAACC	3254
QY	1001	IleGlnIleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLysIleGlu	1020

||||| 4081 GATTATCTTCAGAGACAAGTGAAGATGATGATCTCACTGAAGTGTATGGTTACTGTCTCT 4140
QY ||||| GlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAla 1400
Db ||||| CAGATAAACCCCTTGTGGCCAGATACATTCAGGAACATTTTGAATTTTATGGAGCT 4200
QY ||||| VallysGlyMetSerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeu 1420
Db ||||| GTCAAAGGAATGAGTGAAGTGACATGAAGAAGTCAATAGTCGAATAACACATGCACCT 4260
QY ||||| AspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLys 1440
Db ||||| GATTTAAAGAACATCTTCAGAGACTCTAAAGAACTACCTGCAGGAATCAAACGAAAG 4320
QY ||||| LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
Db ||||| TTGTGTTTCTCTAAGTATGCTAGGGAATCCTCAGATTACTTTGCTAGATGAACCATCT 4380
QY ||||| ThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLys 1480
Db ||||| ACAGGTATGGATCCCAAGCCAAACAGCACATGTGGCGAGCAATTGCAACTGCATTTAAA 4440
QY ||||| AsnArgLysArgAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCys 1500
Db ||||| AACAGAAAGCGGCTGCTATTCTGACCACTCACTATATGGAGGAGGCAGAGCTGTCTGT 4500
QY ||||| AspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeu 1520
Db ||||| GATCGAGTAGCTATCATGTTCTGCGGAGTTAAGATGTATCGAACAGTACAACATCTA 4560
QY ||||| LysSerLysPheGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsn 1540
Db ||||| AAGAGTAAATTTGGAAGAGGCTACTTTTGGAAATTAATTTGAGGACTGGATAGAAAC 4620
QY ||||| LeuGluValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGln 1560
Db ||||| CTAGAAGTAGACCGCTTCAAAGAGAAATTCAGTATATTTTCCCAATGCAAGCCGTCAG 4680
QY ||||| GluSerPheSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSer 1580
Db ||||| GAAAGTTTTTCTCTATTTTGGCTTATAAAATTCCTAAGGAAGATGTTTCAGTCCCTTCA 4740
QY ||||| GlnSerPhePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPhe 1600
Db ||||| CAATCTTTTTTAAAGCTGGAAGAGCTAAACATGCTTTTGGCATTGAAGAAATATAGCTTT 4800
QY ||||| SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620
Db ||||| TCTCAAGCAACATTTGGAACAGAGTCTTTTGTAGAACTCACTAAAGAAACAAGAGGAGAGAT 4860
QY ||||| AsnSerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThrGlnGluAspArgVal 1640
Db ||||| AATAGTTGTGGAACCTTTAAACAGCACACTTTGGTGGGAACGAACACAAGAGATAGAGTA 4920
QY ||||| ValPhe 1642
Db ||||| GTATTT 4926

RESULT 4
US-09-971-121-5
; Sequence 5, Application US/09971121
; Patent No. US20020111477A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: No. US20020111477A1 Human Transporter Proteins and Polynucleoti
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629
; PRIOR FILING DATE: 2000-10-10

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5262
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-971-121-5
Alignment Scores:
Pred. No.: 0 Length: 5262
Score: 8395.00 Matches: 1637
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 5
Query Match: 99.63% Indels: 0
DB: 9 Gaps: 0
US-10-090-458-5 (1-1642) x US-09-971-121-5 (1-5262)
QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLys 20
Db 255 ATGTCCACTGCAATTAGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTACTGAAG 314
QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 315 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 374
QY 41 PhePheLeuPheTrpLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 375 TTTTATTTTGGTTAATATTAATTAGCATGATCCAAATGAAGAAATATGAAGAA 434
QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuLeuGly 80
Db 435 GTGCCTAATATAGAACTCAATCCTATGCACAAAGTTTACTCTTTCTAATCTAATCTTTGGA 494
QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 495 TATACTCCAGTGACTAATATTAACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 554
QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 555 CCTGATGTCTAATTAATGAAGAATATACAAATGAAGAAATGTTAACAATCCAGTCTC 614
QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 615 TCTAAGCCGAGCAACTTTGTAGGTGTGTTTCAAGACTCCATGCTCTATGAACCTTCTGT 674
QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 675 TTTTCTCTGATATGATTCAGTATCTTCTATTTATATGGATTCAAGAGCTGGCTGTTC 734
QY 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 735 AAATCATGTGAGGCTGCTCAGTACTGCTCAGGTTTTCACAGTTTACAGCATCCATA 794
QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200
Db 795 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGAGAGCTGGAGTCAACT 854
QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 855 AAAGCTGTTTATATGGGAGAAACTGCTGTGTGTAGAAATAGATACCTTTCCCGAGGAGTA 914
QY 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240
Db 915 ATTTTAATATACCTAGTTATAGCAATTTTCACCTTTTGGATACCTTTTGGCAATTCATATC 974
QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 975 GTAGCAGAAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTTCATGATACT 1034
QY 261 AlapheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
Db 1035 GCCTTTTGGCTTCTCTGGGTTCTTCTATATAWACAAGTTTAAATTTTCTTATGTCCTTCTT 1094

QY 641 ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLeuLysTyrArg 660
Db 1921 CCAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGA 1980
QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680
Db 1981 AAAGCCAAATCGGGTGACAGTGTTCACTACTCATTTTCATGGATGAAGTCGACATCTTGCA 2040
QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700
Db 2041 GATAGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGGTCTTTCATGTTCCTC 2100
QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720
Db 2101 AAAAGTAAATGGGGATCGGCTACCGCTGAGCATGTACATAGACAAATATTGTGCCACA 2160
QY 721 GluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsn 740
Db 2161 GAATCTCTTCTTCACTGGTTAAACAACATATACCTGGAGCTACTTTATTACACAGAAT 2220
QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760
Db 2221 GACCAACAACCTTGTGTATAGCTTGCTTCAAGGACATGGACAAATTTTCAGGTTGTTT 2280
QY 761 SerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMetThrThr 780
Db 2281 TCTGCCCTAGACAGTCAATTCAAATTTGGGTGGCATTTCTTATGGGGTTTCCATGACGACT 2340
QY 781 LeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSer 800
Db 2341 TTGGAAGACGTATTTTAAAGCTAGAACTTGAAGCAGAAATTGACCAAGCAGATTATAGT 2400
QY 801 ValPheThrGlnGlnProLeuGluGluMetAspSerLysSerPheAspGluMetGlu 820
Db 2401 GTATTTACTCAGCAGCCACTGGAGGAAGAAATGGATTCAAATCTTTTGTATGAAATGGAA 2460
QY 821 GlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSerLeuTrp 840
Db 2461 CAGAGCTTACTTATTTCTTCTGAAACCAAGGCTKCTCTAGTGAGCACCATGAGCCTTTGG 2520
QY 841 LysGlnGlnMetTyrThrIleAlaLysPheHisPhePheThrValGlnIlePheMetPhe 860
Db 2521 AAACAACAGATGATACAAATAGCAAGTTTCATTTCTTACCTTGAAACGTTGAAAGTAAA 2580
QY 861 SerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPhe 880
Db 2581 TCAGTGAGATCAGTGTTGCTTCTGCTTTAAATTTTTCACAGTTCAGATTTTATGTTT 2640
QY 881 LeuValHisHisSerPheLysAsnAlaValProIleLysLeuValProAspLeuTyr 900
Db 2641 TTGGTTCAATCACTCTTTTAAATGCTGTGGTTCCTCATCAAACTGTTCCAGACTTATAT 2700
QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSer 920
Db 2701 TTTCTAAAACCTGGAGACAAACCACATAAATACAAACAAGTCTGCTTCTTCAAAATTC 2760
QY 921 AlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMetValThr 940
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QY 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960
Db 2821 ATGATTAAATGACAGTGACTATGTATCCGTGGCTCCCATAGTGGCGCTTAAATGTGRTG 2880
QY 961 HisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyrSerLeu 980
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QY 981 ProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThr 1000
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Db 3061 CTGTATTTTCAAGCAGCTTTGCTTGGAAATCAATGTTACTGCAATGCCACCTTACTTTGCC 3120
QY 1041 MetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeu 1060
Db 3121 ATGGAAATGCAGAGAAATCAAGATCAAAGCTTAVACTCAACTTAAACTTTCAGGTCTT 3180
QY 1061 LeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIle 1080
Db 3181 TTGCCATCTGCATATTGGATTGGACAAGCTGTTGTTGATATCCCTTATTTTTTATCATT 3240
QY 1081 LeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrVal 1100
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QY 1141 TyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr 1160
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QY 1321 PheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSer 1340
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QY 1341 ThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGly 1360
Db 4021 ACAATTATTAAATATTCTGTTGGTGGTATTTGAACCAACTTCAGGCCCAGGTATTTTAGGA 4080
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; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4929
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-971-121-1

Alignment Scores:
Pred. No.:      0      Length:      4929
Score:          8395.00  Matches:      1637
Percent Similarity: 99.70%  Conservative: 0
Best Local Similarity: 99.70%  Mismatches: 5
Query Match:      99.63%  Indels:      0
DB:               9      Gaps:        0

US-10-090-458-5 (1-1642) x US-09-971-121-1 (1-4929)

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QY 21 AenTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 61 AATTACTTAATTAAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATTCCTTTCCACTA 120

QY 41 PhePheLeuPheTyrLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 121 TTTTTTTATTTTGGTTAATATTAATTAGCATGATGATGCCAAATGATGAAGAA 180

QY 61 ValProAsnIleGluLeuAenProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 181 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTTAATCTTAATCTTGG 240

QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
Db 241 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAAGAAAGTGTCTACTGATCATCTA 300

QY 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
Db 301 CCTGATGTCTAATAATTACTGAAGAATATATACAAATGAAAAAGAAATGTTAACAATCCAGTCTC 360

QY 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140
Db 361 TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTTCAAAGACTCCATGTCTCTATGAACTTCGT 420

QY 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160
Db 421 TTTTTCCTGATATGATCCAGTATCTTCTATTATATATGATGATTCAAGAGCTGGCTGTTC 480

QY 161 LysSerCysGluAlaAlaGlnTyrTyrSerSerGlyPheThrValLeuGlnAlaSerIle 180
Db 481 AAATCATGTGAGGCTGCTCAGTACTGGTCTCCTCAGGTTTCACAGTTTACAGCATCCATA 540

QY 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTyrLysGluLeuGluSerThr 200
Db 541 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGGAGCTGGAGTCAACT 600

QY 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220
Db 601 AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA 660

QY 221 IleLeuIleTyrLeuValIleAlaPheSerProPheGlyTyrPheLeuAlaIleHisIle 240
Db 661 ATTTTAATATACCTAGTTATAGCATTTTCACCTTTTGGATACTTTTGGCAATTCATATC 720

QY 241 ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr 260
Db 721 GTAGCAGAAAGAAAGAAAAATAAAGAAATTTTAAAGATAATGGGACTTCATGATACT 780

QY 261 AlaPheTyrLeuSerTyrValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
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QY 301 LeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu 320
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QY 361 ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe 380
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QY 621 ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAspGlu 640
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RESULT 3

US-09-971-121-1
; Sequence 1, Application US/09971121
; Patent No. US20020111477A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; TITLE OF INVENTION: No. US20020111477A1 Human Transporter Proteins and Polynucleot
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0250-USA
; CURRENT APPLICATION NUMBER: US/09/971,121
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/239,629

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QY 661 LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla 680

Db 2991 AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGTGCATTTCTTGCA 3050

QY 681 AspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMetPheLeu 700

Db 3051 GATAGGAAAGCTGTGATATCACAAAGGAATGCTGAAATGTGTGGTCTTCAATGTTCCCTC 3110

QY 701 LysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThr 720

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QY 741 AspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPhe 760

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QY 881 LeuValHisHisSerPheLysAsnAlaValProIleLysLeuValProAspLeuTyr 900

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QY 901 PheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGlnAsnSer 920

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QY 941 MetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsnValMet 960

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Db 3891 CATTCAGAAAAAGGACTATGTTTTTGCAGCTGTTTTTCAACAGTACTATGGTTTTTCTTTA 3950

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Qy 1441 LeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSer 1460
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Qy 1601 SerGlnAlaThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAsp 1620
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Qy 1641 ValPhe 1642
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US-10-005-338B-1
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; Publication No. US20030044895A1
; GENERAL INFORMATION:
; APPLICANT: DENEFELE, Patrice
; APPLICANT: ROSIER-MONTUS, Marie-Francoise
; APPLICANT: PRADES, Catherine
; APPLICANT: ARNOULD-REGUIGNE, Isabelle
; APPLICANT: DUVERGER, Nicolas
; APPLICANT: ALLIKMETS, Rando
; APPLICANT: DEAN, Michael
; TITLE OF INVENTION: NUCLEIC ACIDS OF THE HUMAN ABCA5, ABCA6, ABCA9, AND ABCA10 GENES
; FILE REFERENCE: ABCA5, 6, 9, 10
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/263,231
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: FR 00403440.1
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 1
; LENGTH: 6525
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4449
; OTHER INFORMATION: n=unknown, may be a or g or c or t
US-10-005-338B-1
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Score: 8422.00 Matches: 1641
Percent Similarity: 99.94% Conservative: 0
Best Local Similarity: 99.94% Mismatches: 1
Query Match: 99.95% Indels: 0
DB: 14 Gaps: 0
US-10-090-458-5 (1-1642) x US-10-005-338B-1 (1-6525)
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Qy 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40
Db 1071 AATTACTTAAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 1130
Qy 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60
Db 1131 TTTTTTTATTGTTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATG 1190
Qy 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80
Db 1191 GTGCCTAATATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTAATCTAATCTTGA 1250
Qy 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100
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Qy 101 ProAspValIleIleThrGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu 120
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Qy 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTyrLysGluLeuGluSerThr 200
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Qy 261 AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu 280
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Alignment Scores:

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-090-458-5 (1-1642) x US-10-090-458-4 (1-5475)

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Db	174	AAATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA	233
QY	41	PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu	60
Db	234	TTTTTTTTTATTTGGTTAATATTAAATTAGCATGATGCATCCAAATAAGAAATATGAAGAA	293
QY	61	ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly	80
Db	294	GTGCCTAATATAGAACTCAATCCTATGGCAAGTTTACTCTTTCTAATCTAATCTTGGGA	353
QY	81	TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu	100
Db	354	TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA	413
QY	101	ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetLeuThrSerSerLeu	120
Db	414	CCTGATGTCATAATTACTGAAGAAATATACAAATGAAAAGAAATGTAAACATCCAGTCTC	473
QY	121	SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg	140
Db	474	TCTAAGCCGAGCAACTTTGTAGGTGTGGTTTCAAAGACTCCCATGTCTATGAACITTCGT	533
QY	141	PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer	160
Db	534	TTTTTCTTGATATGATTCAGTATCTTCTTATTTATATGGATTCAAGAGCTGGCTGTTC	593
QY	161	LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle	180
Db	594	AAATCATGTGAGGCTGCTCAGTACTGGTCCTCAGGTTTCACAGTTTACAAGCATCCATA	653
QY	181	AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr	200
Db	654	GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAGGAGCTGGAGTCAACT	713
QY	201	LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal	220
Db	714	AAAGCTGTTATTATGGGAGAAACTGCTGTTGTAGAAATAGATACCTTTCCCGAGGAGTA	773
QY	221	IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle	240
Db	774	ATTTTAATATACCTAGTTATAGCATTTTCACCTTTTGGATACCTTTTGGCAATTCTATC	833
QY	241	ValAlaGluLysGluLysLysIleLysGluPheLeuLysIleMetGlyLeuHisAspThr	260
Db	834	GTAGCAGAAAAGAAAAAATAAAGAAATTTTAAAGATAATGGGACTTTCATGATACT	893
QY	261	AlaPheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMetSerLeuLeu	280
Db	894	GCCTTTTGGCTTCTCGGGTTCTTCTATATACAAAGTTTAAATTTTCTTATGTCCTTCTT	953
QY	281	MetAlaValIleAlaThrAlaSerLeuLeuPheProGlnSerSerSerIleValIlePhe	300
Db	954	ATGGCAGTCATTGGACAGCTTCTTTGTTATTTCTCAAAGTAGCAGCATTTGTGATATTT	1013
QY	301	IeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThrProLeu	320
Db	1014	CTGCTTTTTTCCTTTATGGATTATCATCTGTATTTTGTGTTTAAATGCTGACACCTCTT	1073

QY	321	PheLysLysSerLysHisValGlyIleValGluPhePheValThrValAlaPheGlyPhe	340
Db	1074	TTTAAAAAATCAAAACATGTGGAAATAGTTGAATTTTCTTACTGTGGCTTTTGGATTT	1133
QY	341	IleGlyLeuMetIleIleLeuIleGluSerPheProLysSerLeuValTrpLeuPheSer	360
Db	1134	ATTGGCCTTATGATAATCCTCATAGAAAAGTTTCCCAAATCGTAGTGTGGCTTTTCAGT	1193
QY	361	ProPheCysHisCysThrPheValIleGlyIleAlaGlnValMetHisLeuGluAspPhe	380
Db	1194	CCTTCTGTCACTGTACTTTTGTGATTGGTATTGCACAGGTGATGCATTTAGAAGATTTT	1253
QY	381	AsnGluGlyAlaSerPheSerAsnLeuThrAlaGlyProTyrProLeuIleIleThrIle	400
Db	1254	AATGAAGGTGCTTCATTTTCAAAATTTGACTGCAGGCCCATATCCTCTAATATTACAAT	1313
QY	401	IleMetLeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnVal	420
Db	1314	ATCATGCTCACACTTAATAGTATATTCTATGCTCTCTTGGCTGTCTATCTTGATCAAGTC	1373
QY	421	IleProGlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp	440
Db	1374	ATTCCAGGGGAATTTGGCTTACGGAGATCATCTTTATATTTTCTGAAGCCTTCATATTGG	1433
QY	441	SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer	460
Db	1434	TCAAAGAGCAAAAGAAATTTATGAGGAGTTATCAGAGGGCAATGTTAATGGAAATATTAGT	1493
QY	461	PheSerGluIleIleGluProValSerSerGluPheValGlyLysGluAlaIleArgIle	480
Db	1494	TTTAGTGAAATTTATGAGCCAGTTTCTTCAGAAATTTGTAGGAAAAGAGCCATAAGAAT	1553
QY	481	SerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsnLeu	500
Db	1554	AGTGGTATTCAGAAAGACATACAGAAAGAGGGTGAAAATGTGGAGGCTTTGAGAAATTTG	1613
QY	501	SerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGlyHisSerGlyThrGlyLys	520
Db	1614	TCATTTGACATATATGAGGTCAGATTACTGCCTTACTTGGCCACAGTGGAAACAGGAAAG	1673
QY	521	SerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSerIle	540
Db	1674	AGTACATTGATGAATATTTCTTGTGGACTCTGCCACCTTCTGATGGGTTTTCATCTATA	1733
QY	541	TyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGlyIle	560
Db	1734	TATGGACACAGAGTCTCAGAAATAGATGAAATGTTTGAAGCAAGAAAAATGATTGGCATT	1793
QY	561	CysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIleLeu	580
Db	1794	TGTCACAGTTAGATATACACTTTGATGCTTTTGACAGTAGAAGAAAAATTTATCAATTTTG	1853
QY	581	AlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeuLeu	600
Db	1854	GCTTCAATCAAAGGGATACCAGCCACAATAATAATACAAGAGTGCAGAAAGGTTTACTA	1913
QY	601	AspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGlnLys	620
Db	1914	GATTAGACATGCAGACTATCAAAGATAACCAAGCTAAAAAATTAAGTGGTGGTCAAAAA	1973
QY	621	ArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuAspGlu	640
Db	1974	AGAAAGCTGTCTATTAGGAATGCTGTTCTTGGGAACCCCAAGATACTGCTGCTAGATGAA	2033
QY	641	ProThrAlaGlyMetAspProCysSerArgHisIleValTrpAsnLeuLysTyrArg	660
Db	2034	CCAAACAGCTGGAATGGACCCCTGTTCTCGACATATTGTATGGAATCTTTTAAATACAGA	2093
QY	661	LysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIleLeuAla	680
Db	2094	AAAGCCAAATCGGGTGACAGTGTTCAGTACTCATTTTCATGGATGAAGCTGACATTCTTGA	2153

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 13, 2004, 00:30:55 ; Search time 860 Seconds
(without alignments)
7162.674 Million cell updates/sec

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Scoring table: BLOSUM62
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2475585 seqs, 1875730760 residues

Total number of hits satisfying chosen parameters: 4951170

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	8426	100.0	5475	13	US-10-090-458-4	Sequence 4, Appli
2	8422	100.0	6525	14	US-10-005-338B-1	Sequence 1, Appli
3	8395	99.6	4929	9	US-09-971-121-1	Sequence 1, Appli
4	8395	99.6	5262	9	US-09-971-121-5	Sequence 5, Appli
5	8309	98.6	4917	13	US-10-090-458-3	Sequence 3, Appli
6	8309	98.6	5463	13	US-10-090-458-1	Sequence 1, Appli
7	8112	96.3	4785	9	US-09-971-121-3	Sequence 3, Appli
8	4930.5	58.5	3347	15	US-10-108-260A-160	Sequence 160, App
9	4847.5	57.5	3268	15	US-10-094-749-984	Sequence 984, App
10	3234	38.4	6181	14	US-10-005-338B-4	Sequence 4, Appli
11	3200.5	38.0	4875	13	US-10-090-454-3	Sequence 3, Appli
12	3200.5	38.0	5018	13	US-10-090-454-1	Sequence 1, Appli
13	3197.5	37.9	5981	14	US-10-005-338B-3	Sequence 3, Appli
14	3124	37.1	5296	14	US-10-005-338B-2	Sequence 2, Appli
15	3117	37.0	4854	13	US-10-090-453A-3	Sequence 3, Appli
16	3117	37.0	5332	13	US-10-090-453A-1	Sequence 1, Appli
17	3107.5	36.9	3928	10	US-09-822-846-98	Sequence 98, Appli
18	2982	35.4	4798	15	US-10-093-463-197	Sequence 197, App
19	2961.5	35.1	4766	15	US-10-093-463-199	Sequence 199, App
20	2908	34.5	5175	15	US-10-085-198-37	Sequence 37, Appl
21	2824.5	33.5	4727	12	US-10-332-447-56	Sequence 56, Appl
22	2660	31.6	1548	10	US-09-822-846-97	Sequence 97, Appl
23	1677	19.9	1346	9	US-09-962-436-337	Sequence 337, App
24	1677	19.9	1346	9	US-09-880-107-3406	Sequence 3406, Ap
25	1677	19.9	1346	9	US-09-954-531-1033	Sequence 1033, Ap
26	1677	19.9	1346	14	US-10-171-581-333	Sequence 333, App
27	1674	19.9	2645	15	US-10-094-749-1290	Sequence 1290, Ap
28	1553.5	18.4	6491	9	US-09-954-456-2118	Sequence 2118, Ap
29	1553.5	18.4	6491	12	US-10-342-887-559	Sequence 559, App
30	1540	18.3	2512	15	US-10-108-260A-1795	Sequence 1795, Ap
31	1481	17.6	8040	15	US-10-191-803-169	Sequence 169, App
32	1480	17.6	8350	14	US-10-072-900-3	Sequence 3, Appli
33	1480	17.6	9112	14	US-10-072-900-1	Sequence 1, Appli
34	1480	17.6	10365	14	US-10-098-939-1	Sequence 1, Appli
35	1480	17.6	10381	14	US-10-098-939-2	Sequence 2, Appli
36	1480	17.6	10423	14	US-10-098-939-3	Sequence 3, Appli
37	1479	17.6	7860	12	US-10-617-334-2	Sequence 2, Appli
38	1479	17.6	7860	15	US-10-452-510-2	Sequence 2, Appli
39	1479	17.6	10412	14	US-10-313-641-7	Sequence 7, Appli
40	1479	17.6	10412	15	US-10-428-551-7	Sequence 7, Appli
41	1477.5	17.5	6786	14	US-10-313-641-8	Sequence 8, Appli
42	1477.5	17.5	6786	15	US-10-428-551-8	Sequence 8, Appli
43	1476	17.5	9870	10	US-09-984-827-103	Sequence 103, App
44	1475	17.5	9497	16	US-10-429-160-3	Sequence 3, Appli
45	1475	17.5	9741	9	US-09-846-456-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-090-458-4
; Sequence 4, Application US/10090458
; Publication No. US20020123107A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hongyun
; APPLICANT: Kilinski, Ligia
; APPLICANT: Le Bihan, Stephane
; TITLE OF INVENTION: NOVEL ABCA5 TRANSPORTER AND USES THEREOF
; FILE REFERENCE: 100103.403
; CURRENT APPLICATION NUMBER: US/10/090,458
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 5475
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 25
; OTHER INFORMATION: n = A,T,C or G
US-10-090-458-4


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QY      1363 rSerGluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAs 1383
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QY      1383 nProLeuTrpProAspThrThrLeuGlnGluHisPheGluIleTyr----- 1398
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Db      3439 TCATGAGGAGATCGTGAGGGCGCGCCAGGGAGGCCAACATCCACAGTTCATCGACTCACT 3498
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Db      3499 GCCTGAGAAATACAAACACCAGAGTGGGAGACAAAGGACTCAGCTGTGCGGCGGGCAGAA 3558
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QY      1458 uProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArgThrAl 1478
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Db      3733 C---GCAGACTTGATCGTGGTGATTTCAGAACGGCCAGGTCAAGGAGCACGGCACCCACCA 3789
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QY      1537 -----TrpIleGluAsnLeu-G 1542
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QY      1542 luValAspArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGluS 1562
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QY      1562 erPheSerSerIleLeu 1567
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Search completed: April 13, 2004, 02:07:49
Job time : 426 secs

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DB	1688	GCCACGTCAGCCTTGGACACAGAAAGCGAAGCCCGTGGTTCAGGCCGCTCTGGATAAGGCT	1747
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DB	1748	AGAGAAGCCCGGACCAACCATTTGTGATAGCTCACCCGCTTGTTCTACAGTGGCGCAATGCTGAC	1807
QY	678	IleLeuAla	695
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QY	696	SerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAsp	715
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DB	1901	ACACAGACTAGAGGAATGAAATTGAA	1936
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QY	756	PheSerGlyLeuPheSerAlaLeuAspSerHisSerAsnLeuGlyVal	773
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DB	2099	GTTCCTTTTGGCAGATCTCTAAAG--CTAATATTAGTGAATGGCCCTATTAGTT	2152
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QY	852	PhePheThrLeuLysArg-GluSerLysSerValArgSerVa	865
DB	2212	TTCAAAGATTGTAGGGTTTTCAGAGACGACGACCATGAAACCAACACCGAATTG	2271
QY	865	LleuLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHisHisSe	885
DB	2272	TAACTTGTTTCCCTTCTCTTCTGGTCATGGGAATGATTTCTTTTGTACGTAC	2326
QY	885	rPheLysAsnAlaValProIleLysLeuValProAspLeuTyrPheLeuLysProGl	905
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DB	2467	GCTCGTAGTGACGCTCTTAATGTTAAAGGGCTATGGCTCCAGGCTTGTCTAGTTAC	2526

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Db	2587	TACACTTTTACTGTAGTAATTATACCACTCATT	2620
QY	996	nValThrGluThrIleGlnIleTyrSerThrPropheGlnGluIleThrAspIleVal	1016
Db	2620		2620
QY	1016	lPheLysIleGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetPr	1036
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QY	1036	oProTyrPheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLy	1056
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Db	2785	CTTGCAGATACCATACAGAAATGCTTTGAAGAAAGCACACGCTCTTTGGGATCACCTTC	2842
QY	1108	sLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSerPheThrPheLy	1128
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QY	1128	sLysIleLeuAsnThrLysGluPheTrpSerPhe	1143
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Db	3055		3055
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QY	1283	sCysGluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLy	1303
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Db 3011 -----GCGAAGGCCAAAGTCTCAGCATCCACATCATCAGGATCATTTGAG-- 3055
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QY 1414 r-----ArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLysTh 1429
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QY 340 -----PheileGlyLeuMetileil 346
Db 9579 GAACTATTAGACTTTAATCAGCAACAGCATACAGAAACTAGTCTTTTGGAAATGTTCTTGAT 9638
QY 346 e-----LeuileGluSerPheProLysSerLeuValTrpLeuPheSe 360
Db 9639 ACTGTAGAATTATCAGAACTTATTAGAAATTTACCCGCCGAAATTAGATTCTTAAGTTG-- 9696
QY 360 rProPheCysHisCysThrPheValileGlyIleAlaGlnVal-----MetHi 376
Db 9697 -----ATGAATATGGTGGTAACCTCTCTGGAGGTGAGATGCAACGGATCTCA 9743
QY 376 sLeu----GluaspPheAsnGluGlyAlaSerPhe-----SerAsnLeuThrAlaGl 392
Db 9744 CTTGCAAGAGGATTACTGAAAGCAGGAGATGTTTATTATTAGATGAATCTT----- 9795
QY 392 yProTyrProLeuileile-----ThrileileMe 402
Db 9796 ----TTGCCAATATTGATGAAGAGACTTGTCTTAAATAAATAAATAAATTGCTGCTTAT 9851
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Db 9852 GCTGAATCACAAGCAAGCAAAATTGTTATTGAAGTTATTCTAATAAT-CTAAATAGATAACTCC 9910
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QY 638 uAspGluProThrAlaGlyMetAspProCysSerArgHisileValTrpAsnLeuLeuLy 658
Db 10637 GGATGAACCGACTAATGGACTTGATCCTATTGTTATTCAGGAGTTGCGTAATCTTATTCG 10696
QY 658 sTyrArgLysAlaAsnArgValThrVal---PheSerThrHisPheMetAspGluAlaAs 677
Db 10697 TTCCCTTCCTACACAAGGAATACAGTTATTATTTCCAGTCATATCTTATCTGAGATTCA 10756
QY 677 pileLeuAlaAspArgLysAlaValileSerGlnGlnMetLeuLysCysValGlySerSe 697
Db 10757 GATGACAGCGGATCATATTGGTATCATCTGCTAATGGCGTACTG----- 10799
QY 697 rMetPheLeuLysSerLysTrpGlyileGlyTyrArgLeuSerMetTyrileAspLysTy 717
Db 10800 -----GGTTATCAG-----GATAGAAT 10816
QY 717 rCysAlaThrGluSerLeuSerSerLeuValLysGln----- 729
Db 10817 TCACCAAGATGAAGACTTGGAAAAACTTTTACTGATGTGGTTATGAGATACCGAGGAGG 10876
QY 730 -----HisileProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLe 744
Db 10877 TGAGTGATATGCTGGGCATGTTTCAGGCAGAAAGGTT----- 10913
QY 744 uValTyrSerLeuProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeuAs 764
Db 10914 -----AAACTGAAGCGAAGTATGCGAAGAAAGTTACTAGTTTGTG 10954
QY 764 pSerHisSerAsnLeuGlyValileSerTyrGlyValSerMetThrThrLeuGluAspVa 784
Db 10955 CCCCCATAAT-----AGCTATTTTATATGTTTATATAGCACCTGTGGGTT 10999
QY 784 lPheLeuLys-----LeuGluValGluAlaGluileAspGlnAlaAsp----- 798
Db 11000 ATTTAGTAATAATGCTTATAATTGGTGTATGTCATGATTTTCCAGGGCTGCTAACCT 11059
QY 799 -----TyrSerValPheThrGlnGlnProLeuGluGluMetAspSerLysSe 815
Db 11060 TATTTGCTGCTTTAATAATACTTTACGAAGAAAAAAGCTGCATTATCGAGCAGTGTTC 11119
QY 815 rPheAspGluMetGluGlnSerLeuLeuileLeuSerGluThrLysAlaSerLeuValse 835
Db 11120 CTTTGCCCATTTCTTTAAGAAAAATTTGGTTTGAAAAATTTTATAACTGTTTATTATC 11179
QY 835 rThrMetSerLeuTrpLysGln---GlnMetTyrThrileAlaLysPheHisPhePheTh 854
Db 11180 TTAATTTTAGTAATGGAGTACTTTGGATAATTACAGTATTACTGAATACTTTTATTATC 11239
QY 854 r-----LeuLysArgGluSerLysSerValArgSerValleuLeuLeuilePh 872
Db 11240 CAAATTATGGAAGA-----CTATACTTACTGTTGGAG 11275
QY 872 ePheThrValGlnilePheMetPheLeuValHisHisSerPheLysAsnAlaValPr 892
Db 11276 AATTAGCACTAGCTCTTTGGTTATAATAGTTACTACACTTTGGCAAAATCCATTTTGTG 11335
QY 892 oileLysLeuValProAspLeuTyrPheLeuLysProGlyAspLysProHisLysTyrLy 912
Db 11336 TGTG-----GCTGACAAAAAAGAAATCGGTTT-- 11360
QY 912 sThrSerLeuLeuGlnAsnSerAlaAspSerAspIleSerAspLeuileSerPhe-- 931
Db 11361 -----TACCATAACGTTGATAAATAATTAATGAGTAATTTTCAATTTTGG 11404
QY 932 -----PheThrSerGlnAsnileMetValThrMet-----Il 942
Db 11405 GAGTTGTTTTTGCACTACTTCTCTGCTGGTGGCTTTGTCCATATAGTTGGGAATACGAT 11464

Qy 1496 AlaGluAlaValCysAspArgValAlaIleMetValSerGlyGlnLeuArgCysIleGly 1515
Db 1651 GCCGAA---TACTGCGACCGGTGCGCATGCTCTCGCGTGGCGCCTGATTGCACCTGGAC 1707
Qy 1516 ThrValGlnHisLeuLys 1521
Db 1708 ACGCCGACGCGCTCAAG 1725

RESULT 13
US-09-627-376-3
; Sequence 3, Application US/09627376
; Patent No. 6342385
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia Caulfield, Page Chen, Ping
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17402/22
; CURRENT APPLICATION NUMBER: US/09/627,376
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 15567
; TYPE: DNA
; ORGANISM: Streptococcus mutans
US-09-627-376-3

Alignment Scores:
Pred. No.: 1.21e-31 Length: 15567
Score: 413.50 Matches: 363
Percent Similarity: 34.48% Conservative: 306
Best Local Similarity: 18.71% Mismatches: 617
Query Match: 4.91% Indels: 659
DB: 4 Gaps: 81

US-10-090-458-5 (1-1642) x US-09-627-376-3 (1-15567)

Qy 17 LeuLeuLeuLysAsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnLuile 36
Db 7990 ATAATAATCAAGATCATCTTTA-----GTAATTACTATA 8025
Qy 37 LeuPheProLeuPheLeuPheTrpLeuIleLeuIleSerMetMetHis-----53
Db 8026 ATCAATATCAGGACAAATTTTATTTTGGCTCCTGGTGGTGAACAACCTTTACTAGACCAAT 8085
Qy 54 -----ProAsnLysLysTyrGluGlu 60
Db 8086 ATGGTCAAGAAGAGTGGTATATATCAGAAACTTTTATGAAGAACAAGTCTTATCAACAA 8145
Qy 61 Val-----ProAsnIleGluLeuAsnProMetAspLysPhe---72
Db 8146 GTAATAATCGAAATATATGATTATGCAGATGGTACTTCTATTTCACAGGAAAGTTTCTG 8205
Qy 73 ---ThrLeuSerAsnLeuIleLeuGlyTyrThrProValThrAsnIleThrSerSerile 91
Db 8206 GAGAGCTTCAGAAAATTATTA-----GTAACCTACCATCTTCAAGGAGATT 8250
Qy 92 MetGlnLysValSerThrAspHisLeuProAspValIleIleThrGluGluTyrThrAsn 111
Db 8251 CTTCAAAAGCTGAGAAGTATT-CTACTAAATCAAGTT-----AATTATACTAGT 8297
Qy 112 Glu-----LysGluMetLeuThr-----117
Db 8298 GATGGTTATAAAGAAATAAGCACTTACAAAAGCTTTGCGAGGTTACTAAATGAAGTGGTTA 8357
Qy 118 -----SerSerLeuSerLysProSerAsnPheValGlyValValPheLys 132
Db 8358 GAAGTTTTGCAAAATTAGTAAAAAAGAAAAAATCTTTATCTTATTGGTTGTATATTTC 8417
Qy 133 AspSerMetSerTyrGluLeuArgPhePheProAspMetIleProValSerSerileTyr 152
Db 8418 -----ATTATGACAGGCTTAATTACTCTACGAATCACCTAC 8453

Qy 153 Met-----AspSerArgAlaGlyCysSerLysSerCysGluAlaAlaGln 167
Db 8454 TTACTTAAGAAATTTAGTTGACAGCAAAATCGTCTTTTAATAATT--TGTTCTTGTCTTGTG 8511
Qy 168 TyrTrpSerSerGlyPheThrValLeuGlnAlaSerIleAspAlaAlaIleIleGlnLeu 187
Db 8512 TTTTGGGATTAGTTCTTTT-ATCATAGATGCTGGTTCACAGTATCTAATTTCATTGATT 8570
Qy 188 LysThrAsnVal-----SerLeuTrpLysGluLeu-----197
Db 8571 GGTAATCAAGTAGTGTTTAACAGTCGAAATAATATTGGAAAAAAATTTCTGATTGGACA 8630
Qy 198 -----GluSerThrLysAlaVal-----IleMetGlyGluThrAlaValVal 211
Db 8631 GATAGTAAAGATGATTCTTCGAAAATGGCAGGCCACCTTATTATAATGATAGTGAACCTGATA 8690
Qy 212 Glu-----IleAspThrPheProArgGlyVal-----220
Db 8691 GAAAAATTTATAATTTCTACTATTCTCAATCAATAAATTCAGTTATTGTTGGATCAGGA 8750
Qy 221 -----IleLeu 222
Db 8751 TCCTTAGTTATGCTATTGTTATTAAATAGTAAATGCTTTAGAAAGTTATAGGATTTGC 8810
Qy 223 IleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAla-----237
Db 8811 TTGCTTTTATTGTTTCATTATGCAACCCCTTTTCTAGAAATTAAGCAAAATAAGTAAAGA 8870
Qy 238 -----IleHisIleValAlaGluLysGluLysLysIleLys 249
Db 8871 ATCCAGGAAGACAAAGCTGAACCTTATTATAATTGCCTCACAGTTGAGAGGACAAGTCAA 8930
Qy 250 GluPheLeuLysIleMetGlyLeuHisAspThrAlaPhe-----262
Db 8931 ACA---ATAAAAAAGCTATAATGCTCAAGATTATGCCTTTCAAAAATTTGATGAGCAAAAT 8987
Qy 262 -----262
Db 8988 CGCCAATTATTCAAGATATCTTAAATAGATAATAAAATTTTAGCATTTACTCTCCTTTT 9047
Qy 263 -----TrpLeuSer-----265
Db 9048 TTAAATATCTTAATTTCTTTTATGATTATAATTGTTGTTGGCTAGGAAATACAGAAAGTA 9107
Qy 266 -----TrpValLeuLeuTyrThrSerLeu 273
Db 9108 CGTTTCAGGAAATCTCAGTGTAGTTGAGCAACTATTTTGTGTTGCTAGGAAATACAGAAATTA 9167
Qy 274 ilePheLeuMetSerLeuLeuMetAlaValIleAlaThrAlaSerLeuLeu-----290
Db 9168 ATTAATCCAATTATGCAATTATCACAATTAGTTGCTCATATGTTGCTTAATGGCGGC 9227
Qy 291 -----PheProGlnSerSerSerile-----297
Db 9228 GTGGAACGCTCTTTGGAGTATAATCAAGCTATTCCAGAAAAAAATGGAATCAAGAAAAATT 9287
Qy 298 -----ValIlePhe-LeuLeuPhePheLeuTyrGlyLeuSerSerValPh 312
Db 9288 GATGAAATAATAATATATCGCGTTTGATAATGTTTTCATTTGCTTATGATAACCAAGAAAAAT 9347
Qy 312 ePheAlaLeuMetLeuThrProLeuPheLysLysSerLysHisValGlyIleValGluPh 332
Db 9348 ATTATTGAAAATGTGAATTTAACCTTTTCAAAAAG-----GTACTTATATTTCCATT 9398
Qy 332 ePheValThrValAlaPheGly-----339
Db 9399 GTTGGTGAAGTGGAGTTGGGAATCAACCTTACTTGTATCTTTTAGAACATAATTATGTA 9458
Qy 339 -----339
Db 9459 CCATCAAAAGACGAATCTTAAATAACGGAATAGACTTTAGAGAATGAATATTAAGACT 9518
Qy 339 -----339

1011 ----- 1011
1139 PheIleTyrSerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMet 1158
1011 ----- 1011
1159 GlyTyrThrIleAlaThrIleLeuHisTyrAlaPheCysIleIleProIleTyrPro 1178
1011 ----- 1011
1179 LeuLeuGlyCysLeuIleSerPheIleIleLysIleSerTrpLysAsnValArgLysAsnVal 1198
1011 ----- 1011
1199 AspThrTyrAsnProTrpAspArgLeuSerValAlaValIleSerProTyrLeuGlnCys 1218
1011 ----- 1011
1219 ValLeuTrpIlePheLeuLeuGlnTyrTyrGluLysLysTyrGlyArgSerIleArg 1238
1012 ----- 1023
1239 LysAspProPhePheArgAsnLeuSerThrLysSerLysAsnArgLysLeuProGluPro 1258
1023 ----- 1023
1259 ProAspAsnGluAspGluAspGluAspValLysAlaGluArgLeuLysValLysGluLeu 1278
1024 ----- 1056
1279 MetGlyCysGlnCysCysGluGluLysProSerIleMetValSerAsnLeuHisLysGlu 1298
1057 ----- 1098
1299 TyrAspAspLysLysAspPheLeuLeuSerArgLysValLysLysValAlaThrLysTyr 1318
1099 TTCGGCGAA-----TTTACCGCCACCGACCAG 1125
1319 IleSerPheCysValLysLysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGly 1338
1126 GTCAGTTTGTGAGGTCAGAAAGGTGAATCTTCGGCTGTCTCGGCCCAACGGCGCGGC 1185
1339 LysSerThrIleIleAsnIleLeuValGlyAspIleGluProThrSerGlyGlnValPhe 1358
1186 AAGTCCACCACCTTCAAGATGCTGTGCGGCTACTGAAACCTACGGTGGTGAAGCGCAT 1245
1359 Leu-----GlyAspTyrSerSerGluThrSerGluAspAspSerLeuLysCysMet 1376
1246 GTGGTGGGTACGATCTGCGCCACGCTACGGCGCCGCCAAGAGCCAGCTC----- 1296
1377 GlyTyrCysProGlnIleAsnProLeuTrpProAspThrThrLeuGlnGluHisPheGlu 1396
1297 GGCTATATGGCGCAGAAAGTTCTCGCTATGCGCTCTTTCGGTGGCGCAAAACCTGGAG 1356
1397 IleTyrGlyAlaValLysGlyMetSerAlaSerAspMetLysGluValIleSerArgIle 1416
1357 TTCTCGGCCGGCTTACGGGCTGGAAGGCAACGTCGGCGCGAGCGCTATCGAGGAAATG 1416
1417 ThrHisAlaLeuAspLeuLysGluHisLeuGlnLysThrValLysLysLeuProAlaGly 1436
1417 ATCGCCACCTTCGATCTCGCGACTGGTTGTTCGCGACGCCGACTCCCTGCGCTGGGG 1476
1437 IleLysArgLysLeuCysPheAlaLeuSerMetLeuGlyAsnProGlnIleThrLeuLeu 1456
1477 CACAAACAGCGCTAGCGTGGCTGCTCGCTCATGTCATCGGCCACCGCTGCTGTTCTCTG 1536
1457 AspGluProSerThrGlyMetAspProLysAlaLysGlnHisMetTrpArgAlaIleArg 1476
1537 GATGAACCTACTTCGGCGCTGGATCCGATCACCGCGCGCAATTCGACCCACATCAAT 1596
1477 ThrAlaPheLysAsnArgLysArgAlaAlaIleLeu--ThrThrHisTyrMetGluGlu 1495
1597 GGCTTG-----GCACGCAAGGCGGTGACCATCATGCTGTCACCGCACTTCATGGACGAA 1650

747 ----- 747
779 ThrThrLeuGluAspValPheLeuLysLeuGluValGluAlaGluIleAspGlnAlaAsp 798
747 ----- 747
799 TyrSerValPheThrGlnProLeuGluGluMetAspSerLysSerPheAspGlu 818
748 -----CGCAAGAGTTGACCGCGCAGCTTGAAGCGCGCAGCTTC---CGC 789
819 MetGluGlnSerLeuLeuIleLeuSerGluThrLysAlaSerLeuValSerThrMetSer 838
790 CTGAAAC-----GTCGGCGCGGCGCGGCTTCTGACCGAGCGCTCGAT 840
839 LeuTrpLysGlnGlnMetTyrThrIleAlaLysPheHisPheThrLeuLysArgGlu 858
841 CTG----- 843
859 SerLysSerValArgSerValLeuLeuLeuLeuIlePhePheThrValGlnIlePhe 878
843 ----- 843
879 MetPheLeuValHisHisSerPheLysAsnAlaValValProIleLysLeuValProAsp 898
843 ----- 843
899 LeuTyrPheLeuLysProGlyAspLysProHisLysTyrLysThrSerLeuLeuGln 918
843 ----- 843
919 AsnSerAlaAspSerAspIleSerAspLeuIleSerPhePheThrSerGlnAsnIleMet 938
844 -----CCAGCGTGCGGAT----- 858
939 ValThrMetIleAsnAspSerAspTyrValSerValAlaProHisSerAlaAlaLeuAsn 958
858 ----- 858
959 ValMetHisSerGluLysAspTyrValPheAlaAlaValPheAsnSerThrMetValTyr 978
858 ----- 858
979 SerLeuProIleLeuValAsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThr 998
858 ----- 858
999 GluThrIleGlnIleTrpSerThrProPhePheGlnGluIleThrAspIleValPheLys 1018
858 ----- 858
1019 IleGluLeuTyrPheGlnAlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyr 1038
859 -----GGCGTGATCCAGGGCGCAGGGGTGCGCGTG 888
1039 PheAlaMetGluAsnAlaGluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSer 1058
889 GTACTGCGGAGGGTGACCAACGAGCAATCCAGGCGCTGGCCGATCGGGCCCCAAGTG 948
1059 GlyLeuLeuProSerAlaTyrTrpIleGlyGlnAlaValValAspIleProLeuPhePhe 1078
949 CAACTGGCTCCAGTGGCGCGCGGTTTCGAAGACGCTTTATTGAT----- 993
1079 IleIleLeuIleLeuMetLeuGlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyr 1098
993 ----- 993
1099 ThrValLysPheLeuAlaValValPheCysLeuIleGlyTyrValProSerValIleLeu 1118
994 -----TTGCTCGGCGCGGCCA----- 1011
1119 PheThrTyrIleAlaSerPheThrPheLysLysIleLeuAsnThrLysGluPheTrpSer 1138

QY 1286 uLysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLe 1306
| | | | | : : : : :
Db 1006 GAAACGGTCATTGAA-GCCAGTCGTTAAAGAAAGTTTGGTGAT----- 1050
| | | | | : : : : :
QY 1306 uLeuSerArgLysValLysLysValAlaThrLysTyrIleSerPheCysValLysLysG1 1326
| | | | | : : : : :
Db 1051 -----TTCCGCCGCTACCGACCATGTCGATTCCAGGTTAAGCGCGG 1091
| | | | | : : : : :
QY 1326 yGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLe 1346
| | | | | : : : : :
Db 1092 TGAAATTTTCGGCCTGCTTGGCCCCACCGCGCGGAAATCCACCACCTTCAAAATGAT 1151
| | | | | : : : : :
QY 1346 uValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluTh 1366
| | | | | : : : : :
Db 1152 GTGCGGCTGCTGGTGCACCTCCGGCAAGCGCTGGTCTGGGAATGGATCTCAAGGT 1211
| | | | | : : : : :
QY 1366 rSerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTr 1386
| | | | | : : : : :
Db 1212 CAGC--TCTGGCAAGCGCGCCAGCATCTGGGCTATATGGCGCAAAATTTTCGCTGTA 1268
| | | | | : : : : :
QY 1386 pProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAl 1406
| | | | | : : : : :
Db 1269 CGGCAACCTCAGCGTCGAGCAAAACCTCGGCTTTTCTCCGGCTCTATGGCCTGCGCGG 1328
| | | | | : : : : :
QY 1406 aSerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLe 1426
| | | | | : : : : :
Db 1329 CCGGGCGCAAAATGAAAAATCGCCGGATGAGCGATGCTTTTGGCCTGAAAAAGTATCGC 1388
| | | | | : : : : :
QY 1426 uGlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSe 1446
| | | | | : : : : :
Db 1389 CCGCCACGCGCGGACGAGCTGCGCTACAGCTACAGCAGCGGCTGGCCTGCTGCTC 1448
| | | | | : : : : :
QY 1446 rMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLy 1466
| | | | | : : : : :
Db 1449 CCTGATGTCATGAACCCGATATTCTGTTCTCGATGAACCCACCTCCGGCTCGACCCCT 1508
| | | | | : : : : :
QY 1466 sAlaLysGlnHisMetTyrArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAl 1486
| | | | | : : : : :
Db 1509 CACCCGCGCGAGTCTGGCTACATATT---AATAGCATGGTTGATAAAAGGCGTGACGGT 1565
| | | | | : : : : :
QY 1486 aIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMe 1506
| | | | | : : : : :
Db 1566 AATGGTCAACCACTTTATGATGAGGCGGAA---TACTGGACCGCATCGGGCTGGT 1622
| | | | | : : : : :
QY 1506 tValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLys 1523
| | | | | : : : : :
Db 1623 CTATCAGGCAAGCTTATCGCAGCGGACCCCGGATGAGCTGAAAGCCAG 1674
| | | | | : : : : :

RESULT 12

US-09-252-991A-1780
; Sequence 1780, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1780
; LENGTH: 1824
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1780

Alignment Scores:

Pred. No.: 3.79e-34 Length: 1824

Score: 421.50 Matches: 200
Percent Similarity: 28.64% Conservative: 111
Best Local Similarity: 18.42% Mismatches: 258
Query Match: 5.00% Indels: 517
DB: 4 Gaps: 22

US-10-090-458-5 (1-1642) x US-09-252-991A-1780 (1-1824)

QY 441 SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsnValAsnGlyAsnIleSer 460
| | | | | : : : : :
Db 4 TCAGAGTCGATCGCAAGCCGACCCAGTATCCCGGGGAGCGTTGAGATGCAGGTAAGC 63
| | | | | : : : : :
QY 461 PheSerGluIleIleGluProValSerSerGluPheValGlyLysGlu---AlaIleArg 479
| | | | | : : : : :
Db 64 CTGCCATCGCCCGCTGCTGCGGGCGCG-----GGCGAAGACGCTGCCGTCGTC 114
| | | | | : : : : :
QY 480 IleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnValGluAlaLeuArgAsn 499
| | | | | : : : : :
Db 115 ATCGAAGACGTGGACAAGCATTTTC-----GGCGACGTAAAGCGCTGCGGGGC 162
| | | | | : : : : :
QY 500 LeuSerPheAspIleTyrGluGlnIleThrAlaLeuLeuGlyHisSerGlyThrGly 519
| | | | | : : : : :
Db 163 TTGAGCGCGCATCTCACTATGGCGGCTGACGGGTCTGGTGGCGCCCGACGGCGTGGC 222
| | | | | : : : : :
QY 520 LysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSerAspGlyPheAlaSer 539
| | | | | : : : : :
Db 223 AAGACGACGTCGATCGGATTCTGACCGGCTCTGGTGGCGAAGCGCGCGCGTCAAC 282
| | | | | : : : : :
QY 540 IleTyrGlyHisArgValSerGluIleAspGluMetPheGluAlaArgLysMetIleGly 559
| | | | | : : : : :
Db 283 TTGGCAGGCTATGACGTGGTCAAGGACAACGACGACCATTCATGTGCGCAGC-----GGC 336
| | | | | : : : : :
QY 560 IleCysProGlnLeuAspIleHisPheAspValLeuThrValGluGluAsnLeuSerIle 579
| | | | | : : : : :
Db 337 TACATGCCGCAACGCTTTGGCCTGTACGAAGACCTGTCGGTGATGAGAGACATGCGCCTG 396
| | | | | : : : : :
QY 580 LeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGluValGlnLysValLeu 599
| | | | | : : : : :
Db 397 TATGCGCAGTTGGTGGCATGGACGCGACGCAACGCGAGCTGTTCGCGAGTGTCTC 456
| | | | | : : : : :
QY 600 LeuAspLeuAspMetGlnThrIleLysAspAsnGlnAlaLysLysLeuSerGlyGln 619
| | | | | : : : : :
Db 457 GACTTCACGCGGCTCGGACCCCTTCACCAAGCGCTCGCCGCGCAAGCTCTCTGGCGCATG 516
| | | | | : : : : :
QY 620 LysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnProLysIleLeuLeuLeuAsp 639
| | | | | : : : : :
Db 517 AAGCAAAACCTGGCCTGGCCTGGCGCTCATGGCGCGGCCCHAGGTCTCTGCTGGAC 576
| | | | | : : : : :
QY 640 GluProThrAlaGlyMetAspProCysSerArgHisIleValTyrAsnLeuLeuLys--- 658
| | | | | : : : : :
Db 577 GAACCTGGAGTGGCGCTTGATCCCGTCAGCCGCCAGGACCTGTGGCGCATGGTGCAGGCG 636
| | | | | : : : : :
QY 659 TyrArgLysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAlaAspIle 678
| | | | | : : : : :
Db 637 CTGACCGATGAGGCGATGGCGGTGGTCTGGTCCACCGCTACCTCGACGAGGCCGAG--- 693
| | | | | : : : : :
QY 679 LeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySerSerMet 698
| | | | | : : : : :
Db 694 -----CGCTGC----- 699
| | | | | : : : : :
QY 699 PheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCys 718
| | | | | : : : : :
Db 699 ----- 699
| | | | | : : : : :
QY 719 AlaThrGluSerLeuSerSerLeuValLysGlnHisIleProGlyAlaThrLeuLeuGln 738
| | | | | : : : : :
Db 700 -----GAGAGCGTGTGTTA 714
| | | | | : : : : :
QY 739 GlnAsnAspGlnGlnLeuValTyrSerLeuProPheLysAspMetAspLysPheSerGly 758
| | | | | : : : : :
Db 715 CTGAACCGAGGGCAGCTCTTGTGTTGATGTCGCG----- 747
| | | | | : : : : :
QY 759 LeuPheSerAlaLeuAspSerHisSerAsnLeuGlyValIleSerTyrGlyValSerMet 778
| | | | | : : : : :

Db	262	CACGCG-----GTGCTCGGCTATATGCGCGCAGAAAGTTTCGGCCCTGTATGAAGATCTGACG	315
QY	573	ValGluGluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIle	592
Db	316	GTGATGGAACCTGACCCCTGTACGCCGACCTGCGCAGCGTCACCGGC-----	363
QY	593	GlnGluValGlnLysValLeuLeuAsp-----LeuAspMetGlnThrIle	607
Db	364	---GAGGCGCGAAGAAATTTTCGACCGCCCTGCTGGAGTTACCTCTCTTGGTCCATTTC	420
QY	608	LysAspAsnGlnAlaLysLysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIle	627
Db	421	ACCGAACGGCTGGCAGGCAAGCTTCCGGCGGGATGAAGCAAAAGTGGGCGCTCGCCTGT	480
QY	628	AlaValLeuGlyAsnProLysIleLeuLeuLeuAspGluProThrAlaGlyMetAspPro	647
Db	481	ACCCTGGTGGCGATCCGAAAGTACTGCTGCTCGATGAGCCCGCGTCGCGCGTCGACCCCT	540
QY	648	CysSerArgHisIleValTrpAsnLeuLeuLysTyrArgLysAlaAsnArgValThrVal	667
Db	541	ATCTCGCGCGCGAGCTATGGCAGATGGTGACGAGCTGGCCGCGACGGCATGCTGATT	600
QY	668	---PheSerThrHisPheMetAspGluAlaAspIleLeuAlaAspArgLysAlaValIle	686
Db	601	CTGTGGAGCACCTCCTATCTCGATGAAGCGGAACAATGCCCGCAC-----	645
QY	687	SerGlnGlyMetLeuLysCysValGlySerSerMetPheLeuLysSerLysTrpGlyIle	706
Db	645	-----	645
QY	707	GlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeuSerSerLeu	726
Db	645	-----	645
QY	727	ValLysGlnHisIleProGlyAlaThrLeuLeuGlnAsnAspGlnGlnLeuValTyr	746
Db	646	-----GTGCTGCTGATGAACGAAGCAAACTGCTCTAC	678
QY	747	SerLeuProPheLysAspMetAspLysPheSerGlyLeuPheSerAlaLeuAspSerHis	766
Db	678	-----	678
QY	767	SerAsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeu	786
Db	678	-----	678
QY	787	LysLeuGluValGluAlaGluIleAspGlnAlaAspTyrSerValPheThrGlnGlnPro	806
Db	679	-----CAGGGTGAGCCGACGGCGGTGACGCA-----	705
QY	807	LeuGluGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeuLeuIleLeu	826
Db	706	-----ACCATGGCGCGCGCAGCTT-----	726
QY	827	SerGluThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGlnMetTyrThr	846
Db	727	-----CTGGTTTCCAGC-----	738
QY	847	IleAlaLysPheHisPheThrLeuLysArgGluSerLysSerValArgSerValLeu	866
Db	739	-----CAGCAGGAGAACACCGCGCGCTGCTG	765
QY	867	LeuLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuValHisHisSerPhe	886
Db	765	-----	765
QY	887	LysAsnAlaValValProIleLysLeuValProAspLeuTyrPheLeuLysProGlyAsp	906
Db	765	-----	765
QY	907	LysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAspIleSer	926

Db	766	-----CAGCGGGCGCTGAAGCTGCCGACAGGTTAGCGACGGGTGATCCAG	810
Qy	927	AspLeuIleSerPhePheThrSerGlnAsnIleMetValThrMetIleAsnAspSerAsp	946
Db	811	-----GGCAAATCGGTGCTGATCTGATCTGAAAGGACGCGCGC	849
Qy	947	TyrValSerValAlaProHisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyr	966
Db	850	ATTGAGGAAGTCCAGCAGCATGGC-----	873
Qy	967	ValPheAlaAlaValPheAsnSerThrMetValTyrSerLeuProIleLeuValAsnIle	986
Db	873	-----	873
Qy	987	IleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThrIleGlnIleTrpSerThr	1006
Db	873	-----	873
Qy	1007	ProPhePheGlnGluIleThrAspIleValPheLysIleGluLeuTyrPheGlnAlaAla	1026
Db	873	-----	873
Qy	1027	LeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsnAlaGluAsn	1046
Db	874	-----GACATGCCGCCCTGCAGGTGGCCGACACCGCG-----	906
Qy	1047	HisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAlaTyrTrp	1066
Db	906	-----	906
Qy	1067	IleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeuIleLeuMetLeuGly	1086
Db	907	-----CCGCGCTTTGAAGATGCGTTTATCGACCTGCTCGGC	942
Qy	1087	SerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPheLeuAlaValVal	1106
Db	943	GGC-----	945
Qy	1107	PheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSerPheThr	1126
Db	945	-----	945
Qy	1127	PheLysLysIleLeuAsnThrLysGluPheTrpSerPheIleTyrSerValAlaAlaLeu	1146
Db	946	-----GCCGGACCGCTGAA-----	960
Qy	1147	AlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyrThrIleAlaThrIleLeu	1166
Db	960	-----	960
Qy	1167	HisTyrAlaPheCysIleIleIleProIleTyrProLeuLeuGlyCysLeuIleSerPhe	1186
Db	960	-----	960
Qy	1187	IleLysIleSerTrpLysAsnValArgLysAsnValAspThrTyrAsnPro-TrpAspAr	1206
Db	961	-----TCGCCGTGGGGCGC	975
Qy	1206	gLeuSerValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuG1	1226
Db	976	ATTATCCATCGCGTTCACGGCA-----	997
Qy	1226	nTyrTyrGluLysTyrGlyGlyArgSerIleArgLysAspProphePheArgAsnLe	1246
Db	997	-----	997
Qy	1246	uSerThrLysSerLysAsnArgLysLeuProGluProProAspAsnGluaspGluaspG1	1266
Db	997	-----	997
Qy	1266	uAspValLysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluG1	1286
Db	998	-----GCAAAAGAG	1005

Db	889	CTAGTGGCAAAATAGCGCACCACTGAATC-----	918
QY	1050	LysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAlaTyrTrpIleGlyGln	1069
Db	918	-----	918
QY	1070	AlaValAlaSpIleProLeuPhePheIleIleLeuIleLeuMetLeuGlySerLeuLeu	1089
Db	918	-----	918
QY	1090	AlaPheHisTyrGlyLeuTyrPheTyrThrValLysPheLeuAlaValPheCysLeu	1109
Db	918	-----	918
QY	1110	IleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSerPheThrPheLysLys	1129
Db	918	-----	918
QY	1130	IleLeuAsnThrLysGluPheTrpSerPheIleTyrSerValAlaAlaLeuAlaCysIle	1149
Db	918	-----	918
QY	1150	AlaIleThrGluIleThrPhePheMetGlyTyrThrIleAlaThrIleLeuHisTyrAla	1169
Db	919	-----GAAGATGTTTATGATG-----	936
QY	1170	PheCysIleIleIleProIleTyrProLeuLeuGlyCysLeuIleSerPheIleLysIle	1189
Db	936	-----	936
QY	1190	SerTrpLysAsnValArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSerVal	1209
Db	936	-----	936
QY	1210	AlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyrGlu	1229
Db	937	-----TTGTTACAGCAAAATCAA	954
QY	1230	LysLysTyrGlyArgSerIleArgLysAspProPhePheArgAsnLeuSerThrLys	1249
Db	955	AAACAACAA-----ATCTCTATTCTCAGCAGGCTTT-----	987
QY	1250	SerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspValLys	1269
Db	988	-----CGATCGAACAACAATAATTCGAATCAGACCAAGCGGTC---	1029
QY	1270	AlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysProSer	1289
Db	1029	-----	1029
QY	1290	IleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSerArg	1309
Db	1030	ATTGTAGTTAAAGATTAGTCAGAACTTTTGGAGAT-----	1065
QY	1310	LysValLysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluIleLeu	1329
Db	1066	-----TTTACTGCTGTGGCCAAATACGTCACTTACTGTACAGCGTGGAGAGATCTTT	1116
QY	1330	GlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGlyAsp	1349
Db	1117	GGGTACTTGGGCCAAATGGAGCTGGTAAACCCAGCAATCCGCATGTTATGTGGGTTA	1176
QY	1350	IleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGluAsp	1369
Db	1177	CTACCGCAAGTAGCGTTACCTAGAAGTTGCAGGTAAAAAACCCTACGGACGCCCGTGCT	1236
QY	1370	AspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAspThr	1389
Db	1237	GAAGCAAGAGCTAAA--GTAGGCTACGTCTCTCAAAAATTTGCACGTATAGCAATT	1293
QY	1390	ThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAspMet	1409

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Db      1294 ACTGTGTTGGAAACTTAAAGTTCTTTGGTGGAGCCCTATGGTTTATCGGCGCAAAAACCTA 1355
QY      1410 LysGluValIleSerArgIleThrHisAlaLeuAaspLeuLysGluHisLeuGlnLysThr 1429
Db      1354 GATCAACAAATTGATAAAGCTTTTACAACAATATGATTTAAAGCCGCAAAATTAAAGC--- 1410
QY      1430 ValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeuGly 1449
Db      1411 ---GGTGATTTACCTGGTGGTTATAAACAGCGCTTATCTATGGCGGCTGCATTATTACAT 1467
QY      1450 AsnProGlnIleThrLeuLeuAaspGluProSerThrGlyMetAaspProLysAlaLysGln 1469
Db      1468 GAACCAGAAATTTTATTTTATAGACGAACCTACGAGTGAATAGACCCGCTGCACGGCGT 1527
QY      1470 HisMetTyrArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeuThr 1489
Db      1528 TTATTTTGGTACAGCATT--GGTAAACTCGCAAATCAAGGCATTACCATCATTTATTACC 1584
QY      1490 ThrHisTyrMetGluGluAlaGluAlaValCysAaspArgValAlaIleMetValSerGly 1509
Db      1585 ACTCATTTTATGGAGGAAGCAGAA--TATTGTGACCGCATTTGCCATACAAAGATGCAGGA 1641
QY      1510 GlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLys 1526
Db      1642 AAGTTACTAGCCCTAGGTTCTCTCTCAACAGGTCGCGAATTGGCAAGTAAA 1692

RESULT 11
US-09-489-039A-6408
; Sequence 6408, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBS
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6408
; LENGTH: 1767
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6408

Alignment Scores:
Pred. No.: 1.2e-34 Length: 1767
Score: 426.00 Matches: 187
Percent Similarity: 29.49% Conservative: 125
Best Local Similarity: 17.67% Mismatches: 231
Query Match: 5.06% Indels: 516
DB: 4 Gaps: 21

US-10-090-458-5 (1-1642) x US-09-489-039A-6408 (1-1767)
QY      473 ValGlyLysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGlu 492
Db      28 ATGAGTGAGACCGTCATCGCCTTAAACGGCCTGAGCCGC-----CGTTTCCCGGTATG 81
QY      493 AsnValGluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeu 512
Db      82 GACAGGCCACGGTAGCGCCGCTCACCTGCACGATCCGCGCCGGCTACGTCACCGGGCTG 141
QY      513 LeuGlyHisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysPro 532
Db      142 GTGGGGCCCGACGCGCGGGGAAAACCAACCCTGATGCGAATGCTCGCCGGATTGCTCAA 201
QY      533 ProSerAaspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAaspGluMetPhe 552
Db      202 CCTGATGAGGCCGCGCCAGCGTGTAGGCTTCGACCCGCTAAAGACGACAGCGCCCTG 261
QY      553 GluAlaArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAaspValLeuThr 572

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Db 2454 AAGCCAACCTCCTGCCACAGCCAGCGGTGAGGTCTCTGCCACTCTCTGGGAGAGGAGGACGA 2513

QY 1266 uAspVallysAlaGluArgLeuLysVallysGluLeuMetGlyCysGlnCysCysGluG1 1286

Db 2514 GGATGTAGCCCGTGAACGGAGCGGTG-----GTCCAAGGAGCCACCCA 2558

QY 1286 uLysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLe 1306

Db 2559 GGGGGATGTGTGGTCTGAGGAACCTGACCAAGGTATAC----- 2598

QY 1306 uLeuSerArgLysVallysLysValAlaThrLysTyrIleSerPheCysVallysLysG1 1326

Db 2599 -----CGTGGCAGAGGATGCCAGCTGTGACCGCTTGTGCTGGGGATTCCCCCTGG 2651

QY 1326 yGluIleLeuGlyLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLe 1346

Db 2652 TGAGTGTTTTGGGCTGCTGGTGTGAATGAGCAGGGAAGACGTCACGTTTCGCATGCT 2711

QY 1346 uValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluTh 1366

Db 2712 GACGGGGACACATTTGGCCAGCAGGGGCGGAGCTGTGCTGGCAGGCAC---AGCGTGGC 2768

QY 1366 rSerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTr 1386

Db 2769 CCGGGAACCCAGTGTGCGCACCTCAGCATGGGATACTGCCCTCATCCGATGCCATCT 2828

QY 1386 pProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaVallysGlyMetSerAl 1406

Db 2829 TGAGCTGTGACGGGCGCGAGCACCTGGAGCTGCTTGGCGCCCTGGCGGTGTCCCGGA 2888

QY 1406 aSerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLe 1426

Db 2889 GGCCACAGTTGCCAGACCGCTGGCTCGGGCTGGCGCTCTGGGACTCTCATGGTACGC 2948

QY 1426 uGlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSe 1446

Db 2949 AGACCGGCTGACGGCACCTACAGCGGAGGGAACAAACGCAAGTGGCGACGGCCCTGGC 3008

QY 1446 rMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLy 1466

Db 3009 GCTGGTTGGGACCCAGCGTGTGTTTCTGGACGAGCCGACCAAGCATGGACCCGAG 3068

QY 1466 sAlaLysGlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAl 1486

Db 3069 CGCGCGCGCTTCCTTTGAAACAGCCTT---TTGCCGTGGTGGGAGGGCCGTTTCAGT 3125

QY 1486 aIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMe 1506

Db 3126 GATGCTCACCTCCCATAGCATGGAGGAGTGTGAAGCGCTCTGTCGCGCTGGCCATCAT 3185

QY 1506 tValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLy 1526

Db 3186 GGTGAATGGCGGTTCCGCTGCTGGCAGCCCGCAACATCTCAAGGGCAGATTTCGCGGC 3245

QY 1526 sGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLe 1546

Db 3246 GGGTCACACACTGACCCCTGCGG-----GTGCCCGCGCAAGGTC 3284

QY 1546 uGlnArgGluIleGlnTyrIle-----PheProAsnAlaSerArgGlnGluSerPh 1563

Db 3285 CCAGCGCGCAGCGCCTTCGTGGCGGCGGAGTTCCCTGGGCGGAGCTGCGGAGGCACA 3344

QY 1563 eSerSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPh 1583

Db 3345 TGGAGCGCGCTGCGCTTCCAGTCCCGCGGAGGGCGGTGCGCCCTGGCGCGCTCTT 3404

QY 1583 ePheLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAl 1603

Db 3405 TGGAGAGCTGGCGGTGCACGGCGCAGAGCACGGCGTGGAGGACTTTTCC----- 3453

QY 1603 aThrLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAspAsnSer 1622

Db 3454 -----GTATTCTTGTACTTCTCCAAGGACCGAGGGAAGGAGGACACC 3498

RESULT 8

US-09-621-976-409

; Sequence 409, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 409

; LENGTH: 485

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 185..484

US-09-621-976-409

Alignment Scores:

Pred. No.:	4,44e-45	Length:	485
Score:	515.00	Matches:	100
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	6.11%	Indels:	0
DB:	4	Gaps:	0

US-10-090-458-5 (1-1642) x US-09-621-976-409 (1-485)

QY 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLys 20

Db 185 ATGTCCACTGCAATTAGGGAGGTAGGAGTTTGGAGACAGACCAGAACTTCTACTGAAG 244

QY 21 AsnTyrLeuIleLysCysArgThrLysLysSerValGlnGluIleLeuPheProLeu 40

Db 245 AATTACTTAATTAATGCAGAACCAAAAGAGTAGTGTTCAGGAAATCTTTTCCACTA 304

QY 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60

Db 305 TTTTITTTATTTGGTTAATATTAAATTAGCATGATGCATCCAAATAGAAATATGAAGAA 364

QY 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80

Db 365 GTGCTAATATAGAACTCAATCCTATGGACAAAGTTTACTCTTTCTAATCTAATCTTTGA 424

QY 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100

Db 425 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 484

RESULT 9

US-09-833-381-962

; Sequence 962, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 962

; LENGTH: 2075

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:


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; SEQ ID NO 1082
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1082

Alignment Scores:
Pred. No.:      3,87e-85      Length:      1350
Score:          900.50        Matches:      186
Percent Similarity: 69.14%    Conservative: 56
Best Local Similarity: 53.14% Mismatches:      96
Query Match:     10.69%      Indels:       12
DB:              4          Gaps:         3

US-10-090-458-5 (1-1642) x US-09-833-381-1082 (1-1350)

QY 1285 GluGluLysProSerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAsp 1304
Db 6 GATGAGAAACCTGTTATAATTGCCAGCTGTCTACACAAAGAAATATGCAGGCCAGAGAAA 65

QY 1305 PheLeuLeuSerArgLysValLysValAlaThrLysTyrIleSerPheCysValLys 1324
Db 66 AGTTGCTTTCAAAGAGGAAGAAATAATAGCAGCAAGAAATATCTCTTCTGTGTCAA 125

QY 1325 LysGlyGluIleLeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsn 1344
Db 126 GAAGATGAATTTTGGGATTGCTAGGACCCCAATGGTGTGGAAAAAGTTTCATCTATTAGA 185

QY 1345 IleLeuValGlyAspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSer 1364
Db 186 ATGATATCTGGGATCAAAAGCCAACTGCTGGAGAGGTGGAACCTGAAAGGCTGCAGTTCA 245

QY 1365 GluThrSerGluAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnPro 1384
Db 246 -----GTTTGGGCCACCTGGGGTACTGCGCTCAAGAACGTCG 284

QY 1385 LeuTyrProAspThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMet 1404
Db 285 CTGTGGCCCATGCTGACGTTGAGGGAACACCTGGAGGTGTATGTCGCGTCAAGGGGCTC 344

QY 1405 SerAlaSerAspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGlu 1424
Db 345 AGGAAAGCGGACGCGAGGCTCGCCATCGCAAGATTAGTGAGTGTCTTCAAACACTGCATGAG 404

QY 1425 HisLeuGlnLysThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAla 1444
Db 405 CAGCTGAATGTTCTGTGCAGAAATTAACAGCAGGAATCACAGAGAAAGTTGTGTTTGTG 464

QY 1445 LeuSerMetLeuGlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAsp 1464
Db 465 CTGAGCCTCCTGGAAACTCCCTTCCGTGCTCTGGATGAACCATCTACGGGCATAGAC 524

QY 1465 -ProLysAlaLysGlnHisMetTyrArgAlaIleArgThrAlaPheLysAsnArgLysAr 1484
Db 525 CCCACAGGGCAGCCAGCAAAATGTGGCAGGCAATCCAGGCAGTCGTTTAAAAACACAGAGAG 584

QY 1484 gAlaAlaIleLeuThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAl 1504
Db 585 AGGTGTCCTCCTGACCAACCATAACTGGCTGAGCGGGAAGCCTTGTGTGACCGTGTGGC 644

QY 1504 aIleMetValSerGlyGlnLeuArgCysIleGlyThrValGlnHisLysSerLysph 1524
Db 645 CATCATGGTGTCTGGAAGGCTTAGATGCATTGGCTCCATCCACACCTGAAAAACAAACT 704

QY 1524 eGlyLysGlyTyrPheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAs 1544
Db 705 TGGAAGGATTACATTCTAGAGCTAAAAGTGAAG-----GAAACGCTCTCAAGTGAC 755

QY 1544 pArgLeuGlnArgGluIleGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSe 1564
Db 756 TTTGGTCCACACTGAGATTCTGAAGCTTTTCCACACAGCTGCAGGGCAGGAAAGGTATTTC 815

QY 1564 rSerIleLeuAlaTyrLysIleProLysGluAspValGlnSerLeuSerGlnSerPhePh 1584
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Db 816 CTCCTTTGTTAACTATAAGCTGCGCGTGGCAGACGTTTACCTCTATCACAGACCTTCA 875

QY 1584 eLysLeuGluGluAlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaTh 1604
Db 876 CAAATTAGAAGCAGTGAAGCATAACTTTAACTGGAGAAATACAGCCTTCTCAGTCAC 935

QY 1604 rLeuGluGlnValPheValGluLeuThrLysGluGlnGluGluAspAsnSerCysGl 1624
Db 936 ACTGGAGAGGTATTCTTAGAGCTTCTTAAAGAACAG---GAAGTAGGAAATTTTGATGA 992

QY 1624 yThrLeuAsnSerThrLeuTyrTrpGlu 1633
Db 993 AGAAATTGATACAACAATGAGATGGAAA 1020

RESULT 7
US-09-833-381-958
; Sequence 958, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 958
; LENGTH: 3609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-958

Alignment Scores:
Pred. No.:      1.62e-57      Length:      3609
Score:          647.00        Matches:      269
Percent Similarity: 37.34%    Conservative: 194
Best Local Similarity: 21.69% Mismatches:      420
Query Match:     7.68%      Indels:       357
DB:              4          Gaps:         38

US-10-090-458-5 (1-1642) x US-09-833-381-958 (1-3609)

QY 639 AspGluProThrAlaGlyMetAspProCysSerArg-----HisIleVal-TrpAsnLe 656
Db 84 GAACAAAGCTACAGCGCGCTCCGTCCTCCCAAGATCAACCGCTCCATGCAGAACTGGCACCA 143

QY 656 uLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPheMetAspGluAl 676
Db 144 GCTAGAA--AACCTGTCCAACCTTCATCAAGGCCATGGTCAGCTACGGCATGAACCTGT 200

QY 676 aAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLysCysValGlySe 696
Db 201 GGACCTGTTTCGAGGCCAACGACCTGTTTGAGAGTGGGAACATGACGGCAGGTGCTGTC 260

QY 696 rSerMetPheLeuLysSerLys-----TrpGl 705
Db 261 TCTTCTGCGCCTGGCGGGAAGGTCAACCAATGCCTTCTCCAGGGAGACTGGGGTGGG 320

QY 705 yIleGlyTyrArgLeuSerMetTyrIleAspLysTyrCysAlaThrGluSerLeuSerSe 725
Db 321 CGTGAGCGGGGCTCCCTGAAGCACCCCTTTGTGCACACAGGCACCTCCTCAGCTGCTGGC 380

QY 725 rLeuValLysGlnHisIleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnLeuVa 745
Db 381 CCTGTACAGCACTGGGTGCGCGGGGCACGGCTGTGTGGAGAGTGCACACAGAGCTGGT 440

QY 745 lTyrSerLeuProPheLysAspMet-----AspLysPheSerGlyLeuPheSerAlaLe 763
Db 441 GCTGTGCTGCCCTACACGGGTGCCCATGACGGCAGCTTCGCCACACTCTTCGAGAGCT 500
```

Db 6135 GTTGGCAAGTTGGTGAGTGGCGGATTCGGAAACTGGGCCCTCGTGAAGTATGGAGAAAA 6194

Qy 1429 ThrValLysLysLeuProAlaGlyIleLysArgLysLeuCysPheAlaLeuSerMetLeu 1448

Db 6195 TATGCTGGTAACATATAGTGGAGGCAACAAACGAAGCTCTCTACAGCCATGGCTTTGATC 6254

Qy 1449 GlyAsnProGlnIleThrLeuLeuAspGluProSerThrGlyMetAspProLysAlaLys 1468

Db 6255 GCGGGCCCTCCTGTGGTGTCTTGATGAACCCACCACAGGATGGATCCCAAAGCCCGG 6314

Qy 1469 GlnHisMetTrpArgAlaIleArgThrAlaPheLysAsnArgLysArgAlaAlaIleLeu 1488

Db 6315 CGGTCTCTGTGGAATTGTGCCCTAAGTGTGTCAAG---GAGGGAGATCAGTAGTGCTT 6371

Qy 1489 ThrThrHisTyrMetGluGluAlaGluAlaValCysAspArgValAlaIleMetValSer 1508

Db 6372 ACATCTCATAGTATGAAGAATGTGAAGCTCTTGACACTAGGATGGCAATCATGGTCAAT 6431

Qy 1509 GlyGlnLeuArgCysIleGlyThrValGlnHisLeuLysSerLysPheGlyLysGlyTyr 1528

Db 6432 GGAAGGTTTCAGTGCCCTTGGCAGTGTCCAGCATCTAAATAATAGTTTGGAGATGGTTAT 6491

Qy 1529 PheLeuGluIleLysLeuLysAspTrpIleGluAsnLeuGluValAspArgLeuGlnArg 1548

Db 6492 ACAATAGTTTACGAATAGCAGG-----TCCAACCCCGACCTGAAGCCTGTCCAGGAT 6545

Qy 1549 GluIleGlnTyrIlePheProAsnAlaSerArgGlnGluSerPheSerIleLeuAla 1568

Db 6546 TTCTTTGGACTTCGATTTCTCTGGAGTGTCTAAAGAGAAACACCGGAACATGCTACAA 6605

Qy 1569 TyrLysIleProLysGluAspValGlnSerLeuSerPhePheLysLeuGluGlu 1588

Db 6606 TACCAGCTTCCA---TCTTCATTATCTCTCTGGCCAGGATATTCAGCATCCTCTCCCGAG 6662

Qy 1589 AlaLysHisAlaPheAlaIleGluGluTyrSerPheSerGlnAlaThrLeuGluGlnVal 1608

Db 6663 AGCAAAAAGCGACTCCACATAGAAGACTCTGTGTTCTCAGACAACTTGACCAAGTA 6722

Qy 1609 PheValGluLeuThrLysGluGlnGluGluAspAsn----- 1621

Db 6723 TTTGTGAACCTTGGCAAGGACCAAAAGTGATGATGACCACTTAAAGACCTCTCATTTACAC 6782

Qy 1622 -----SerCysGlyThrLeuAsnSerThrLeuTrpTrpGluArgThr 1635

Db 6783 AAAAACCCAGACAGTAGTGACGTTGCAGTGTCTCACATCTTTTCTACAGGATGAGAAAGTG 6842

Qy 1636 GlnGluAsp-----ArgValValPhe 1642

Db 6843 AAAGAAAGCTATGATGATGAAGAATCCTGTTT 6872

RESULT 5

US-09-833-381-1085

; Sequence 1085, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; PRIOR FILING DATE: 2001-04-11

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1085

; LENGTH: 974

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-833-381-1085

Alignment Scores: 3.24e-122 Length: 974

Pred. No.: 1248.00 Matches: 245

Score:

Percent Similarity: 100.00% Conservative: 2

Best Local Similarity: 99.19% Mismatches: 0

Query Match: 14.81% Indels: 0

DB: 4 Gaps: 0

US-10-090-458-5 (1-1642) x US-09-833-381-1085 (1-974)

Qy 1 MetSerThrAlaIleArgGluValGlyValTrpArgGlnThrArgThrLeuLeuLys 20

Db 233 ATGTCCACTGCAATTAGGGAGGTAGGAGTTGGAGACAGACCAGAACACTTCTTACTGAAG 292

Qy 21 AsnTyrLeuIleLysCysArgThrLysLysSerSerValGlnGluIleLeuPheProLeu 40

Db 293 AATTACTTAATAATGCAGAACCAAAAAAGAGTAGTGTTCAGGAATTCCTTTTCCACTA 352

Qy 41 PhePheLeuPheTrpLeuIleLeuIleSerMetMetHisProAsnLysLysTyrGluGlu 60

Db 353 TTTTTTTATTGTTTAAATATTATTAGCATGATGCATCCAAATAAAGAAATATGAAGAA 412

Qy 61 ValProAsnIleGluLeuAsnProMetAspLysPheThrLeuSerAsnLeuIleLeuGly 80

Db 413 GTGCCATAATAGAACTCAATCCTATGGACAAGTTTACTCTTTCTTAATCTAATTTCTTGA 472

Qy 81 TyrThrProValThrAsnIleThrSerSerIleMetGlnLysValSerThrAspHisLeu 100

Db 473 TATACTCCAGTGACTAATATTACAAGCAGCATCATGCAGAAAGTGTCTACTGATCATCTA 532

Qy 101 ProAspValIleIleThrGluGluTyrThrAsnGluLysGluMetIleuThrSerSerLeu 120

Db 533 CCTGATGTCATAATTACTGAAGAATATACAAATGAAAGAAATGTTAACATCCAGTCTC 592

Qy 121 SerLysProSerAsnPheValGlyValValPheLysAspSerMetSerTyrGluLeuArg 140

Db 593 TCTAAGCCGAGCAACTTTGTAGGTGGTGTTCAAAGACTCCATGTCCTATGAACCTCGT 652

Qy 141 PhePheProAspMetIleProValSerSerIleTyrMetAspSerArgAlaGlyCysSer 160

Db 653 TTTTCTCTGATGATGATCCAGTATCTTCTATTTATATGGATTCAAGAGCTGGCTGTTCA 712

Qy 161 LysSerCysGluAlaAlaGlnTyrTrpSerSerGlyPheThrValLeuGlnAlaSerIle 180

Db 713 AAATCATGTGAGGCTGCTCAGTACTGGTCTCAGGTTTCACAGTTTTACAGCATCCATA 772

Qy 181 AspAlaAlaIleIleGlnLeuLysThrAsnValSerLeuTrpLysGluLeuGluSerThr 200

Db 773 GATGCTGCCATTATACAGTTGAAGACCAATGTTTCTCTTTGGAAGAGCTGGAGTCAACT 832

Qy 201 LysAlaValIleMetGlyGluThrAlaValValGluIleAspThrPheProArgGlyVal 220

Db 833 AAAGCTGTTATTATCGGAGAAACTGCTGTGTAGAAATAGATACCTTTCCCGAGGAGTA 892

Qy 221 IleLeuIleTyrLeuValIleAlaPheSerPropheGlyTyrPheLeuAlaIleHisIle 240

Db 893 ATTTTAATATACCTAGTTATAGCATTTTTCACCTTTTGGATACCTTTTGGCAATTCATATC 952

Qy 241 ValAlaGluLysGluLysLys 247

Db 953 GTAGCAAAAAAATAAAAAA 973

RESULT 6

US-09-833-381-1082

; Sequence 1082, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; PRIOR FILING DATE: 2001-04-11

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSeq for Windows Version 3.0

QY 882 ----- 882
Db 4176 GTGCCACCCTTTGGCAAGTACCCGAGCCTGGAACCTTCAGCCCTGGATGTACAAAGAACAG 4235
QY 882 ----- 882
Db 4236 TACACATTGTCAGCAATGATGCTCCTGAGGACACGGGAACCCCTGGAACCTCTTAAACGCC 4295
QY 882 ----- 882
Db 4296 CTCACCAAGACCCTGGCTTCGGGACCCGCTGTATGGAAGAAACCCCAATCCAGACACG 4355
QY 883 -----HisHisSerPheLysAsnAlaValProIleLysLeuValPro 897
Db 4356 CCCTGCCAGCGAGGAGGAGAGAGTGGAACCACTGCCCCAGTTCCC--CAGACCATCATG 4412
QY 898 AspLeuTyr----- 900
Db 4413 GACCTCTTCCAGAATGGAACTGGACAATGCAGAACCCCTTCACCTGCATGCCAGTGTAAGC 4472
QY 901 -----PheLeuLysProGly-----Asp 906
Db 4473 AGGACAAAATCAAGAAGATGCTGCCTGTGTGTCCTCCCGGAGGGGGCTGCCTCCT 4532
QY 907 LysProHisLysTyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAspIleSer 926
Db 4533 CCACAAAGAAAACAAACACTGCAGATATCCTTCAGGACCTGCAGAGAAAGAAACATTTCCG 4592
QY 927 Asp-----LeuIleSerPhePheThrSerGlnAsnIleMet 938
Db 4593 GATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGCTTAAAGAACAGATCTGG 4652
QY 939 ValThr----- 940
Db 4653 GTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGTAATACTCAAGCATTCTCCT 4712
QY 941 -----MetIleAsnAspSer-----AspTyrValSerValAlaPro 952
Db 4713 CCGAGTCAAGAGTTAATGATGCCATCAAAACAAATGAAGAAACACCTAAAGCTGGCCAAAG 4772
QY 953 HisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyrVal----- 967
Db 4773 GACAGTTCTGCAGATCGATTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACC 4832
QY 968 -----PheAlaAlaValPheAsnSerThrMetValTyrSerLeuProIleLeuVal 984
Db 4833 AGAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTG 4892
QY 985 AsnIleIleSerAsnTyrTyrLeu----- 992
Db 4893 AATGTCATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAGAACCCCTAGCCAT 4952
QY 993 -----TyrHisLeuAsnValThrGluThrIleGlnIleTrpSer 1005
Db 4953 TATGGAATTACTGCTTTCAATCATCCCTGAAATCTCAACCAAGCAG--CAGCTCTCAGAG 5009
QY 1006 ThrProPhePheGlnGluIleThrAspIleValPheLysIleGluLeuTyrPheGlnAla 1025
Db 5010 GTGGCTCTGATGACCACATCAGTGGATGTCTCTGTGTCCATCTGTGTCTATCTTT----- 5063
QY 1026 AlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsnAlaGlu 1045
Db 5064 -----GCAATGTCCTTCGTCCCGAGCAGCTTTGTGCTATTCTCTGATCCAG 5108
QY 1046 AsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAlaTyr 1065
Db 5109 GAGCGGGTCAGCAAGCAAAACACCTGCAGTTTCATCATGTGAGTGAAGCCTGTCTATCTAC 5168
QY 1066 TrpIleGlyGlnAlaValAlaAspIleProLeuPhePheIleIleLeuIleLeuMetLeu 1085
Db 5169 TGGCTCTCTAATTTTGTCTGGGATATGTGCAATTACGTGTCCTGCCACACTGGTTCATT 5228
QY 1086 GlySerLeuLeuAlaPheHisTyrGlyLeuTyrPheTyrThrValLysPheLeuAlaVal 1105

Db 5229 ATCATCTTCATCTGCTTCCAGCAGAAAGTCTCTATGTGCTCTCCACCAATCTGCCTGTGCTA 5288
QY 1106 ValPheCysLeuIleGlyTyrValProSerValIleLeuPheThrTyrIleAlaSerPhe 1125
Db 5289 GCCCTTCTACTTTTGTGTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCTCTTT 5348
QY 1126 ThrPheLysLysIleLeuAsnThrLysGluPheTrpSerPheIleTyrSerValAlaAla 1145
Db 5349 GTGTTCAAG-----ATCCCAGC 5366
QY 1146 LeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyr-----ThrIleAla 1163
Db 5367 ACAGCCTATGTGTGCTCACCGAGGTGAACCTCTTCAATTGGCATTAATGGCAGCGTGCC 5426
QY 1164 Thr-----IleLeuHis 1167
Db 5427 ACCTTTGTGCTGGAGCTGTTCCACCGACAATAAGCTGAATAATATCAATGATATCCTGAAG 5486
QY 1168 TyrAlaPheCysIleIleIleProIleTyrProLeuLeuGlyCysLeuIleSerPheIle 1187
Db 5487 TCCGTGTTCTTGGATCTTCCACATTTTGCCTGGGACGAGGGCTCATCGACATGGTG 5543
QY 1188 Lys----- 1188
Db 5544 AAAAACCCAGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAAATCGCTTTGTGTACCA 5603
QY 1189 IleSerTrpLysAsnValArgLysAsnValAspThrTyrAsnProTrpAspArgLeuSer 1208
Db 5604 TTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCC-----ATGGCC 5645
QY 1209 ValAlaValIleSerProTyrLeuGlnCysValLeuTrpIlePheLeuLeuGlnTyrTyr 1228
Db 5646 GTGGAAGGGTGGTGTCTTCTCTCATTTACTGTT-----CTGATCCAGTAC-- 5690
QY 1229 GluLysLysTyrGlyArgSerIleArgLysAspProphePheArgAsnLeuSerThr 1248
Db 5691 -----AGATTCTTC-----ATCAGGCCC 5708
QY 1249 LysSerLysAsnArgLysLeuProGluProProAspAsnGluAspGluAspVal 1268
Db 5709 AGACCTGTAAATGCAAGCTA-----TCTCCTCTGAAT--GATGAAGATGAAGATGTG 5759
QY 1269 LysAlaGluArgLeuLysValLysGluLeuMetGlyCysGlnCysCysGluGluLysPro 1288
Db 5760 AGCGGGAAGACAGAGAAATCTTGTATGTTGGAGGC-----CAGAATGAC 5804
QY 1289 SerIleMetValSerAsnLeuHisLysGluTyrAspAspLysLysAspPheLeuLeuSer 1308
Db 5805 ATCTTAGAAATCAAGGAGTTGACGAAGATATAT----- 5837
QY 1309 ArgLysValLysLysValAlaThrLysTyrIleSerPheCysValLysLysGlyGluIle 1328
Db 5838 AGAAGGAAGCGGAAGCCTGCTGTGTGACAGGATTTGCGTGGGCATTCCTCCTGGTGTGAGTGC 5897
QY 1329 LeuGlyLeuLeuGlyProAsnGlyAlaGlyLysSerThrIleIleAsnIleLeuValGly 1348
Db 5898 TTTGGCTCCTGGGAGTTAATGGGCTGGAAATCATCAACTTTCAAGATGTTAACAGGA 5957
QY 1349 AspIleGluProThrSerGlyGlnValPheLeuGlyAspTyrSerSerGluThrSerGlu 1368
Db 5958 GATACCACTGTTACCAGAGGAGATGCTTTTCTT--AACAAAAATAGTATCTTATCAAAAC 6014
QY 1369 AspAspAspSerLeuLysCysMetGlyTyrCysProGlnIleAsnProLeuTrpProAsp 1388
Db 6015 ATCATGAAGTACATCAGAAACATGGGCTACTGCCCTCAGTTTGTATGCCATCAGAGCTG 6074
QY 1389 ThrThrLeuGlnGluHisPheGluIleTyrGlyAlaValLysGlyMetSerAlaSerAsp 1408
Db 6075 TTGACTGGGAGAGAACACCGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA 6134
QY 1409 MetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeuGlnLys 1428

Db 2055 TATGAGAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGCGCTGGACAAACAGCATC 2114
Qy 262 PheTrpLeuSerTrpValLeuLeuTyrThrSerLeuIlePheLeuMet-----Ser 278
Db 2115 CTCTGGTTTAGTGGTTCATT-----AGTAGCCTCATTCCTCTCTTGTGTAGCGCTGGC 2168
Qy 279 LeuLeuMetAlaValIleAlaThrAlaSerLeuPheProGlnSerSerSerIleVal 298
Db 2169 CTGCTAGTGGTCATCCTGAAGTTAGGAACCTGCTG---CCCTACAGTGATCCCAGCGTG 2225
Qy 299 IlePheLeuLeuPhePheLeuTyrGlyLeuSerSerValPhePheAlaLeuMetLeuThr 318
Db 2226 GTGTTTGTCTTCTCTCGTGTGTTTGTGTGGTGACAATCCTGCAGTGTCTTCTGTATTAGC 2285
Qy 319 ProLeuPheLysSerLysHisVal-----GlyIleValGluPhePheVal 334
Db 2286 ACACCTCTTCCAGAGCCAACTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTG 2345
Qy 335 ThrValAlaPhe-----GlyPheIleGlyLeuMetIleIleLeu 347
Db 2346 TACCTGCCCTACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATC 2405
Qy 348 IleGluSerPheProLysSerLeuValTrpLeuPheSerProPheCysHisCysThrPhe 367
Db 2406 TTCGCTAGC-----CTGCTGTCTCCT-----GTGGCTTTT 2435
Qy 368 ValIleGlyIleAlaGlnValMetHisLeuGluAspPheAsnGluGlyAlaSerPheSer 387
Db 2436 GGGTTTGGCTGTGAGTACTTTTGCCCTTTTGTGAGGAGCAGGGCATGGAGTGCAGTGGGAC 2495
Qy 388 AsnLeuThrAlaGlyPro-----TyrProLeuIleIleThrIleMet 402
Db 2496 AACCTGTTTGAGAGTCTGTGGAGGAAGATGGCTTCAATCTCACACTTCGGTCTCCATG 2555
Qy 403 LeuThrLeuAsnSerIlePheTyrValLeuLeuAlaValTyrLeuAspGlnValIlePro 422
Db 2556 ATGCTGTTTGACACCTTCTCTATGGGFGATGACCTGGTACATTGAGGCTGTCTTTCCA 2615
Qy 423 GlyGluPheGlyLeuArgArgSerSerLeuTyrPheLeuLysProSerTyrTrp----- 440
Db 2616 GGCCAGTACGGAATCCAGGCCCTGGTATTTTCTTGACCAAGTCTACTGTTTGGC 2675
Qy 441 -----SerLysSerLysArgAsnTyrGluGluLeuSerGluGlyAsn 454
Db 2676 GAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAGAGAAATATCAGAA----- 2729
Qy 455 ValAsnGlyAsnIleSerPheSerGluIleIleGluProValSerSerGluPheValGly 474
Db 2730 -----ATCTGCATGGAGGAG-----GAACCCACCCTTG----- 2759
Qy 475 LysGluAlaIleArgIleSerGlyIleGlnLysThrTyrArgLysLysGlyGluAsnVal 494
Db 2760 AAGCTGGCGTGCTCCATTAGAACCTGGTAAAGTCTACCGA---GATGGATGAAGGTG 2816
Qy 495 GluAlaLeuArgAsnLeuSerPheAspIleTyrGluGlyGlnIleThrAlaLeuLeuGly 514
Db 2817 ---GCTGTCGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACCTCCTTCTCTGGGC 2873
Qy 515 HisSerGlyThrGlyLysSerThrLeuMetAsnIleLeuCysGlyLeuCysProProSer 534
Db 2874 CACAATGAGGGGGGAGACGACCACTGTCATCTCTGACCGGGTGTTCCTCCCGGACC 2933
Qy 535 AspGlyPheAlaSerIleTyrGlyHisArgValSerGluIleAspGluMetPheGluAla 554
Db 2934 TCGGGCACCGCTACATCTCTGGGAAAAGACATTGCG-----TCTGAGATGAGCACCATC 2987
Qy 555 ArgLysMetIleGlyIleCysProGlnLeuAspIleHisPheAspValLeuThrValGlu 574
Db 2988 CGGCAGAACCTGGGGGTCTGTCCCCAGCATACGTGCTGTTTGACATGCTGACTGTICGAA 3047
Qy 575 GluAsnLeuSerIleLeuAlaSerIleLysGlyIleProAlaAsnAsnIleIleGlnGlu 594
Db 3048 GAACACATCTGGTTCTATGCCCGCTTGAAAGGGCTCTCTGAGAAGCACGTGAAGCGGAG 3107

Qy 595 ValGlnLysValLeuLeuAspLeuAspMetGlnThrIleLys---AspAsnGlnAlaLys 613
Db 3108 ATGGAGCAGATGGCCCTGGATGTTGGTTTGCATCAAGCAAGCTGAAAAACAAGC 3167
Qy 614 LysLeuSerGlyGlyGlnLysArgLysLeuSerLeuGlyIleAlaValLeuGlyAsnPro 633
Db 3168 CAGCTGTAGGTGAATGCAGAGAAAGCTATCTGTGGCCTTGGCCCTTGTTCGGGGATCT 3227
Qy 634 LysIleLeuLeuAspGluProThrAlaGlyMetAspProCysSerArgHisIleVal 653
Db 3228 AAGGTTGTCTATTCTGGATGAACCCACAGCTGGTGTGGACCTTACTCCCGCAGGGGAATA 3287
Qy 654 TrpAsn---LeuLeuLysTyrArgLysAlaAsnArgValThrValPheSerThrHisPhe 672
Db 3288 TGGGAGCTGCTGCTGAAATACCGACAA---GGCCGCACCATATTATTCTCTACACACCAC 3344
Qy 673 MetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLys 692
Db 3345 ATGGATGAAGCGGACGTCCTGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGC 3404
Qy 693 CysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMet 712
Db 3405 TGTGTGGCTCCTCCTGTTTCTGAAGAACACAGCTGGGAACAGGCTACTACCTGACCTTG 3464
Qy 712 ----- 712
Db 3465 GTCAAGAAAGATGTGGAATCCTCCCTCAGTTCCTGCAGAAACAGTAGTACACTGTGTCA 3524
Qy 713 TyrIleAspLysTyrCysAla-----ThrGluSerLeuSerSerLeuValLysGlnHis 730
Db 3525 TACCTGAAAAAGGAGGACAGTGTTCCTCAGAGCAGTTCTGATGCTGGCCTGGGCAGCGAC 3584
Qy 720 -----ThrGluSerLeuSerSerLeuValLysGlnHis 730
Db 3585 CATGAGAGTGACACGCTGACCATCGATGTCTCTGCTATCTCCAACCTCATCAGGAAGCAT 3644
Qy 731 IleProGlyAlaThrLeuLeuGlnGlnAsnAspGlnGlnLeuValTyrSerLeuProphe 750
Db 3645 GTGTCTGAAGCCCGCTGGTGGGAAGACATAGGCGCATGAGCTGACCTATGTGCTGCCATAT 3704
Qy 751 LysAspMetAspLys-----PheSerGlyLeuPheSerAlaLeuAspSerHis---Ser 767
Db 3705 GAAGCTGTCTAAGAGGGAGACCTTTTGTGGAACTCTTTTCATGAGATTGATGACCGGCTCTCA 3764
Qy 768 AsnLeuGlyValIleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLys 787
Db 3765 GACCTGGGCATTTCTAGTTATGGCATCTCAGAGACGACCCCTGGAAGAAATATTCTCTCAAG 3824
Qy 788 LeuGluValGluAlaGluIleAsp----- 795
Db 3825 GTGGCCGAAGAGAGTGGGTGGATGCTGAGACCTCAGATGGTACCTGCCAGCAAGACGA 3884
Qy 796 -----GlnAlaAspTyrSerValPheThrGln----- 804
Db 3885 AACAGCGGGGCCTTCGGGGACAAGCAGAGCTGTCTTCGCCCGTTCACTGAAGATGATGCT 3944
Qy 805 ---GlnProLeuGluGluMetAspSerLysSerPheAspGluMetGluGlnSerLeu 823
Db 3945 GCTGATCCAAATGATTCTGACATAGACCCAGAATCC-----AGAGAGACAGACTTG 3995
Qy 824 LeuIleLeuSerGluThrLysAlaSerIleu---ValSerThrMetSerLeuTrpLysGln 842
Db 3996 CTCAGTGGGATGGATGGCAAAGGGTCTCTACCAGGTGAAAGGCTGGAACCTTACACAGCAA 4055
Qy 843 GlnMetTyrThrIleAlaLysPheHisPheThrLeuLysArgGluSerLysSerVal 862
Db 4056 CAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCCAGACGAGGTGCGAAAGGATTT 4115
Qy 863 ArgSerValLeuLeuLeuIlePhePheThrValGlnIlePheMetPheLeuVal 882
Db 4116 TTTGCTCAGATTGCTTGGCAGCTGTGTTGTCTGCAATTGCCCTTGTGTTTCAGCCTGATC 4175

Db 2048 ATCTGGGATCTTCTCAGCGGCAGAAAAGTAGCCGCACCATCGTGTGTGACCCACCTTC 2107
QY 673 MetAspGluAlaAspIleLeuAlaAspArgLysAlaValIleSerGlnGlyMetLeuLys 692
Db 2108 ATGGACGAGGCTGACTGTGGGAGACCGCATGCCATCATGGCCAAAGGGGAGCTGCAG 2167
QY 693 CysValGlySerSerMetPheLeuLysSerLysTrpGlyIleGlyTyrArgLeuSerMet 712
Db 2168 TGCTGCGGTCTCTCGCTGTCTCTCAAGCAGAAATACGGTGCCGGGTATCATGACGCTG 2227
QY 713 TyrIleAspLysTyrCysAlaThrGluSerLeuSerSerLeuValLysGlnHisIlePro 732
Db 2228 GTGAAGGAGCGCGACTGCAACCCGGAAGACATCTCCAGCTGGTCCACCACCGTGCCC 2287
QY 733 GlyAlaThrLeuLeuGlnGlnAsnAspGlnLeuValTyrSerLeuProPheLysAsp 752
Db 2288 AACGCCACGCTGGAGACGCGCTGGGGCCGAGCTGTCTTTCATCTCTCCAGAGAGAGC 2347
QY 753 MetAspLysPheSerGlyLeuPheSerAlaLeuAsp---SerHisSerAsnLeuGlyVal 771
Db 2348 ACGCACAGGTTTGAAAGTCTCTTTGCTAAACTGGAGAAGACGAGAAAGAGCTGGGCATT 2407
QY 772 IleSerTyrGlyValSerMetThrThrLeuGluAspValPheLeuLys----- 787
Db 2408 GCCAGCTTTGGGGCATCCATCACCAACCATGGAGGAAGTCTTCTCCTCGGTCGGGAAGCTG 2467
QY 788 -----LeuGluValGluAlaGlu 793
Db 2468 GTGGACAGCAGTATGGACATCCAGGCCATCCAGCTCCCTGCCCTGCAGTACCAGCAGAG 2527
QY 794 IleAspGlnAlaAspTyrSerValPheThrGlnGlnProLeuGluGluMetAspSer 813
Db 2528 AGGCGCGCCAGCGACTGGGCTGTG-----GACAGC 2557
QY 814 LysSerPheAspGluMetGluGlnSer-----LeuLeuIleLeuSerGlu 828
Db 2558 AACCTCTGTGGGCCATGGACCCCTCCGACGGCATTTGGAGCCCTCATCGAGGAGGAGCGC 2617
QY 829 ThrLysAlaSerLeuValSerThrMetSerLeuTrpLysGlnGlnMetTyrThrIleAla 848
Db 2618 ACCGCTGTCAAGCTCAACACTGGGCTCGCCCTGCACCTGCCAGCAATTCTGGGCCATG--- 2674
QY 849 LysPheHisPheThrLeuLys-----ArgGluSerLysSerValArg 863
Db 2675 -----TTCCTGAAGAAGCGCGCATACAGCTGGCGGAGTGGAAAATGTTGGCG 2722
QY 864 Ser-----ValLeuLeuLeuLeuIlePhePheThr 874
Db 2723 GCACAGGTCTGTGTGCTCTGACCTGCGTGCACCTGGCCCTCTCTGGCCATCACTACTCC 2782
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Db 2783 TCGGAGCTCTTCGACGACCCCATGTCTGAGGCTGACCTTGGCGGAGTACGGCAGAACCGTC 2842
QY 891 ValProIleLysLeuValProAspLeuTyrPheLeuLysProGlyAspLysProHisLys 910
Db 2843 GTGCCC-----TTCAGTTCCCGGACCTCCAGCTGGGT 2878
QY 911 TyrLysThrSerLeuLeuLeuGlnAsnSerAlaAspSerAsp----- 924
Db 2879 CAGCAGCTGTACAGGATCTGAAAGACGCACCTGCAGGCTGAGGGACAGAGACCCCGCGAG 2938
QY 925 ---IleSerAspLeuIleSerPhe-----Phe 932
Db 2939 GTGCTCGGTGACCTGGAGGAGTTCTTGATCTTCAGGGCTTCTGTGGAGGGGGCGGCTTT 2998
QY 933 ThrSerGlnAsnIleMetValThrMetIleAsnAspSerAspTyrValSerValAlaPro 952
Db 2999 AATGAGCGGTGCCTTGTGGCAGCGTCTCTTCAGAGAT-----GTGGGA 3040
QY 953 HisSerAlaAlaLeuAsnValMetHisSerGluLysAspTyr-----Val 967

Db 3041 GAGCGCACGGTCTGTCAACGCCCTTGTTCACAAACCAGGGGTACCACTCTCTCCAGCCACTGCC 3100
QY 968 PheAlaAlaValPheAsnSerThrMetValTyrSerLeu-----ProIleLeuVal 984
Db 3101 CTGGCCGTCTGTGGCAAC-----CTTCTGTCAAGCTGTGTGGGGCTCAGCCCTCC 3154
QY 985 AsnIleIleSerAsnTyrTyrLeuTyrHisLeuAsnValThrGluThrIleGlnIleTrp 1004
Db 3155 ATTGTGTCTCCAACTTC-----CCCCAGCCCCGAGCGCCCTGCAGGCTGCC 3202
QY 1005 SerThrProphePheGlnGluIleThrAspIleValPheLysIleGluLeuTyrPheGln 1024
Db 3203 AAGGACCAGTTTAAACGAGGGCCGGAAGGAGTTCGACATTGCCCTCAACCTGCTCTTCGCC 3262
QY 1025 AlaAlaLeuLeuGlyIleIleValThrAlaMetProProTyrPheAlaMetGluAsnAla 1044
Db 3263 ATGGCATTCTTGCC-----AGCACGTTCTCCATCCTGCGGTC 3301
QY 1045 GluAsnHisLysIleLysAlaTyrThrGlnLeuLysLeuSerGlyLeuLeuProSerAla 1064
Db 3302 ACGAGAGGGCCGTGCAGGCCAAGCATGTGCAGTTGTGAGTGGAGTCCAGTGGCCAGT 3361
QY 1065 TyrTrpIleGlyGlnAlaValValAspIleProLeuPhePheIleIleLeuLeuMet 1084
Db 3362 TTCTGGCTCTCTGCTCTGTGGACCTCATCTCTCTCATCCCCAGTCTGCTGCTG 3421
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Db 3422 CTGGTGGTGTTTAAGGCTTCGACGTGCGTGCCTTCACGGGACGGCCACATGGCTGAC 3481
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Db 3482 ACCCTGCTGCTGCTCTCTACGGCTGGGCCATCATCCCCCTCATGTACCTGATGAAC 3541
QY 1125 PheThrPhe-----LysLysIleLeuAsnThrLysGluPheTrpSerPheIleTyr 1141
Db 3542 TTCTTCTTCTTGGGGCGCCACTGCCCTACACGAGGCTGACCATCTTCAACATCCTGTCA 3601
QY 1142 SerValAlaAlaLeuAlaCysIleAlaIleThrGluIleThrPhePheMetGlyTyrThr 1161
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QY 1196 -----LysAsnValAspThrTyrAsnProTrp 1204
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Db 4349 CACATGACAGGCCGCGGAGATGCTGGTTCATGTACGCTCGGCTCCGGGCGCATCCCTGAGCGC 4408
QY 1408 AspMetLysGluValIleSerArgIleThrHisAlaLeuAspLeuLysGluHisLeuGln 1427
Db 4409 CACATCGGGGCTCGGTGGAGAACACTCTGGGGGCTGCTGTGGAGCCACATGCCAAC 4468
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Db 4646 ATCACCTCCACAGCATGGAGGAGTGTGAGGCCCTGTGCACCCCGCTGGCCATCATGGTG 4705
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QY 1608 ValPheValGluLeuThrLysGluGln 1616
Db 5003 GTCTTCTGAGTTCGCTCCACCTGCAG 5029
RESULT 3
US-08-762-500-24
; Sequence 24, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
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; NAME: Dugan, Deborah A.
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; TELEPHONE: (508) 872-8400
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; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..5053
US-08-762-500-24
Alignment Scores:
Pred. No.: 8.3e-150 Length: 5894
Score: 1521.50 Matches: 469
Percent Similarity: 44.83% Conservative: 333
Best Local Similarity: 26.22% Mismatches: 666
Query Match: 18.06% Indels: 321
DB: 3 Gaps: 56
US-10-090-458-5 (1-1642) x US-08-762-500-24 (1-5894)

